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OM nucleic - nucleic search, using sw model

Run on: December 4, 2004, 05:07:05 ; Search time 26244 Seconds
(without alignments)
11757.556 Million cell updates/sec

Title: US-10-005-338B-1
Perfect score: 6525
Sequence: 1 aaaatgttgatatttcctct........ttgatcataataagtgaaat 6525

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 452629 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Accession	Description
1	6524	100.0	6525	6	AX473847	AX473847	Sequence
2	6524	100.0	6525	9	AY028897	AY028897	Homo sapi
3	6122.8	93.8	6369	6	AX392931	AX392931	Sequence
4	5373.2	82.3	5475	6	AX537473	AX537473	Sequence
5	5255.8	80.5	5463	6	AX537470	AX537470	Sequence
6	5247.4	80.4	5262	6	AX417828	AX417828	Sequence
7	5039	77.2	5096	9	HSA275973	AJ275973	Homo sapi
8	4918.4	75.4	4929	6	AX417824	AX417824	Sequence
9	4807.4	73.7	4917	6	AX537472	AX537472	Sequence
10	4754.8	72.9	4785	6	AX417826	AX417826	Sequence
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13	3868.8	59.3	4929	10	AB097675	AB097675	Mus muscu
14	3816.2	58.5	4945	10	RNO550165	AJ550165	Rattus no
15	3811.6	58.4	4078	9	HSM806823	BX540746	Homo sapi
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22	2773.6	42.5	2845	9	AJS12612	HSA512612	Homo sapi
23	2591.4	39.7	5243	9	BX647447	HSM807592	Homo sapi
24	1809.4	27.7	2325	6	AX780218	AX780218	Sequence
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26	-1743	26.7	3324	9	BX648540	HSM808688	Homo sapi
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ALIGNMENTS

RESULT 1
AX473847

LOCUS   AX473847   6525 bp   DNA   linear   PAT 09-AUG-2002
DEFINITION   Sequence 1 from Patent WO0246458.
ACCESSION   AX473847
VERSION   AX473847.1   GI:2220806
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Denefle,P., Rosier-Montus,M.F., Prades,C., Arnould-Reguigne,I.,
    Duverger,N., Allikmets,R. and Dean,M.
TITLE   Nucleic acids of the human abca5, abca6, abca9, and abca10 genes,
    vectors containing such nucleic acids and uses thereof
JOURNAL   Patent: WO 0246458-A 1 13-JUN-2002;
    Aventis Pharma S.A. (FR) ; The Secretary, Department of Health and
    Human Services (US)
FEATURES   Location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
ORIGIN

Query Match   100.0%;   Score 6524;   DB 6;   Length 6525;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 6525;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy    1 AAAATGTTGATATTTCCTCTAGCAGGCTGCTCAACCAGGTTAGGTCAGGTCATAAGTTT 60
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Qy  121 TACTTTTTGGTCGTCGTGTGTGCCTTGCCTTGCGCAGTGAACAGTCTGGATTTGGACAGTGGT 180
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Qy   181  CTGTCTGTTAGTTCAGTTTCTCAAGCCTTGTCACACTAATAGGATTGGATTATGTATG  240
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Qy   301  TCTTTCATTTGTTCCCCCTTCTACTTTTGCTTCCCTGTGCTGCTGTTTCTATCCTCC   360
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Db   301  TCTTTCTATTTGTTCCCCCTTCTACTTTTGCTTCCCTGTGCTGCTGTTTCTATCCTCC  360

Qy   361  AGCCAGAGAGCTAGTGTTTATTTCTCCATTGTTACACACTTGTCAGCTGCAACCAC     420
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Qy   421  CATATCCAGGGCCCAATGTAGGAGGTAGAAGAAAGCAAAAGGGATTGGCCTCATCC    480
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Qy   601  ATACAGGAGAATTCAGAAAGAAAAAAAGATTTGCTATTTCTACATTCTCCCTGAGCATT    660
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Qy   661  AAGACCTCCCTGCCCATTCCTCAATTCCTCAAAGCTAAGCTTCTTCTGGAGCTGCCCTGT  720
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Db   661  AAGACCCTCCCTGCCCATTCCTCAATTCCTCAAAGCTAAGCTTCTTCTGGAGCTGCCCTGT 720

Qy   721  GGGCGGTTCGGGGGATACCAAAGGAGAAAAAGTACCACTGTGATATGGTGGTATTTCAA   780
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Qy   781  ATTCTGGTCTACCCTATTTCACATGCCTTGTTTACTTTTCAGAGCTGACAGATTGCTGCT  840
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Qy   901  CTGGGACTGAAACAGCTGCTTATTTGCCGTTAAAAATTACATGCCAGTTACTGCGGTGGC  960
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Qy  1021  CAATTAGGGAGGTTGGAGACAGACCAGAACTTCTACTGAAGAATTACTTAA          1080
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Qy  1081  TTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTCTTTTTCCACTATTTTTTTTTAT 1140
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Qy  1321  TAATTACTGAAGAATATACAAATGAAAGAAATGTTAACATCCAGTCTCTCAAGCCGA    1380
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Qy  1381  GCAACTTGTAGTGTGGTTTCAAAGACTCCATGTCCATGAACTCGTTTTTTTCCTG       1440
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Qy  1861  TTGGCACAGCTTCTTCTTGTATTTCCTCAAAGTAGCAGCATTGTGATATTCTGCTTTTTT  1920
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Db  1921  TCCTTTATGGATTATCATCTGTATTTTTGCTTTAAATGCTGACACCCTCTTTTAAAAAAT 1980

Qy  1981  CAAAACATGTGGAATAGTTGAATTTTCCCAAATCGTTAGTGTGGCTTTTCAGTCC      2040
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Qy  3361 TATTTTAAAGCTAGAAGTTGAAGCAGAAGTTGACCAAGCAGATTATAGTGTATTCTTC 3420
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Db  3361 TATTTTAAAGCTAGAAGTTGAAGCAGAAGTTGACCAAGCAGATTATAGTGTATTCTTC 3420
Qy  3421 AGCAGCCACTGGAGGAGAAGAAAATGGATTCAAAATCTTTTGATGAAATGAACAGAGCTTAC 3480
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Qy  3481 TTATTCTTCTGAAACCAAGGCTTCTCTCAGTGAGCACCATGTGAGCCTTTGGAAACAACAGA 3540
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Qy  3601 CAGTGTTGCTTCTGCTTCTTTAATTTTTTTCACAGTTCAGATTTTTATGTTTTTGGTTCATC 3660
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Qy  3781 ATATCAGTGACTCTTATTAGCTTCACAAGCCAGAACAATAATGGTGACGATGAATAATG 3840
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Qy  3841 ACAGTGACTATGTATCCGTGCTGCCCCATAGTGCGGCTTAAATGTTGATCATTCAGAAA 3900
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Db  3841 ACAGTGACTATGTATCCGTGCTGCCCCATAGTGCGGCTTAAATGTTGATCATTCAGAAA 3900
Qy  3901 AGGACTATGTTTTGCAGCTGTTTCAAGAAATTACTGGATTATTCTTTACCTATATTAG 3960
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Qy  3961 TGAATATCATTAGTAACTACCATCTTATCATTAAATGACTGAAACCATCAGATCT 4020
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Qy  4021 GGAGTACCCCATTCTTCAAGAAATCAGAACTTATACTTCAGTGTGTATTTTC 4080
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Db  4021 GGAGTACCCCATTCTTCAAGAAATCAGAACTTATACTTCAGTGTGTATTTTC 4080
Qy  4081 AAGCAGCTTGCTTGGAATCATTGTTACTGCCAACCTTACTTGCCATGGAAAATG 4140
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Qy  4141 CAGAGAATCATAAGATCAAAGCTTATACAACTTTCAGTCTTTTGCCATCTG 4200
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Qy  4201 CATATTGGATTGGACAAGCTGTGTTGATATCCCCCTATATTTTATCATTCTTATTTTGA 4260
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Qy  4501 CTATTCTTCATTATGCCTTTGTGTATCATCATTCCAATCTATCCAACTTCCAGGTTGCCTGA 4560
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Qy  4681 TCTTACAATACTATGAGAAAAATATGGAGGCAGATCAATAAGAAAAGATCCCTTTTTCA 4740
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Qy  4741 GAAACCTTCAACGAAGCTAAAAATAGGAAGCTTCAGAACCACCAGACAATGAGGATG 4800
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Qy  4801 AAGATGAAGATGTCAAAGCTGAAAGACTAAAGTCAAAGAGCTCAAAGAGTCAAAAG 4860
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Qy  4861 GTGAGGAGAAACCATCCATTATGTCAGCAATTGCATAAGAATATGATGACAAGAAAG 4920
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Qy  5161 CTTTGTGGCCAGATACTACACATTGCAGGAACATTTGAAATTTATGGAGCTGTCAAAGGAA 5220
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Qy  5461 CTATCATGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTAAAGAGTAAAT 5520
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Db  6121 GTATAATTAAGTGAGCTGCATGTTTGTATTGAACTATTAGTTTTGTATG 6180

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Db  6421 TGTCATCCGTAAAAGCTGAAGTGTAAGCACTGAAGAATTCAATATAGAGATTTGAAAT 6480

Qy  6481 AGTTATATCCACTAGGTGGCAGTCAGTGGCAGTCATTGATCATAATAAGTGAAAT 6525
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Db  6481 AGTTATATCCACTAGGTGGCAGTCAGTGGCAGTCATTGATCATAATAAGTGAAAT 6525
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Schneider,T., Maintoux,C., Lemoine,C., Debono,D., Devaud,C.,
Naudin,L., Bauche,S., Annat,M., Alikmets,R., Denefle,P., Rosier,M.
and Dean,M.

TITLE   Identification and characterization of a cluster of five new
          ATP-binding cassette transporter genes on human chromosome 17q24: a
          novel sub-group within the ABCA sub-family

JOURNAL   Unpublished

REFERENCE 2 (bases 1 to 6525)

AUTHORS   Schriml,L.M., Arnould,I., Prades,C., Lachtermacher-Rocha,M.,
          Schneider,T., Maintoux,C., Lemoine,C., Debono,D., Devaud,C.,
          Naudin,L., Bauche,S., Annat,M., Alikmets,R., Denefle,P., Rosier,M.
          and Dean,M.

TITLE   Direct Submission

JOURNAL   Submitted (20-MAR-2001) Evry Genomics Center, Aventis Pharma, 2 Rue
          Gaston Cremieux, Evry 91057, France

FEATURES   Location/Qualifiers

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ORIGIN
Query Match   100.0%;   Score 6524;   DB 9;   Pred. No. 0;
Best Local Similarity 100.0%;   Matches 6525; Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Db   121 TACCTTTTGGTCTGTCTGTGTGTGTGCCTTGCAGTGAACAGTCTGGATTGGACAGTGGT   180

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Qy   661 AAGACCTCCCTGCCCATTCCTCAATTCCTCAAAGCTCAAAGGCTTCTCTGGAGCTGCCTCTGT   720
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Qy   721 GGGCGGTTCGGGAGATACCACCACTGTTGATGATGGTGGTATTTCAA   780
            |||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GGGCGGTTCGGGAGATACCACCACTGTTGATGATGGTGGTATTTCAA   780

Qy   781 ATTCTGTCTACCCTATTCACAGCTTGGGAGTATGCTTAATCCATCTTAC   840
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ATTCTGTCTACCCTATTCACAGCTTGGGAGTATGCTTAATCCATCTTAC   840

Qy   841 CCATGCATTCGTCCAGTTTCCTAAGAGACAGCAGCTGGAGTATGCTTAATCCATCTTAC   900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CCATGCATTCGTCCAGTTTCCTAAGAGACAGCAGCTGGAGTATGCTTAATCCATCTTAC   900

Qy   901 CTGGGACTGAAACAGCTGCTTATTTTGCCGTAAAAATTACTGGCGGTGGC   960
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CTGGGACTGAAACAGCTGCTTATTTTGCCGTAAAAATTACTGGCGGTGGC   960

Qy   961 TCCGGGTTTGTTGTTGTTGTTGTTTTGCCCTTTAAATAGGTTTATTCAGAAAACATGTCCACTG   1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TCCGGGTTTGTTGTTGTTGTTGTTTTGCCCTTTAAATAGGTTTATTCAGAAAACATGTCCACTG   1020

Qy   1021 CAATTAGGGAGTAGGAGTTTGGACAGACAGACCAGAACACTTCTACTGAAGAATTACTTAA   1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CAATTAGGGAGTAGGAGTTTGGACAGACAGACCAGAACACTTCTACTGAAGAATTACTTAA   1080

Qy   1081 TTAAATGCAGAACCAAAAAGAGTAGTTCAGGAAATTCTTTTTCCACTATTTTTTTAT   1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TTAAATGCAGAACCAAAAAGAGTAGTTCAGGAAATTCTTTTTCCACTATTTTTTTAT   1140

Qy   1141 TTTGGTTAATATTAATTAGCATGATGCATCCAAATAAGAAGATATGCAGTGCCTAATA   1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TTTGGTTAATATTAATTAGCATGATGCATCCAAATAAGAAGATATGCAGTGCCTAATA   1200

Qy   1201 TAGAACTCAATCCTATGGACAAGTTTACTCTTTCCAATCTAATTCTTGGATATACTCCAG   1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TAGAACTCAATCCTATGGACAAGTTTACTCTTTCCAATCTAATTCTTGGATATACTCCAG   1260

Qy   2341 AAAGAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGTTTTAGTGAAA 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AAAGAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGTTTTAGTGAAA 2400

Qy   2401 TTATTGAGCCAGTTCTTCAGAATTGTGGGAAAAGAGCCATAAGAATTAGTGGTATTC 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TTATTGAGCCAGTTCTTCAGAATTGTGGGAAAAGAGCCATAAGAATTAGTGGTATTC 2460

Qy   2461 AGAAGACATACAGAAGAGGGTGAAAATGTGGAGGCTTGAGAAATTTGTCATTTGACA 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 AGAAGACATACAGAAGAGGGTGAAAATGTGGAGGCTTGAGAAATTTGTCATTTGACA 2520

Qy   2521 TATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAACAGGAAAGAGTACATTGA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAACAGGAAAGAGTACATTGA 2580

Qy   2581 TGAATATTCTTGTGGACTCTGCCCACCTTCGATGGGTTGCATCTATATATGGACACA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGAATATTCTTGTGGACTCTGCCCACCTTCGATGGGTTGCATCTATATATGGACACA 2640

Qy   2641 GAGTCTCAGAAATAGATGAAATGTTGAAGCAAGAGAAAAATGATTGGCATTTGTCCACAGT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GAGTCTCAGAAATAGATGAAATGTTGAAGCAAGAGAAAAATGATTGGCATTTGTCCACAGT 2700

Qy   2701 TAGATATACACTTTGATGTTTTGACAGTAGAAGAAATTTATCAATTTTGGCTTCAATCA 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TAGATATACACTTTGATGTTTTGACAGTAGAAGAAATTTATCAATTTTGGCTTCAATCA 2760

Qy   2761 AAGGGATACCACCAACAATATAATACAAGAAGTGCAGAAGGTTTACTAGATTAGACA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 AAGGGATACCACCAACAATATAATACAAGAAGTGCAGAAGGTTTACTAGATTAGACA 2820

Qy   2821 TGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGCGTGGTCAAAAAAGAAAGCTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TGCGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGCGTGGTCAAAAAAGAAAGCTGT 2880

Qy   2881 CATTAGGAATTGCTGTTCCTTGGGAACCCAAAGATACTGCTGCTAGAAGATCAGCTG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CATTAGGAATTGCTGTTCCTTGGGAACCCAAAGATACTGCTGCTAGAAGATCAGCTG 2940

Qy   2941 GAATGACCCCTGTTCTCGACATATGTATGGAATCTTTAAAATACAGAAAAGCCAATC 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 GAATGACCCCTGTTCTCGACATATGTATGGAATCTTTAAAATACAGAAAAGCCAATC 3000

Qy   3001 GGGTGACAGTGTTCAGTACTCATTTCATGGATGAAGCTGACATTCTTGCAGATAGGAAAG 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GGGTGACAGTGTTCAGTACTCATTTCATGGATGAAGCTGACATTCTTGCAGATAGGAAAG 3060

Qy   3061 CTGTGATATCACAAGGAATGCTGAAATGTCGTTGGTTCTCAATGTTCCTCAAAAGTAAAT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 CTGTGATATCACAAGGAATGCTGAAATGTCGTTGGTTCTCAATGTTCCTCAAAAGTAAAT 3120

Qy   3121 GGGGATCGGCTACCCGCTAAACAACATATACCTGGAGCTACTTTATTACAACAGAATGACCAACAAC 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGGGATCGGCTACCCGCTAAACAACATATACCTGGAGCTACTTTATTACAACAGAATGACCAACAAC 3180

Qy   3181 CTTCACTGGTTAAAGCTGCCTTTGCACAGGTCAAATTTTCAGGTTTGTTTTCTGCGCCCTAG 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CTTCACTGGTTAAAGCTGCCTTTGCACAGGTCAAATTTTCAGGTTTGTTTTCTGCGCCCTAG 3240

Qy   3241 TTGTGTATAGCTTGCCTTTCAAATTTGGGTGTCATTTCCATGACGACTTTGAAGAGCG 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TTGTGTATAGCTTGCCTTTCAAATTTGGGTGTCATTTCCATGACGACTTTGAAGACG 3300

Qy   3301 ACAGTCATTCAAATTGGGTGTCATTTCTATGGTGTTCCATGACGACTTTGGAAGACG 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 ACAGTCATTCAAATTGGGTGTCATTTCTATGGTGTTCCATGACGACTTTGGAAGACG 3360

Qy   3361 TATTTTTAAAGCTAGAAGTTGAAGCAGAAGAATTATGACCAAGCAGATTATAGTGTATTTACTC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TATTTTTAAAGCTAGAAGTTGAAGCAGAAGAATTGACCAAGCAGATTATAGTGTATTTACTC 3420

Qy   3421 AGCAGCCACTGAGGAAGAAATGGATTCAAAATCTTTGATGAAATGGAACAGAGCTTAC 3480

Qy   1261 TGACTAATATTACAAGCAGCATCATGCGCAGAAAGTGTCTACTGCATCATCTACCTGATGTCA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGACTAATATTACAAGCAGCATCATGCGCAGAAAGTGTCTACTGCATCATCTACCTGATGTCA 1320

Qy   1321 TAATTACTGAAGAATATACAAATGAAAAGAAATGTTAACATCCAGTCTCTCTAAGCCGA 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TAATTACTGAAGAATATACAAATGAAAAGAAATGTTAACATCCAGTCTCTCTAAGCCGA 1380

Qy   1381 GCAACTTTGTAGGTGTGTTTCAAAGACTTCCATGTCCATGAACTTCGTTTTTTTCCTG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAACTTTGTAGGTGTGTTTCAAAGACTCCATGTCCATGAACTTCGTTTTTTTCCTG 1440

Qy   1441 ATATGATTCCAGTATCTTCTATTATATGGATTCAAGAGCTGGCTGTTCAAAATCATGTG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATATGATTCCAGTATCTTCTATTATATGGATTCAAGAGCTGGCTGTTCAAAATCATGTG 1500

Qy   1501 AGGCTGCTCAGTACTGGTCCTCCTCAGGTTCACAGTTTTACAAGCATCCATAGATGCTGCCA 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGCTGCTCAGTACTGGTCCTCCTCAGGTTCACAGTTTTACAAGCATCCATAGATGCTGCCA 1560

Qy   1561 TTATACAGTTGAAGACCAATGTTCTCTTTGGAAGGAGACTGGAGTCAACTAAAGCTGTTA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TTATACAGTTGAAGACCAATGTTCTCTTTGGAAGGAGACTGGAGTCAACTAAAGCTGTTA 1620

Qy   1621 TTATGGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCCGAGGAGTAATTTAATAT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TTATGGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCCGAGGAGTAATTTAATAT 1680

Qy   1681 ACCTTATAGCATTTCACCTTTGGATACTTTTGGCAATTCATATCGTAGCAGAAAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ACCTAGTTATAGCATTTCACCTTTGGATACTTTTGGCAATTCATATCGTAGCAGAAA 1740

Qy   1741 AAGAAAAAAAATAAAGAATTTTAAGAATAATGGGACTTCATGATACTGCCTTTTGGC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AAGAAAAAAAATAAAGAATTTTAAGAATAATGGGACTTCATGATACTGCCTTTTGGC 1800

Qy   1801 TTTCCTGGGGTTCTTCTATATACAAGTTTAATTTTCTTATGTCCCTTCTTATGGCAGTCA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TTTCCTGGGGTTCTTCTATATACAAGTTTAATTTTCTTATGTCCCTTCTTATGGCAGTCA 1860

Qy   1861 TTGCGACAGCTTCTTCTTGTATTTCTATGTAGCAGATTGTAATTCTGCTTTTTT 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TTGCGACAGCTTCTTCTTGTATTTCTATGTAGCAGATTGTAATTCTGCTTTTTT 1920

Qy   1921 TCCTTTATGGATTATCATCGTATTTTTGTATTTTTGCTTAATGCTGACACCTCTTTTTTAAAAAAT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TCCTTTATGGATTATCATCGTATTTTTGTATTTTTGCTTAATGCTGACACCTCTTTTTTAAAAAAT 1980

Qy   1981 CAAAACATGTGGAATAGTTGAATTGTAATTTTGTTGGTACTGTTTATTGGCCTTA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAAAACATGTGGAATAGTTGAATTGTAATTTTGTTGGTACTGTTTATTGGCCTTA 2040

Qy   2041 TGATAATCCTCATAGAAAGTTTTCCCAAATCGTTAGTGTGGCCTTTCAGTCCTTTCTGTC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGATAATCCTCATAGAAAGTTTTCCCAAATCGTTAGTGTGGCCTTTCAGTCCTTTCTGTC 2100

Qy   2101 ACTGTACTTTGTGATTGGTATTGCACAGTCATGCAGGTCATTAGAAGATTTAATGAAGGTG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ACTGTACTTTGTGATTGGTATTGCACAGTCATGCAGGTCATTAGAAGATTTAATGAAGGTG 2160

Qy   2161 CTTCATTTTTCAAATTTGACTGCAGGCCCCATATCCTCTAATTATTACAATTATCATGCTCA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CTTCATTTTTCAAATTTGACTGCAGGCCCCATATCCTCTAATTATTACAATTATCATGCTCA 2220

Qy   2221 CACTTAATAGTAGTATATTCTATGTCCTCTGGCTGTCATCTTGTCATCAAGTCATTCCAGGGGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CACTTAATAGTAGTATATTCTATGTCCTCTGGCTGTCGTCTCTTGTCATCAAGTCATTCCAGGGGG 2280

Qy   2281 AATTTGGCTTACCGAGATCATCATCTTTATATTTCTGAAGCCTTCATATTGGTCAAAGAGTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AATTTGGCTTACCGAGATCATCATCTTTATATTTCTGAAGCCTTCATATTGGTCAAAGAGTA 2340

Db 3421 AGCAGCCACTCGGAGGAAGAAATGGATTCAAAAATCTTTGATGAAATGGAACAGAGCTTAC 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3481 TTATTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTCGAAACAACAGA 3540

Db 3481 TTATTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTCGAAACAACAGA 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3541 TGTATACAATAGCAAAGTTTCATTTCTTTACCTTGAAAGTGAAAGTAAATCAGTGAGAT 3600

Db 3541 TGTATACAATAGCAAAGTTTCATTTCTTTACCTTGAAAGTGAAAGTAAATCAGTGAGAT 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3601 CAGTGTTGCTTCTGCTTGTTTAATTTTTCACAGTTTTATGTTTTTGGTTCATC 3660

Db 3601 CAGTGTTGCTTCTGCTTGTTTAATTTTTCACAGTTTTATGTTTTTGGTTCATC 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3661 ACTCTTTTAAAAATGCTGTGGTCCCATCAAACTTGTTCCAGATTTTCTAAAAC 3720

Db 3661 ACTCTTTTAAAAATGCTGTGGTCCCATCAAACTTGTTCCAGATTTTCTAAAAC 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3721 CTGGGACAAACCACATAAATACAAAACAAGTCTGCTTCTTCAAAATTCTGCTGACTCAG 3780

Db 3721 CTGGGACAAACCACATAAATACAAAACAAGTCTGCTTCTTCAAAATTCTGCTGACTCAG 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3781 ATATCAGTGATCTTATTAGCTTTTTCACAAGCTTTTCACAAGCCAGACATAATGGTGACGATGATTAATG 3840

Db 3781 ATATCAGTGATCTTATTAGCTTTTTCACAAGCCAGACATAATGGTGACGATGATTAATG 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3841 ACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGGCTTTAAATGTGATCGATTCAGAAA 3900

Db 3841 ACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGGCTTTAAATGTGATCGATTCAGAAA 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3901 AGGACTATGTTTTGCAGCTTTTCAACAGTACTATGTTATTCTTTACCTATATTAG 3960

Db 3901 AGGACTATGTTTTGCAGCTTTTCAACAGTACTATGTTATTCTTTACCTATATTAG 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3961 TGAAATATCATTAGTAACTACTATCTTTATCATTAAATGTGACTGAAACCATCCAGATCT 4020

Db 3961 TGAAATATCATTAGTAACTACTATCTTTATCATTAAATGTGACTGAAACCATCCAGATCT 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4021 GGAGTACCCCATTCTTCAAGAAATATACTGATATAGTTTTAAAATTGAGCTGTATTTTC 4080

Db 4021 GGAGTACCCCATTCTTCAAGAAATATACTGATATAGTTTTAAAATTGAGCTGTATTTTC 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4081 AAGCAGCTTGCTTGGAATCATTGTACTGACTACCTTGTTGCCACCTTACTTTGCCATGG 4140

Db 4081 AAGCAGCTTGCTTGGAATCATTGTACTGACTACCTTGTTGCCACCTTACTTTGCCATGG 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4141 CAGAGAATCATAAGATCAAAGCTTATACTCAACTTAAACTTTCAGGTCTTTTGCCATCTG 4200

Db 4141 CAGAGAATCATAAGATCAAAGCTTATACTCAACTTAAACTTTCAGGTCTTTTGCCATCTG 4200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4201 CATATTGGATTGGACAAGCTGTTGTGATATCCCCTATTTTTATCATTCTTATTTTGA 4260

Db 4201 CATATTGGATTGGACAAGCTGTTGTGATATCCCCTATTTTTATCATTCTTATTTTGA 4260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4261 TGCTAGGAAGCTTACTGGCATTTCATTGGTGTTAAGAAAATTGGTCATTTATCATCATTCTTGTGG 4320

Db 4261 TGCTAGGAAGCTTACTGGCATTTCATTGGTGTTAAGAAAATTGGTCATTTATCATTCTTGTGG 4320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4321 CTGTGGTTTTTGCCTTATTGGTATGTTCCATCAGTTATTCTTGTTCACTTATATTGCTT 4380

Db 4321 CTGTGGTTTTTGCCTTATTGGTATGTTCCATCAGTTATTCTTGTTCACTTATATTGCTT 4380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4381 CTTTCACCTTTAAGAAGAAATTTAAATACCAAAGAAATTTGGTCATTTATCATTCATCATTCTGTGG 4440

Db 4381 CTTTCACCTTTAAGAAGAAATTTAAATACCAAAGAAATTTGGTCATTTATCATTCATTCTGTGG 4440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4441 CAGCGTTGNCTTGTATTGCAATCTGTAATTGCAATCTGAAATAACTTTCTTTATGGGATACACAACAATTGCAA 4500

Db 4441 CAGCGTTGNCTTGTATTGCAATCTGAAATAACTTTCTTTATGGGATACACAACAATTGCAA 4500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4501 CTATTCTTCATTATGCCTTTGTATCATCATCTCCAATCATCCACTTCTAGGTTGCCTGA 4560

Db 4501 CTATTCTTCATTATGCCTTTGTATCATCATCTCCAATCATCCACTTCTAGGTTGCCTGA 4560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4561 TTTCTTCTTCATAAGATTTCTGAAGAATGTAGCACCATATAAATAATGTGGACACCTA-TAATCCAT 4620

Db 4561 TTTCTTCTTCATAAAGATTCTTCTGAAGAATGTAGCACCTA-TAATCCAT 4620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4621 GGGATAGGCTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTACTGTGATTTCC 4680

Db 4621 GGGATAGGCTTCAGTAGCTGTGTTATATCGCCCTTACCTGCAGTGTACTGTGATTTCC 4680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4681 TCTTACAATACTATGAGAAAAATATGGAGGCAGATCAATCAATAAGAAAGATCCTTTTCA 4740

Db 4681 TCTTACAATACTATGAGAAAAATATGGAGGCAGATCAATAAGAAAGATCCTTTTCA 4740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4741 GAAACCTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGACAAGCTTCCAGACAATGAGGATG 4800

Db 4741 GAAACCTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGACAATGAGGATG 4800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4801 AAGATGAAGATGTCAAAGCTGAAAGACTAAAGACTAAAGGTCAAAGGTTGCCAGTGTT 4860

Db 4801 AAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGGTTGCCAGTGTT 4860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4861 GTGACGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGAATTGCATAAAGAATGACAAGAAAG 4920

Db 4861 GTGACGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGAATGACAAGAAAG 4920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4921 ATTTTCTTCTTCAAGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTCTGTGTGA 4980

Db 4921 ATTTTCTTCTTCAAGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTCTGTGTGA 4980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4981 AAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGCTGGCAAAGCACAATTATTA 5040

Db 4981 AAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGCTGGCAAAGCACAATTATTA 5040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5041 ATATCTGGTGGTGATATTCAGGCAGTATTTTTAGGAGATTATTTCTT 5100

Db 5041 ATATCTGGTGGTGATATTCAGGCCAGGTATTTTTAGGAGATTATTTCTT 5100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5101 CAGAGACAAGTGAAGATGATTCACTGAAGTGTATGGTTACTGTCCTCAGATAAACC 5160

Db 5101 CAGAGACAAGTGAAGATGATTCACTGAAGTGTATGGTTACTGTCCTCAGATAAACC 5160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5161 CTTTGTGGCCAGATACTACATTGGAAATTTATGGAGTCGTGTCAAAGGAA 5220

Db 5161 CTTTGTGGCCAGATACTACATTGCAGGAACATTATGGAGTCGTGTCAAAGGAA 5220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5221 TGAGTGCAAGTGACATGACAAGAAGTCATAAGTCGAACAATGACACTGATTGAAAAAG 5280

Db 5221 TGAGTGCAAGTGACATGACAAGAAGTCATAAGTCGAACAATGACACTGATTGAAAAAG 5280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5281 AACATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAGTTGTGTTTTG 5340

Db 5281 AACATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAGTTGTGTTTTG 5340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5341 CTCTAAGTATGCTGGGGAATCCTCAGATTGCTAGATGAACCATCACAGGTATGG 5400

Db 5341 CTCTAAGTATGCTGGGGAATCCTCAGATTGCTAGATGAACCATCACAGGTATGG 5400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5401 ATCCCAAAGCCAAAGCAAATCGAGCAATTGAACTGCATTTAAAACAGAAAGC 5460

Db 5401 ATCCCAAAGCCAAAGCAAATCGAGCAATTGAACTGCATTTAAAAACAGAAAGC 5460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5461 GGGCTGCTATTCTGACCACTCACTATGGAGGCTGATCGAGGCTAG 5520

Db 5461 GGGCTGCTATTCTGACCACTCACTATGGAGGCTGATCGAGGCTAG 5520
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Qy 5521 CTATCATGGTGTCTCGGGCAGTTAAGATGTCACAACATCTAAAGAGTAAAT 5580

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REFERENCE   1
AUTHORS   Yue,H., Thornton,M., Ramkumar,J., Tang,Y.T., Azimzai,Y.,
             Baughn,M.R., Yang,J., Yao,M.G., Lal,P., Walia,N.K., Gandhi,A.R.,
             Hafalla,A.J., Nguyen,D.B., Patterson,C., Elliott,V.S.,
             Tribouley,C.M., Lu,D.A., Xu,Y., Reddy,R., Hernandez,R.,
             Borowsky,M.L., Lo,T.P., Lu,Y., Policky,J.L., Greene,B.D.,
             Sanjanwala,M.S., Raumann,B.E., Burford,N., Ison,C.H., Lee,E.A.,
             Ding,L., Das,D., Kallick,D.A., Khan,F.A. and Seilhamer,J.J.
JOURNAL   Patent: WO 0212340-A 33 14-FEB-2002;
FEATURES   Location/Qualifiers
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             /db_xref="taxon:9606"
             /note="Incyte ID No: 2798241CB1"

ORIGIN

Query Match   93.8%;   Score 6122.8;   DB 6;   Length 6369;
Best Local Similarity 99.9%;   Pred. No. 0;
Matches 6127;   Conservative 0;   Mismatches 8;   Indels 0;   Gaps 0;

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Qy   61 CTACCCACATTCTTTGAACTGTAGTGTCATTTTAGTTTATTTTTCAAAAACTTTTGCAG 120
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Qy  3301 ACAGTCATTCAAATTTGGGTGTCATTTCTTATGGTGTTCCATGACGACTTTGGAAGACG 3360
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Qy  3661 ACTCCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTATATTTTCTAAAAC 3720
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Qy  3721 CTGGAGACAAAACCACAATAACAAAACAAGCTCGCTTCTTCAAATTCTGCTGACTCAG 3780
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Qy  3781 ATATCAGTGATCTTATTAGCTTTTTTGCACAGTTATGGTTTATTCTTTACCTATATTAG 3840
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Db  4188 TGAATATCATTAGTAACTACTATCTTTATCATTTAAATGTACTGAACCATCCAGATCT 4247

Qy  4021 GGGAGTACCCCATTCTTTCAAGAAATTCTTTCAAGAAATTACTGATATAGTTTTTAAAATTGAGCTGTATTTTC 4080
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Qy  4548 CTGTGTGTTTTTTGCCTTATGGTTATGTTCCATCAGTTATTCTGTTCACTTATATTGCTT 4607
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Qy  5208 AAAAAGGAGAGATCTTAGGACTAATGGGTCTGGCAAAAGCACACAATTATTA 5267
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Db  5041 ATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGTGTATTTTAGGAGATTATTCTT 5100

Qy  5268 ATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGTGTATTTTAGGAGATTATTCTT 5327
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Qy  5328 CAGAGACAAGTGAAGATGAATGATTCACTGAAGTGTATGGGTTACTGTCCTCAGATAAACC 5387
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VERSION     AX537473.1  GI:25269282
KEYWORDS
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  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Chen,H., Kilinski,L. and le Bihan,S.
  TITLE     Abca5 transporter and uses thereof
  JOURNAL   Patent: WO 02070690-A 4 12-SEP-2002;
            Active Pass Pharmaceuticals, Inc. (CA)
FEATURES             Location/Qualifiers
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ORIGIN

   Query Match            82.3%;  Score 5373.2;  DB 6;  Length 5475;
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   Matches 5375;  Conservative 0;  Mismatches 0;  Indels 4;  Gaps 0;
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Qy    994 AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 1053
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Db     97 AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA  156

Qy   1054 GAACACTTCTACTGAAGAATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGG  1113
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Qy   1114 AAATTCTTTTCCACTATTTTTTATTTTGGTTAATATTAATTAGCATGCATGATGCATCCAA 1173
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Qy   1234 CTAATCTAATTCTTGGATATATCCAGTGACTACTAATATTACAACAGCATCATGCAGAAAG 1293
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Db    337 CTAATCTAATTCTTGGATATATCCAGTGACTACTAATATTACAACAGCATCATGCAGAAAG  396

Qy   1294 TGTCTACTGATCATCCACCTGATGTCATAATTACTGGAGAATATACAAATGAAAAAGAAA 1353
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Db    397 TGTCTACTGATCATCCACCTGATGTCATAATTACTGGAGAATATACAAATGAAAAAGAAA  456

Qy   1354 TGTTAACATCCAGTCCTGTCTCTCTGAAGCCGAGCAACTTGTAGGTGTGGTTTTCAAAGACTCCA 1413
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Db    457 TGTTAACATCCAGTCCTGTCTCTCTGAAGCCGAGCAACTTGTAGGTGTGGTTTTCAAAGACTCCA  516

Qy   1414 TGTCCTATGAACTTCGTTTTTTCGTTTTTTCCTGATATGATTATATGGATT         1473
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Qy   1534 TTTTACAAGAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTTGGA 1593
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Qy   1594 AGGAGCTGGAGTCAACTAAAGCTAAAGCTGTTATTATGGGAGAAACTGCTGTGTTGTAGAAATAGATA 1653
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Db    697 AGGAGCTGGAGTCAACTAAAGCTAAAGCTGTTATTATGGGAGAAACTGCTGTGTTGTAGAAATAGATA  756

Qy   1654 CCTTTCCCCGAGGAGTAATTTTAATATACCTAGTATATAGCATTTGACCCTTTTGGATACT 1713
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Qy   1714 TTTTGGCAATTCATATCGTAGCAGCAGAAAAAGAGAAAATAAAGAATTTTTAAAGATAA   1773
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Qy   5161 CTTTGTGGCCAGATACTACATTGCAGGAACACATTTTGAAATTTATGGAGCTGTCAAAGGAA 5220
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Qy   5221 TGAGTGCAAGTGACATGAGAAGAAGTCATAAGTGAATAACACATGCACTTGATTTAAAAG 5280
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Qy   5281 AACACTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAGTTGTGTTTTG 5340
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Qy   5341 CTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCTCACAGGTATGG 5400
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Qy   5461 GGGCTGCTATTCTGACCACTCCACTATATGGAGGAGCAGAGGCTGTCTGTTGTGATCGAGTAG 5520
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Qy   5521 CTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTAAAGAGTAAAT 5580
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Qy   5641 ACCGCCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAGGAAAGTTTT 5700
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Qy   5701 CTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTCACAATCTTTT 5760
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Db   5928 CTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTCACAATCTTTT 5987

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Qy   6001 TTTAAAAGTTTTTATTGGAATGGTAACTGGAGCGCACTTGAAGAAATTTTTC 6060
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DEFINITION  Sequence 4 from Patent WO02070690.
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Qy 1894  GCAGCATTGTGATATTCTGCTTTTTTCCTTATGATTATCATCTGTATTTTTTGCTT 1953
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Qy 1954  TAATGCTGCACACCTCTTTTTAAAAAATCAAAACATGTGGAATAGTTGAATTTTTGTTA 2013
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Qy 2014  CTGTGGCTTTGATTATTGGCCTTATGAATCCTCATAGAAAGTTTCCCAAATCGT 2073
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Qy 2794  TGCAGAAGGTTTTACTAGATTTAGACATCAGACTATCAAAGATAACCAAGCTAAAAAT 2853
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Db 1897  TGCAGAAGGTTTTACTAGATTTAGACATCAGACTATCAAAGATAACCAAGCTAAAAAT 1956
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Db 1957  TAAGTGTGGTCAAAAAAAGAGAAGCTGTCATTAGGAATTGTGTTCTTGGGAACCCAAAGA 2016

Qy 2914  TACTGCTGCTAGATGAACCACAGCTGGAATGGACACCCCTGTTCTGACACATATTGTATGGA 2973
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Qy 2974  ATCTTTAAAATACAGAAAAGCCAATCGGGTGACAGTGTTCAGTACTCATTCATGGGATG 3033
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Qy 3034  AAGCTGACATTCTTGCAGATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTG 3093
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Qy 3094  GTTCTTCAATGTCTTCCACAGAATCTCTTTCTCACTGGTTAAACACATACCTGAGCTA 3153
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RESULT 5
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REFERENCE   1
  AUTHORS   Chen,H., Kilinski,L. and le Bihan,S.
  TITLE   Abca5 transporter and uses thereof
  JOURNAL   Patent: WO 02070690-A 1 12-SEP-2002;
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ORIGIN

Query Match   80.5%; Score 5255.8; DB 6; Length 5463;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 5340; Conservative 0; Mismatches 0; Indels 8; Gaps 3;

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Qy   1054 GAACACTTCTACTGAAGAATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGG 1113
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Qy   1234 CTAATCTAATTCTTGGATATACCCCAGTGACTAATAATACAGAGCAGCATCATGCAGAAAG 1293
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Mon Dec 6 10:08:08 2004

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Db 3726 GTAGCTGTTATATCGCCTTACCTGCGCAGTGTGTACTGTGGATTTCCTCCTTACAATACTAT 3785
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Qy 5895 ACACTTGGTGGGAACGAACAACAACAAGAAGATAGAGTAGTATTTGAATTGTATTGTTCGG 5954
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RESULT 6
AX417828
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DEFINITION   Sequence 5 from Patent WO0231147.
ACCESSION   AX417828
VERSION   AX417828.1 GI:21522944
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hu,Y. and Nepomnichy,B.
  TITLE   Human transporter proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 0231147-A 5 18-APR-2002;
                LEXICON GENETICS INC (US)
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                     /mol_type="unassigned DNA"
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ORIGIN

Query Match   80.4%; Score 5247.4; DB 6; Length 5262;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 5248; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy   757 ACTGTTGATATGGTGGTATTTCAAATTCTGGTCTCACCCTATTTCACATGCCTTGTTTACT 816
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Db   1 ACTGTTGATATGGTGGTATTTCAAATTCTGGTCTCACCCTATTTCACATGCCTTGTTTACT 60

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Db  1141  GCATTGTGATATTCTGCTTTTTCCTTTATGATGAATCATCTGTATTTTTGCTTTAA  1200
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Qy  1957  TGCTGACACCTCTTTTTAAAAAATCAAAACATGTGGGATTAGTTGAATTTTTGTTACTG  2016
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Db  1201  TGCTGACACCTCTTTTTAAAAAATCAAAACATGTGGGATTAGTTGAATTTTTGTTACTG  1260

Qy  2017  TGGCTTTTGGATTATTGGCCTTATATACCCATAGATAATCCCAAATCGTTAG  2076
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Db  1261  TGGCTTTTGGATTATTGGCCTTATATACCCATAGATAATCCCAAATCGTTAG  1320

Qy  2077  TGTGGCTTTTCAGTCCTTCTGTCCACTGTACTTTGTGATTGGGATTGGACCAGTCATGC  2136
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Db  1321  TGTGGCTTTTCAGTCCTTCTGTCCACTGTACTTTGTGATTGGTATTGGCACAGGTCATGC  1380

Qy  2137  ATTTGAAGATTTAATGAAGGTGCTTCATTTCAAATTTGACTGCAGGCCCCATATCCTC  2196
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Db  1381  ATTTGAAGATTTAATGAAGGTGCTTCATTTCAAATTTGACTGCAGGCCCCATATCCTC  1440

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Db  1441  TAATTATTACAATTATCATGTCACACTTAATAGTATATTCTATGTCCTCTGGCGTCT  1500

Qy  2257  ATCTTGATCAAGTCATTCCAGGGGAATTTGGCTTACGGACGATCATCTTATATTTTCTGA  2316
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Db  1501  ATCTTGATCAAGTCATTCCAGGGGAATTTGGCTTACGGAGATCATCTTATATTTTCTGA  1560

Qy  2317  AGCCTTCATATTGGTCAAAGAGTAAAAGAAATTATGATGAGGAGTTATCAGAGGGCAATGTTA  2376
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Qy  2437  AAGCCATAAGAATTAGTGGTATTCAGAAGACATACAGAAAGAAGGGTGAAAATGTGGCCACA  2496
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Qy  2497  CTTTGAGAAAATTGTCATTTGACATATATGGGGGTCAGATTACTTGGCCTTCTGATG  2556
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Db  1741  CTTTGAGAAAATTGTCATTTGACATATATGGGGGTCAGATTACTTGGCCTTCTGATG  1800

Qy  2557  GTGGAACAGGAAAAGTACATTGATGAATATTCTTTGTGGACTCTGTGCCCACCTTCTGATG  2616
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Db  1801  GTGGAACAGGAAAAGTACATTGATGAATATTCTTTGTGGACTCTGTGCCCACCTTCTGATG  1860

Qy  2617  GGTTTGCATCTATATATGGACACAGAGTCTCAGAAATGTTGAAGCAAGAA  2676
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Db  1861  GGTTTGCATCTATATATGGACACAGAGTCTCAGAAATGTTTGAAGCAAGAA  1920

Qy  2677  AAATGATTGGCATTTGTCCCACAGTTTAGATATTAAAAGATATGG  2736
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Db  1921  AAATGATTGGCATTTGTCCCACAGTTTAGATATTAAAAGATATGG  1980

Qy  2737  ATTTATCAATTTGGCTTCAATCAAAGGAGTACCAGCCAACAATATAATACAAGAAGTGC  2796
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Db  1981  ATTTATCAATTTGGCTTCAATCAAAGGAGTACCAGCCAACAATATAATACAAGAAGTGC  2040

Qy  2797  AGAAGGTTTTACTAGACATGCAGAGACTCGAGAATAACCAAGCTAAAAATTAA  2856
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Db  2041  AGAAGGTTTTACTAGACATGCAGAGACTCGAGAATAACCAAGCTAAAAATTAA  2100

Qy  2857  GTGGTGGTCAAAAAGGAAAGCTGTCATTAGGAATTGCTTCTTGGGAACCCAAAGATAC  2916
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Qy  2917  TGCTGCTAGATGAACCAACAGCTGTGATCTGGAATGAGCACCCCGTTCTCGACATATTGTATGGAATC  2976
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Db  2161  TGCTGCTAGATGAACCAACAGCTGTGATCTGGAATGAGCACCCCGTTCTCGACATATTGTATGGAATC  2220

Qy  2977  TTTTAAAATACAGAAAAGCCAATCGGTGACGTGTTCAGTACTCATTTCATGGATGAAG  3036
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Qy   817  TTTCAGAGCTGACAGATTGCTGCTCCATGCATTCTGTCCAGTTCCTAAGAGAGACAGCT   876
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Db    61  TTTCAGAGCTGACAGATTGCTGCTCCATGCATTCTGTCCAGTTCCTAAGAGAGACAGCT   120

Qy   877  TGGAGTATGCTTAATCATCTTACCTGGACTGAAACAGCTGCTTATTTGCCGTTAAAA   936
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Db   121  TGGAGTATGCTTAATCATCTTACCTGGACTGAAACAGCTGCTTATTTGCCGTTAAAA   180

Qy   937  ATTACATGCAGTTTACTGCGTGGCTCCGGGTTGTTGTTTGTTTTCCTCTTAATAGG   996
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Qy   997  TTTATTCAGAAAACATGTCCACTGCAATTAGGGAGTTAGGAGTTGGAGACAGACCAGAA  1056
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Db   241  TTTATTCAGAAAACATGTCCACTGCAATTAGGGAGTTAGGAGTTGGAGACAGACCAGAA   300

Qy  1057  CACTTCTACTGAAGAATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAA  1116
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Qy  1417  CCTATGAACTTCGTTTTTTCCTGATATGATTCCAGTATCTTCAGTTTTCACAGTTT  1476
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Qy  1537  TACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCCTTGGAGG  1596
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3517 CCATGAGCCCTTTGGAAACAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCTTGA 3576

Db  2761 CCATGAGCCCTTTGGAAACAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCTTGA 2820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3577 AACGTGAAAGTAAATCAGTGAGATCAGTCGTTGCTGTTCTGCTTTTAAATTTTTTCACAGTTC 3636

Db  2821 AACGTGAAAGTAAATCAGTGAGATCAGTCGTTGCTGTTGCTTCTGCTTTTAATTTTTTCACAGTTC 2880
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Qy  3637 AGATTTTTATGTTTTGGTTCATCACTCTTTAAAAATGCTGTGTGGTTCCCATCAAACTTG 3696

Db  2881 AGATTTTTATGTTTTGGTTCATCACTCTTTAAAAATGCTGTGTGGTTCCCATCAAACTTG 2940
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Qy  3697 TTCTTCAAAATTCTGCTACTGGAGACAAACCTGAGCAAATAACACATAAAACAGAACAGTCTCGC 3756

Db  2941 TTCTTCAAAATTCTGCTACTGGAGACAAACCTGAGCAAATAACACATAAAACAGAACAGTCTCGC 3000
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Db  3001 TTCTTCAAAATTCTGCTCAGATCAGTGATCTTATTAGCTTTCAGAAATTACTGATATAG 3060
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Db  3061 ACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGG 3120
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Db  3121 CTTTAAATGTGARTCATTCATTGCATTCAGAAAAGGACACTARTGTTTTTTCAACAGTACTA 3180
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Db  3181 TGGTTTATTCTTTACCTATATTAGTGAATAACATTAGTAATCATTCTTTATCATTTAA 3240
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Qy  3997 ATGTGACTGAAACCATCCAGTTGGAGTACCCCATTCTTTCAAGAAATTACTGATATAG 4056

Db  3241 ATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGATATAG 3300
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Qy  4057 TTTTAAAATTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGC 4116

Db  3301 TTTTTAAAATTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGC 3360
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Qy  4117 CACCTTACTTTGCCATGAAATGCAGAGAATCATAGAGATCAAAGCTTATACTCAACTTA 4176
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Db  3361 CACCTTACTTTGCCATGGAAAAATGCAGAGAATCAATAGATCAAAGCTTAYACTCAACTTA 3420

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Db  3421 AACTTTCAGGTCTTTGCCATCTGCATATTGGATTGGACAAGCTGTGTTGATATCCCCT 3480

Qy  4237 TATTTTTATCATTCTATTTGATGCTAGGAAGCTTACTGGCATTCATTATGGATTAT 4296
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Qy  4297 ATTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTGCCTTATTGGTTATGTTCCATCAG 4356
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Qy  4357 TTATTCGTTCACTTATATTGCTTCTTCACCTTTAAGAAAATTTAAATACCAAAGAAT 4416
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Qy  4477 TCTTTATGGATACACAATTGCAACTATTCCTCATTATGCTTTTGTATCATCATTCCAA 4536
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Qy  4537 TCTATCCACTTCTAGGTTGCCTGATTTCTCTCTAGTGAGCA 4596
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Qy  4597 AAAAGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTTACC 4656
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Db  3841 AAAAGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTTACC 3900

Qy  4657 TGCAGTGTGTACTGTGATTTTCCTCTTGCATGAGAAAAAAATATGGAGGCAGAT 4716
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Qy  4717 CAATAAGAAAAGATCCCTTTCAACGAGTCTAAAAATAGGAAGCTTC 4776
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Qy  4777 CAGAACCACCAGACAATGAGGATGAAGATGAAGATCAAGCTCAAAGCTAAAGGTCA 4836
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Qy  4837 AAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGC 4896
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Qy  4897 ATAAAGAATATGATGACAAGAAAGATTTTCTTCTTTCAAGAAAAGTAAAGAAAGTGGCAA 4956
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Qy  5017 GTGCTGCAAAGCACAATTATTAATATTCTCGGTTGGTTGGTTGGTTGTGATATTGAACCAACTTCAGGCC 5076
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Db  4261 GTGCTGCAAAGCACAATTATTAATATTCTCGGTTGGTTGGTTGTGATATTGAACCAACTTCAGGCC 4320

Qy  5077 AGTATTTTAGGAGATTATTCTTCAGAGACAAGTGAAGTGTTACTGAGTGTA 5136
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Db  4321 AGTATTTTTAGGAGATTATTCTTCAGAGACAAGTGAAGTGTTACTGAGTGTA 4380

Qy  5137 TGGGTTACTGTCCTCAGATAAACCCTTGTGTGCCAGTAACTACATTTTG 5196
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Db  4381 TGGGTTACTGTCCTCAGATAAACCCTTGTGTGCCAGTAACTACATTTTG 4440
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JOURNAL      Unpublished
REFERENCE    2
AUTHORS      Hirsch-Ernst.K.I.
TITLE        Direct Submission
JOURNAL      Submitted (02-MAR-2000) Hirsch-Ernst K.I., Department of
             Toxicology, University of Goettingen, Robert-Koch-Strasse 40,
             Lowery Saxony, D-37075, GERMANY
REMARK       revised by [3]
REFERENCE    3  (bases 1 to 5096)
AUTHORS      Hirsch-Ernst.K.I.
TITLE        Direct Submission
JOURNAL      Submitted (20-NOV-2001) Hirsch-Ernst K.I., Department of
             Toxicology, University of Goettingen, Robert-Koch-Strasse 40,
             Lowery Saxony, D-37075, GERMANY
COMMENT      On Aug 1, 2002 this sequence version replaced gi:17046099.
FEATURES             Location/Qualifiers
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                     KSCEAAQYWSSGFTVLQASIDAAIIQLKTNVSLWKELESTKAVIMGETAVVEIDTFPR
                     GVILYLVIAFSPFGYFLAIHIVAEKEKKIKEFLKIMGLHDTAFWLLSWVLLYTSIFL
                     MSLLMAVIATASLLFPQSSIVIFLLFFLYGLSSVFFALMLTPLFKKSKHVGIVEBFV
                     TVAFGFIGLMIILIESFPKSLVWLFSPECHCTFVIGIAQVMHLEDFNEGASFSNLTAG
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                     HFDVLTVEENLSIIASIKGIPANNIGEVQKVLLDLDMQTIKDNDQAKKLSGGQKRKLS
                     LGIAVLGNPKILLLDEPTAGMDPCSRHIVWNLLKYRKANRVTVFSTHFMDEADILADR
                     KAVISQGMLKCVGGSMFLKSKWGIGYRLSMYIDKYCATESLSSLWQHIPGATLLQQN
                     DQQLVYSLEPFKDMDKFSGLFSALDSHSNLGVISYGVSMTTLEDVFLKLEVEAEIDQAD
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                     RESKSVRSVLLLLFFTVQIFMPJ.VHHSFKNAVVPIKLVPGDKPHYKTS
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                     NSTMVYSLPILVNIISNYILYEKKVGGRSIRKDPFFRNLSTKSKNRKLPEPPDNE
                     IVTAMPPYFAMENAENHKIKAYTOLKLSGLLPSAYWIGQAVVDIPLFFIILLMLGSL
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                     DRLSVAVISPYLQCVMIFLLQYYEKKYGGRSIRKDPFFRNLSTKSKNRKLPEPPDNE
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                     FCVKKGEILGLLGPNGAGKSTIINLVGDIEPTSGQIFLGDYSSESSEDDDSLKCMGY
                     CPQINPLWPDTTLQEHFEIYGAVKGMSASDMKBVISRITHALDLKEHLQKTVKKLPAG
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ORIGIN

Query Match            77.2%;  Score 5039;  DB 9;  Length 5096;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 5042;          Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;

Qy    994 AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGAGGTAGGAGTTTGGAGACAGACCA 1053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     49 AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGAGGTAGGAGTTTGGAGACAGACCA 108

Qy   1054 GAACACTTCTACTGAAGAATTACTTAATTAAATCAGAACCAAAAAGAGTAGTGTTCAGG 1113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    109 GAACACTTCTACTGAAGAATTACTTAATTAAATCAGAACCAAAAAGAGTAGTGTTCAGG 168
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Sequence alignment block (left portion):

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Qy   5197 AAATTTATGGAGCTGTCAAGGAATGAGTGCAAGTGACATGAAAGAAGTCATAAGTCGAA 5256
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Db   4441 AAATTTATGGAGCTGTCAAGGAATGAGTGCAAGTGACATGAAAGAAGTCATAAGTCGAA 4500

Qy   5257 TAACACATGCACTTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTGCAG 5316
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Db   4501 TAACACATGCACTTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTGCAG 4560

Qy   5317 GAATCAAACGAAAGTTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGC 5376
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 GAATCAAACGAAAGTTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGC 4620

Qy   5377 TAGATGAACCATTCACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTC 5436
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Db   4621 TAGATGAACCAACTACACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTC 4680

Qy   5437 GAACTGCATTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTCAGTGAGGAGG 5496
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Db   4681 GAACTGCATTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTCAGTGAGGAGG 4740

Qy   5497 CAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAA 5556
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Db   4741 CAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAA 4800

Qy   5557 CAGTACAACACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTTGGAAATTAAATTGAAGG 5616
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Db   4801 CAGTACAACACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTTGGAAATTAAATTGAAGG 4860

Qy   5617 ACTGGATGAAAAACCTAGAAGTAGACCCCTTCAAAGAGAAATTCAGTATATTTTCCCAA 5676
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Db   4861 ACTGGATAGAAAAACCTAGAAGTAGACCCCTTCAAAGAGAAATTCAGTATATTTTCCCAA 4920

Qy   5677 ATCGAAGCCGTCAGGAAAGTTTTCTTCTATTTGGCTTATAAAATTCCTAAGGAAGATG 5736
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Db   4921 ATCGAAGCCGTCAGGAAAGTTTTCTTCTATTTGGCTTATAAAATTCCTAAGGAAGATG 4980

Qy   5737 TTCAGTCCCTTTCACAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTG 5796
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Db   4981 TTCAGTCCCTTTCACAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTG 5040

Qy   5797 AAGGAATATAGCTTTTCTCAAGCAACATTGGAACAAGGTTTTGTAGAACTCACTAAAGAAC 5856
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Db   5041 AAGGAATATAGCTTTTCTCAAGCAACATTGGAACAAGGTTTTGTAGAACTCACTAAAGAAC 5100

Qy   5857 AAGAGGAGGAAGATAATAGTGTGGAACTTAAACAGCACACTTGGTGGGAACGAACAC 5916
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 AAGAGGAGGAAGATAATAGTGTGGAACTTAAACAGCACACTTGGTGGGAACGAACAC 5160

Qy   5917 AAGAGAGATAGAGTAGTATTTGAATTTGTATTGTTCGGTCTGCTTACTGGGACTTCTTTC 5976
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Db   5161 AAGAGAGATAGAGTAGTATTTGAATTTGTATTGTTCGGTCTGCTTACTGGGACTTCTTTC 5220

Qy   5977 TTTTTCACTTAATTTAACTTTGGTTTAAAAAGTTTTT 6014
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Db   5221 TTTTTCACTTAATTTAACTTTGGTTTAAAAAGTTTTT 5258
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RESULT 7
HSA275973
LOCUS       HSA275973          5096 bp     mRNA     linear      PRI 31-JUL-2002
DEFINITION  Homo sapiens mRNA for ATP-binding cassette protein of the (ABCA
            subfamily).
ACCESSION   AJ275973
VERSION     AJ275973.3  GI:22080663
KEYWORDS    ABCA subfamily; ATP-binding cassette protein.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petry,F., Kotthaus,A. and Hirsch-Ernst,K.I.
  TITLE     Molecular cloning and tissue distribution of a novel ATP-binding
            cassette (ABC) transporter belonging to the subfamily ABCA
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Qy   1114 AAATTCTTTTCCACTATTTTTTTATTTGGTTAATATTAATTAGCATGATGCATCCAA 1173
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Db    169 AAATTCTTTTCCACTATTTTTTTATTTGGTTAATATTAATTAGCATGATGCATCCAG  228

Qy   1174 ATAAGAAATATGAAGAAGTGCCTAATACAGAACTCAATCCTATGGACAAGTTTACTCTTT 1233
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Qy   1234 CTAATCTAATTCTTGGATATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAG 1293
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Qy   1294 TGTCTACTGATCATCTACCTGATGTCATPATTACTGAAGAATATACAAATGAAAAGAAA 1353
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Db    349 TGTCTACTGATCATCTACCTGATGTCATPATTACTGAAGAATATACAAATGAAAAGAAA  408

Qy   1354 TGTTAACATCCAGTCTCTCTAAGCCGAGCAACTTGTAGGTGGTTTTCAAAGACTCCA 1413
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Db    409 TGTTAACATCCAGTCTCTCTAAGCCGAGCAACTTGTAGGTGGTTTTCAAAGACTCCA  468

Qy   1414 TGTCCTATGAACTTCGTTTTTTTCCTGATGATTCCAGTATCTTCTATTTATATGGATT 1473
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Db    469 TGTCCTATGAACTTCGTTTTTTTCCTGATGATTCCAGTATCTTCTATTTATATGGATT  528

Qy   1474 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGTTTCACAG 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGTTTCACAG  588

Qy   1534 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCCAATGTTTCTCTTTGGA 1593
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Db    589 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCCAATGTTTCTCTTTGGA  648

Qy   1594 AGGAGCTGGAGTCAACTAAAGCTGTATTATGGGAGAAACGTCTGTTGTGAGAAATAGATA 1653
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Db    649 AGGAGCTGGAGTCAACTAAAGCTGTATTATGGGAGAAACGTCTGTTGTGAGAAATAGATA  708

Qy   1654 CCTTTCCCGAGGAGTAATTTAATATACCTAGTTATAGCATTTCACCTTTTGGATACT 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    709 CCTTTCCCCAGGAGTAATTTAATATACCTAGTTATAGCATTTCACCTTTTGGATACT  768

Qy   1714 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAATAAAGAAATTTTAAAGATAA 1773
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Db    769 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAATAAAGAAATTTTAAAGATAA  828

Qy   1774 TGGGACTTCATGATACTGCCCTTTGGCTTTCCTGGGTTCTTCTATATACAAGTTAATT 1833
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Db    829 TGGGACTTCATGATACTGCCCTTTGGCTTTCCTGGGTTCTTCTATATACAAGTTAATT  888

Qy   1834 TTCCTATGTCCCTTCTTATGGCAGTCATTGCGACAGCTTCTTCTTGTATTTCCTTCAAAGTA 1893
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    889 TTCCTATGTCCCTTCTTATGGCAGTCATTGCGACAGCTTCTTCTTGTATTTCCTTCAAAGTA  948

Qy   1894 GCAGCATTGTGATATTCTGCTTTTTTCCTTTATGGATTATCATCTGTATTTTTTGCTT 1953
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Db    949 GCAGCATTGTGATATTCTGCTTTTTTCCTTTATGGATTATCATCTGTATTTTTTGCTT 1008

Qy   1954 TAATGCTGACACCTCTTTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTTTGTTA 2013
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Qy   2014 CCGTGTGGCTTTTGGATTTATTGGCCTTATGGCCTTATGATAATCCTCATAGAAAGTTTTCCCAAATCGT 2073
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Db   1069 CCGTGTGGCTTTTGGATTTATTGGCCTTATGGCCTTATGATAATCCTCATAGAAAGTTTTCCCAAATCGT 1128

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Db   1129 TAGTGTGGCTTTTCAGTCGTTTCTCGTCACTGTACTTTTGTGATTGGTATTGCACAGGTCA 1188

Qy   2134 TGCATTTAGAAGATTTAATGAAGGTGCTTCATTTTCAAATTTCAAATTTGACTGCAGGCCCCATATC 2193
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1189 TGCATTTAGAAGATTTAATGAAGGTGCTTCATTTTCAAATTTCAAATTTGACTGCAGGCCCCATATC 1248

Qy   2194 CTCTAATTATTACAATTATCATGCTCACACTAATAGTATATATTCTATGTCCTCTTGGCTG 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Qy   1249 CTCTAATTATTACAATTATCATGCTCACACTTAATAGTATATATTCTATGTCCTCTTGGCTG 1308
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2254 TCTATCTTGATCAAGTCATTCCAGGGGAATTGGCTTAACTTAATATATGTTACGGAGATCATCTTTATATTTTC 2313

Qy   1309 TCTATCTTGATCAAGTCATTCCAGGGGAATTGGCTTAACTTAATATATGTTACGGAGATCATCTTTATATTTTC 1368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2314 TGAAGCCTTCATATTGGTCAAAGAGTAAAGAAATATGAGGAGTTATGGAGTTATCAGAGGGCAATG 2373

Qy   1369 TGAAGCCTTCATATTGGTCAAAGAGTAAAGAAATATGAGGAGTTATGGAGTTATCAGAGGGCAATG 1428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2374 TTAATGAAAATATTAGTTTAGTGAAATTATTGAGCCAGTTTCTTCAGAATTTGTAGGAA 2433

Qy   1429 TTAATGAAAATATTAGTTTAGTGAAATTATTGAGCCAGTTTCTTCAGAATTTGTAGGAA 1488
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2434 AAGAAGCCATAAGAATTAGTGGTATTCAGGAGACATACAGAAAGAAGGGTGAAAATGTGG 2493

Qy   1489 AAGAAGCCATAAGAATTAGTGGTATTCAGAGAGACATACAGAAAGAAGGGTGAAAATGTGG 1548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2494 AGGCTTTGAGAAATTTGTCATTTGACATATATGAGGGTCAGATTACGCCTCACTTGGCC 2553

Qy   1549 AGGCTTTGAGAAATTTGTCATTTGACATATATGAGGGTCAGATTACTACTTGCCTTACTTGGCC 1608
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2554 ACAGTGGAACAGGAAAGACTACATTGATGAATATTCTTTGTGGACTCTGCCCACCTTCTG 2613

Qy   1609 ACAGTGGAACAGGAAAGACTACATTGATGAATATTCTTTGTGGACTCTGCCCACCTTCTG 1668
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Db   2614 ATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGATGAAAATGTTTGAAGCAA 2673

Qy   1669 ATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGATGAAAATGTTTGAAGCAA 1728
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Qy   1729 GAAAAATGATTGCAGTTGTCCACAGTTAGATATACACTTTGATGTTTTGACAGTAGAAG 1788
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2794 TGCAGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAAT 2853

Qy   1849 TGCAGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAAT 1908
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2854 TAAGTGGTGGTCAAAAAGAAGCTGTCATTAGGAATGCTGTTCTTGGGAACCCAAAGA 2913

Qy   1909 TAAGTGGTGGTCAAAAAGAAGCTGTCATTAGGAATGCTGTTCTTGGGAACCCAAAGA 1968
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2914 TACTGCTGCTGATGAATGGACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGA 2973

Qy   1969 TACTGCTGCTGATGAATGGACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGA 2028
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Qy   2029 ATCTTTTAAAATACAGAAAGCCAATCGGGTGACAGTGTTCAGTGTTCAGTTCATCGATG 2088
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Qy   2209 ACAAATATTGTGCCACAGAATCTCTTTCTTCACTGGTTAAACACATATACCTGAGCTA 2268
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Db   3214 CTTTATTACAACAGAATGACCAACAACTTGTGTATAGCTTGTATAGCTTGTATAGCTTCAAGGACATGGACA 3273

Qy   2269 CTTTATTACAACAGAATGACCAACAACTTGTGTATAGCTTGTATAGCTTCAAGGACATGGACA 2328
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Db  2389  GTGTTCCATGACGACTTGGAAGACGTATTTAAAGCTAGAAGTTGAAGCAGAAATTG  2448
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Qy  3454  CTTTTGATGAAATGGAACAGAGAGCTTACTTATTCTTCGAAACCAAGGCTTCTCTAGTGA  3513
Db  2509  CTTTTGATGAAATGGAACAGAGAGCTTACTTATTCTTCGAAACCAAGGCTTCTCTAGTGA  2568
Qy  3514  GCACCATGAGCCTTGGAAACAACAGATGTATACAATAGCAAAGTTCATTCTTTACCT  3573
Db  2569  GCACCATGAGCCTTGGAAACAACAGATGTATACAATAGCAAAGTTCATTCTTTACCT  2628
Qy  3574  TGAAACGTGAAAGTAAATCAGTGAAGTGCTTTCTGCTTTAATTTTTTTCACAG  3633
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Qy  3634  TTCAGATTTTATGTTTTGGTCATCACTCTTTAAAATGCTGTGTTCCCATCAAAC  3693
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Db  2929  CGGCTTTAAATGTGATGCATTCAGAAAGGACTATGTTTTCAGCTGTTTTCAACAGTA  2988
Qy  3934  CTATGGTTTATTCTTTACCTATATTAGTGAATATCATCAGTAGTAACTACTACTCTTATCATT  3993
Db  2989  CTATGGTTTATTCTTTACCTATATTAGTGAATATCATCAGTAGTAACTACTACTATCATT  3048
Qy  3994  TAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTCAAGAAATTACTGATA  4053
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Qy  4054  TAGTTTAAAATTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAA  4113
Db  3109  TAGTTTAAAATTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAA  3168
Qy  4114  TGCCACCTTACTTTGCCATGAAAATGCTTATAAGATCAAAGCTTATACTCAAC  4173
Db  3169  TGCCACCTTACTTTGCCATGAAAATGCTTATAAGATCAAAGCTTATACTCAAC  3228
Qy  4174  TATATTTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTGCCTTATTGGTTATGTTCCAT  4233
Db  3229  TATATTTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTGCCTTATTGGTTATGTTCCAT  3288
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Qy  4294  TATATTTTTATACTGTAAAGTTCCTTGGTTTTTGCCTTATTGGTTATGTTCCAT  4353
Db  3349  TATATTTTTATACTGTAAAGTTCCTTGGTTTTTGCCTTATTGGTTATGTTCCAT  3408
Qy  4354  CAGTTATTCGTGTTCACTTATATTCGTTCTTCTTCACCTTTCACCTTTAAGAAAATTTTAAATACCAAAG  4413
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Db  4414  AATTTGGTCATTTATCTATTCGTGTGCGTTGCGTTGCTTGATTGCAATCACTGAAATAA  4473
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Qy  3529  CTTTCTTATGGGATACACAATTGCAACTATTCTTCATTATGCCTTTGTATCATCATTC  3588
Db  4534  CAATCTATCCACTTCTTAGGTTGCCTGATTTCTTCATTAAAGAATTCTTGGAGAATGTAC  4593
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Qy  3769  GATCAATAAGAAAGATCCCTTTTCAGAAACCTTTCAACGAAGTGAAGAGTCTAAAAATAGGAAGC  3828
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Qy  3949  TGCATAAAGAATGATGAGAAGTATTCTTCAGAGACAAGTGAAGAGTAAAGAAAGTGG  4008
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Qy  4009  CAACTAAAATACATCTCTTTCTGTGAAAAAGGAGATCTTAGGAGACTATTGGGTCCAA  4068
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Qy  4129  GCCGAGTATTTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATGAAGAAGT  4188
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Qy  4189  GTATGGGTACTGTCCTCAGATAAACCCTTTGTGGCCAGATACTACCATTGCGAGGAACATT  4248
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Qy  4249  TTGAAATTTATGGAGCTGTCAAAGAGTGAGTGCAAGTGCAAGTGAAGAAGTCATAAGTC  4308
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Qy  4309  GAATAACACATGCACTTGATTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTG  4368
Db  5314  CAGGAATCAAACGAAAGTTGTGTTTTGCTCTAAGATGCCTAGGGAATCCTCAGATTACTT  5373
Qy  4369  CAGGAATCAAACGAAAGTTGTGTTTTGCTCTAAGATGCCTAGGGAATCCTCAGATTACTT  4428
Db  5374  TGCTAGATGACCATCACAGGTATGGCAGTATGGCAAAGCCCAAACACACAGCACATGGGCGAGCAA  5433
Qy  4429  TGCTAGATGACCATCACAGGTATGGCAGTATGGCAAAGCCCAAACAGCACATGTGGCGAGCAA  4488
Db  5434  TTCGGACTGCATTTAAAAACACAGAAAAGCGGGCCGTATTCTGACCACCTCACTATATGGGAGG  5493
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Qy   120 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCTTTTCCACTA
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Qy  1131 TTTTTTTATTTGGTTAATTAATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 1190
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Db   121 TTTTTTTATTTGGTTAATTAATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA  180

Qy  1191 GTGCCTAATATAGAACTCAATCCTATGGCACAAGTTACTCTTTCTAATCTAATTCTTGGA 1250
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Db   181 GTGCCTAATATAGAACTCAATCCTATGGCACAAGTTACTCTTTCTAATCTAATTCTTGGA  240

Qy  1251 TATACTTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAGTGTCTACTGATCATCTA 1310
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Db   241 TATACTTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAGTGTCTACTGATCATCTA  300

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Qy  1371 TCTAAGCGAGCAACTTGTAGTGTGGTTTGTGGTTTCAAAGACTCCATGCCTATGAACTTCGT 1430
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Qy  1431 TTTTTTCTGATATGATTCCAGTATCTTCTATTTATATGGATTCAAGAGCTGGCTGTGTTCA 1490
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Qy  1671 ATTTTAATATACCTAGTTATAGCATTTTGGATACTTTTGGCAATTCATATC 1730
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Qy  1851 ATGGCAGTCATTGCGACAGCTTCTTGTTATTCCCAAAGTAGCAGCATTGTGATATTT 1910
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Qy  1911 CTGCTTTTTCCTTATGGATTATCATCTGTATTTTTGCTTAATGCTGACACCTCTT 1970
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Qy  1971 TTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTTGTTACTGGCTTTTGGATTT 2030
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Qy  6034 GAACCAAG 6041
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RESULT 8

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AX417824
LOCUS       AX417824                4929 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 1 from Patent WO0231147.
ACCESSION   AX417824
VERSION     AX417824.1  GI:21522942
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hu,Y. and Nepomnichy,B.
  TITLE     Human transporter proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 0231147-A 1 18-APR-2002;
            LEXICON GENETICS INC (US)
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                     /db_xref="taxon:9606"
ORIGIN
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  Matches 4919;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy  1011 ATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGACAGACCAGAACACTTCTACTGAAG 1070
         |||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db     1 ATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGACAGACCAGAACACTCTACTGAAG   60

Qy  1071 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCTTTTCCACTA 1130
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Qy  3291 TCTGCCCTAGACAGTCATTCAAATTGGGGTGTCATTCTTATGGTGTTCCATGACGACT 3350
         ||||||||||||||| |||||||| |||||||  |||||||||||| |||||||||||||
Db  2281 TCTGCCCTAGACAGTTCATTCAAATTTGGGGTGCCATTCTTATGGGTTTCCATGACGACT 2340

Qy  3351 TTGGAAGACGTATTTTAAAGCTAGAGTGAAGCAGAAATTGACCAAGCAGATTATAGT 3410
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TTGGAAGACGTATTTTAAAGCTAGAGTGAAGCAGAAATTGACCAAGCAGATTATAGT 2400

Qy  3411 GTATTACTCAGCAGCCACTGGAGAAGAAATGAATCAAAATCTTTGATGAAATGGAA 3470
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GTATTACTCAGCAGCCACTGGAGAAGAAATGAATCAAAATCTTTGATGAAATGGAA 2460

Qy  3471 CAGAGCTTACTTATTCTTTCTGAAACCAAGCTTCCTCAGTGACCATGAGCCCTTTGG 3530
         |||||||||||||||||||||  ||||||||||||||||||||||||||||::||||
Db  2461 CAGAGCTTACTTATTCTTTCTGAAACCAAGCTKCCTCAGTGAGCACCATGAGCCCTTTGG 2520

Qy  3531 AAACAACAGATGTATACAAATAGCAAAGTTCATTCTTTACCTTGAAACGTGAAAGTAAA 3590
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 AAACAACAGATGTATACAAATAGCAAAGTTTCATTTCTTTACCTTGAAACGTGAAAGTAAA 2580

Qy  3591 TCAGTGAGATCAGTGTTGCTTCTGCTTTAATTTTTTCACAGTTCAGATTTTTATGTTT 3650
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 TCAGTGAGATCAGTGTTGCTTCTGCTTTAATTTTTTCACAGTTCAGATTTTTATGTTT 2640

Qy  3651 TTGGTTCATCACTCTTTAAAAATGCTGGTTCCCATCAAACTTGTTCCGACTTATAT 3710
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 TTGGTTCATCACTCTTTAAAAATGCTGGTTCCCATCAAACTTGTTCCGACTTATAT 2700

Qy  3711 TTTCTAAAACCTGGACAACAATACCATACAAAACAAGTCTCGCTTCTTCAAAATTCT 3770
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 TTTCTAAAACCTGGACAACAATACCATACAAAACAAGTCTCGCTTCTTCAAAATTCT 2760

Qy  3771 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTCACAAGCCAGAACATAATGGTGACG 3830
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTCACAAGCCAGAACATAATGGTGACG 2820

Qy  3831 ATGATAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGGCTTTAAATGTGATG 3890
         |||||||||||||||||||||||||||||||||||||||||||||||||::|||||||
Db  2821 ATGATAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGGCTTTAAATGTGRTG 2880

Qy  3891 CATTCAGAAAAGGACTATGTTTTGCAGCTGTTTTCAACAGTGTTTATTCTTTA 3950
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 CATTCAGAAAAGGACTATGTTTTGCAGCTGTTTTCAACAGTGTTTATTCTTTA 2940

Qy  3951 CCTATATTAGTGAATATCATTAGTAACTAACTCTTTATCATTTAAAGTGACTGAAACC 4010
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 CCTATATTAGTGAATATCATTAGTAACTAACTCTTTATCATTTAAAGTGACTGAAACC 3000

Qy  4011 ATCCAGATCTGGAGTACCCCATTCTTCTTCAAGAAATTACTGATATAGTTTAAAATTGAG 4070
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 ATCCAGATCTGGAGTACCCCATTCTTCTTCAAGAAATTACTGATATAGTTTAAAATTGAG 3060

Qy  4071 CTGTATTTTCAAGCAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCC 4130
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 CTGTATTTTCAAGCAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCC 3120

Qy  4131 ATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATACTTAAACTTTCAGGTCTT 4190
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 ATGGAAAATGCAGAGAATCATAAGATCAAAGCTTAYACTTAAACTTTCAGGTCTT 3180

Qy  4191 TTGCCATCTGCATATTGGATTGGACAAGCTGTGTTGTGATATCCCCTTATTTTTATCATT 4250
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 TTGCCATCTGCATATTGGATTGGACAAGCTGTGTTGTGATATCCCCTTATTTTTATCATT 3240

Qy  4251 CTTATTTTGATGCGTAGGAAGCTACTGGCATTTCATTATGGATTATTTTATACTGTA 4310
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 CTTATTTTGATGCGTAGGAAGCTACTGGCATTTCATTATGGATTATTTTATACTGTA 3300

Qy  4311 AAGTTCCTTGCTGTGGTTTTTTTGCCTATTGGTTATGTTCCATCAGTTATTCTGTTCACT 4370
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 AAGTTCCTTGCTGTGGTTTTTTTGCCTATTGGTTATGTTCCATCAGTTATTCTGTTCACT 3360
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Db  1141 AATGAAGGTGCTTCATTTCAAATTTGACTGCAGGCGCCCATATCCTCTAATTATTACAATT 1200
Qy  2211 ATCATGCTCACACTTAATAGTATATTCTATGTCCTCTGGCGTCTATCTTGATCAAGTC 2270
Db  1201 ATCATGCTCACACTTAATAGTATATTCTATGTCCTCTGGCGTCTATCTTGATCAAGTC 1260

Qy  2271 ATTCCAGGGGAATTGGCTTACGGAGATCATCTTATATTTCTGAAGCCTTCATATTGG 2330
Db  1261 ATTCCAGGGGAATTGGCTTACGGAGATCATCTTATATTTCTGAAGCCTTCATATTGG 1320

Qy  2331 TCAAAGTAAAAGAAATTATGAGGAGTTATCAGAGAGGCAATGTTAATGGAAATATTAGT 2390
Db  1321 TCAAAGTAAAAGAAATTATGAGGAGTTATCAGAGAGGCAATGTTAATGGAAATATTAGT 1380

Qy  2391 TTTAGTGAAATTATTGACCCAGTTCTTCAGAATTGTAGGAAAAGAAGCCATAGAATT 2450
Db  1381 TTTAGTGAAATTATTGAGCCAGTTCTTCAGAATTGTGAGGAAAAGAAGCCATAGAATT 1440

Qy  2451 AGTGGTATTCAGAAGACATACAGAAGAGGGTGAAAAATGTGGAGCTTTGAGAAATTTG 2510
Db  1441 AGTGGTATTCAGAAGACATACAGAAGAGGGTGAAAAATGTGGAGCTTTGAGAAATTTG 1500

Qy  2511 TCATTTGACATATATGAGGGTCAGATTACTTGCCTTACTGGCCACAGTGGAACAGAGAAAG 2570
Db  1501 TCATTTTGACATATATGAGGGTCAGATTACTTGCCTTACTGGCCACAGTGGAACAGAGAAAG 1560

Qy  2571 AGTACATTGATGAATATTCTTTGTGGACTCTGTGCCCACCTTCTGATGGGTTTGCATCCATA 2630
Db  1561 AGTACATTGATGAATATTCTTTGTGGACTCTGTGCCCACCTTCTGATGGGTTTGCATCCATA 1620

Qy  2631 TATGGACACCAGAGTCTCAGAAATAGATGAAATGTGAAGCAAGAGAAATGATTGGCATT 2690
Db  1621 TATGGACACCAGAGTCTCAGAAATAGATGAAATGTGAAGCAAGAGAAATGATTGGCATT 1680

Qy  2691 TGTCCACAGTTAGTATACACTTTGATGTTTTGACAGTAGAAGAAAATTTATCAATTTG 2750
Db  1681 TGTCCACAGTTAGTATACACTTTGATGTTTTGACAGTAGAAGAAAATTTATCAATTTG 1740

Qy  2751 GCTTCAATCAAAGGGATACCAGCCAACATATAATACAAGAAGTGCAGAAGGTTTTACTA 2810
Db  1741 GCTTCAATCAAAGGGATACCAGCCACCATATAATACAAGAAGTGCAGAAGGTTTTACTA 1800

Qy  2811 GATTTAGAACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGTGTCAAAAA 2870
Db  1801 GATTTAGAACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGTGTCAAAAA 1860

Qy  2871 AGAAAGCTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTAGCTGGATGAA 2930
Db  1861 AGAAAGCTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTAGCTGGATGAA 1920

Qy  2931 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTAAAATACAGA 2990
Db  1921 CCAACAGCTGGAATGGACCCCCTGTTCTCGACATATTGTATGGAATCTTTAAAATACAGA 1980

Qy  2991 AAAGCCAATCGGGTGACAGTGTTCAGTTCAGTTCATGGATGAAGCTGACATTCTTGCA 3050
Db  1981 AAAGCCAATCGGGTGACAGTGTTCAGTTCAGTTCATGGATGAAGCTGACATTCTTGCA 2040

Qy  3051 GATAGGAAGCTGTGATATCACAAGAGAATGCTGAAAGTGTTGGTTCTTCAATGTTCCTC 3110
Db  2041 GATAGGAAGCTGTGATATCACAAGAGAATGCTGAAAGTGTTGGTTCTTCAATGTTCCTC 2100

Qy  3111 AAAAGTAAATGGGGGATCCGGCTACCGCGTTTAAACCCAAATATTGTGCCACA 3170
Db  2101 AAAAGTAAATGGGGGATCCGGCTACCGCGTTTAAACCCAAATATTGTGCCACA 2160

Qy  3171 GAATCTCTTTCTTCACTGGTTAAACACAGATACCTGGAGCTACTTTATTACAACAGAAT 3230
Db  2161 GAATCTCTTTCTTCACTGGTTAAACACAGATACCTGGAGCTACTTTATTACAACAGAAT 2220

Qy  3231 GACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAAATTTTCAGGTTGTT 3290
Db  2221 GACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAAATTTTCAGGTTGTT 2280
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Qy   4371  TATATTGCTTCTTCACCTTTAAGAAAATTTAAATACCAAAGAATTTGGTCATTTATC  4430
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361  TATATTGCTTCTTCACCTTTAAGAAAATTTAAATACCAAAGAATTTGGTCATTTATC  3420

Qy   4431  TATTCTGTGCAGGGTTGNCTTGTATTGCAATCACTTCTTTATTGGGATAC  4490
           |||||||||||||||| ||||||||||||||||||||||||||||||||
Db   3421  TATTCTGTGCAGGGTTGCCTTGTATTGCAATCACTTCTTTATTGGGATAC  3480

Qy   4491  ACAATTGCAACTATTCTTCATTATGCCTTTGTATCATCATCCAATCTATCCACTTCTA  4550
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  ACAATTGCAACTATTCTTCATTATGCCTTTGTATCATCATCCAATCTATCCACTTCTA  3540

Qy   4551  GGTTGCCTGATTTCTTCATAAGAATTCTTGGAAGAATTGTACGGAAAAAATGTGGACACC  4610
           |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   3541  GGTTGCCTGATTTCTTCATAAGAATTCTTGGAAGAATTGTACGAAAAAATGTGGACACC  3600

Qy   4611  TATAATCCATGGGATAGGCTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTACTG  4670
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  TATAATCCATGGGATAGGCTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTACTG  3660

Qy   4671  TGGATTTCTCCTACAATACTATGAGAAAAATATGAGGAGGCAGATCAATAAGAAAGAT  4730
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  TGGATTTCTCCTACAATACTATGAGAAAAATATGAGGAGGCAGATCAATAAGAAAGAT  3720

Qy   4731  CCCTTTTCAGAAACCTTTCAACGAGTCTAAAAATAGGAAGCTTCCAGAACCACCAGAC  4790
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721  CCCTTTTCAGAAACCTTTCAACGAGTCTAAAAATAGGAAGCTTCCAGAACCACCAGAC  3780

Qy   4791  AATGAGGATGAAGATGAAGATGTCAAAGTCAAAGGTCAAAGAGCTGATGGGT  4850
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781  AATGAGGATGAAGATGAAGATGTCAAAGTCAAAGGTCAAAGAGCTGATGGGT  3840

Qy   4851  TGCCAGTGTGTGAGGAGAAAACATCCATTATGGTCAGCAATTTGCATAAAGAATATGAT  4910
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Db   3841  TGCCAGTGTGTGAGGAGAAAACATCCATTATGGTCAGCAATTTGCATAAAGAATATGAT  3900

Qy   4911  GACAAGAAAGATTTTCTTCTTCTTCAAGAAAAGTAAGAAAGTGGCAACTAAATACATCTCT  4970
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901  GACAAGAAAGATTTTCTTCTTCTTCAAGAAAAGTAAGAAAGTGGCAACTAAATACATCTCT  3960

Qy   4971  TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGTGCTGGCAAAAGC  5030
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961  TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGTGCTGGCAAAAGC  4020

Qy   5031  ACAATTAATAATAATATCTCGGTTGGTGATATTGAACCAACTTCAGGCCAGTATTTTTAGGA  5090
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021  ACAATTAATAATAATATCTCGGTTGGTGATATTGAACCAACTTCAGGCCAGTATTTTTAGGA  4080

Qy   5091  GATTATTCTTCAGAGACAAGCAAGTGACATGATGAAGTCACTGAAGTGTATGGGTTACTGTCCT  5150
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081  GATTATTCTTCAGAGACAAGCAAGTGACATGATGAAGTCACTGAAGTGTATGGGTTACTGTCCT  4140

Qy   5151  CAGATAAACCCTTGTGGGCCAGATACTACATTGCAGGAACATTTGAAATTTATGGAGCT  5210
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Db   4141  CAGATAAACCCTTGTGGGCCAGATACTACATTGCAGGAACATTTGAAATTTATGGAGCT  4200

Qy   5211  GTCAAAGGAATGAGTGCAAGTGCAAGTGACATGAAAGAAGTCATAAGTCGAATAACACATGCACTT  5270
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201  GTCAAAGGAATGAGTGCAAGTGCAAGTGACATGAAAGAAGTCATAAGTCGAATAACACATGCACTT  4260

Qy   5271  GATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAG  5330
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261  GATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAG  4320

Qy   5331  TTGTGTTTTGCTCTAAGTAGTGCTCAGATTACTTTGCTAGATGAACCATCT  5390
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321  TTGTGTTTTGCTCTAAGTAGTGCTCAGATTACTTTGCTAGATGAACCATCT  4380

Qy   5391  ACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGGAGCAATTGCATTTAAA  5450
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381  ACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGGAGCAATTGCATTTAAA  4440

Qy   5451  AACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGGAGGCGTGTCGT  5510
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Db   4441  AACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGGAGGCGGTCTGT  4500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5511  GATCGAGTAGCTATCATGGTGTCTCGGCAGTGCAGTTAAGATGTATCGGAACACAGTACAACATCTA  5570
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   4501  GATCGAGTAGCTATCATGGTGTCTCGGCAGTGCAGTTAAGATGTATCGGAACAGTACAACATCTA  4560

Qy   5571  AAGAGTAAATTGGAAAAGGCTACTTTTGGAAATTAAATTAAATTGAAGGACTGGATAGAAAAAC  5630
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561  AAGAGTAAATTGGAAAAGGCTACTTTTGGAAATTAAATTAAATTGAAGGACTGGATAGAAAAAC  4620

Qy   5631  CTAGAAGTAGACCGCCTTCAAAGAAATTCAGTAGTATATTTCCCAAATGCAAGCCGTCAG  5690
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621  CTAGAAGTAGACCGCCTTCAAAGAAATTCAGTAGTATATTTCCCAAATGCAAGCCGTCAG  4680

Qy   5691  GAAAGTTTTCTTCTATTTGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTTCA  5750
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Db   4681  GAAAGTTTTCTTCTATTTGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTTCA  4740

Qy   5751  CAATCTTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTT  5810
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741  CAATCTTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTT  4800

Qy   5811  TCTCAAGCAACATTGGAACAGTTTTTGTAGAACTCACTAAAGAACCACTAAAGAACAACAAGAGGAGGAAGAT  5870
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801  TCTCAAGCAACATTGGAACAGTTTTTGTAGAACTCACTAAAGAACCACTAAAGAACAACAAGAGGAGGAAGAT  4860

Qy   5871  AATAGTTGTGGAACTTTAAACAGCACACTTTGGTGGGAACCAAGAGATAGAGTA  5930
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861  AATAGTTGTGGAACTTTAAACAGCACACTTTGGTGGGAACCAAGAGATAGAGTA  4920

Qy   5931  GTATTTTGA  5939
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Db   4921  GTATTTTGA  4929
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RESULT 9

AX537472

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LOCUS       AX537472                4917 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 3 from Patent WO02070690.
ACCESSION   AX537472
VERSION     AX537472.1  GI:25269279
KEYWORDS    
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Chen,H., Kilinski,L. and le Bihan,S.
  TITLE     Abca5 transporter and uses thereof
  JOURNAL   Patent: WO 02070690-A 3 12-SEP-2002;
            Active Pass Pharmaceuticals, Inc. (CA)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Query Match             73.7%;  Score 4807.4;  DB 6;  Length 4917;
Best Local Similarity   98.8%;  Pred. No. 0;
Matches 4891;  Conservative    0;  Mismatches    7;  Indels   50;  Gaps    3;
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Qy   1011  ATGTCCACTGCAATTAGGAGTTGGAGACAGCCAGAGCACTTCTACTGAAG  1070
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  ATGTCCACTGCAATTAGGAGTTGGAGACAGCCAGAGCACTTCTACTGAAG  60

Qy   1071  AATTACTTAATTAAATCGAGACCAAAAAGAGTAGTGTTCAGAAATTCTTTTCCACTA  1130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  AATTACTTAATTAAATCGAGACCAAAAAGAGTAGTGTTCAGAAATTCTTTTCCACTA  120

Qy   1131  TTTTTTTTTATTTTGGTTAATATTAATTAGCATGATGCATCAAATAAGAAAATATGAAGAA  1190
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Qy  2271  ATTCCAGGGAATTGGCTTACGGAGATCATCTTTATATTTCTGAAGCCTTCATATTGG  2330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  ATTCCAGGGAATTGGCTTACGGAGATCATCTTTATATTTCTGAAGCCTTCATATTGG  1320

Qy  2331  TCAAAGAGTAAAAGAAATATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT  2390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  TCAAAGAGCAAAAGAATTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT  1380

Qy  2391  TTTAGTGAAATTATTGAGCCAGTTTCTTCAGAATTGTAGGAAAAGAAGCCATAAGAATT  2450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  TTTAGTGAAATTATTGAGCCAGTTTCTTCAGAATTGTAGGAAAAGAAGCCATAAGAATT  1440

Qy  2451  AGTGGTATTCAGAAGACATCAGAAAAGAAGAGGTGAAAATGTGGAGGCTTTGAGAAATTTG  2510
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Db  1441  AGTGGTATTCAGAAGACATACAGAAAAGAAGAGGTGAAAATGTGGAGGCTTTGAGAAATTTG  1500

Qy  2511  TCATTTGACATATATGAGGGTCAGATTACTGCCTTACTGGCCACAGTGGAACGAGGAAAG  2570
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Db  1501  TCATTTGACATATATGAGGGTCAGATTACTGCCTTACTGGCCACAGTGGAACGAGGAAAG  1560

Qy  2571  AGTACACAGAGTCTCAGAAATAGTCTTGTGGACACTGCGCCCACCTTCGATGGGTTGCATCTATA  2630
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Db  1561  AGTACATTGATGAATTCTTGTGGACCTCTGCGCCCACCTTCGATGGGTTGCATCTATA  1620

Qy  2631  AGTACACAGAGTCTCAGAAATAGTTGAAGCAAGAAAATGATTGGCATT  2690
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  AGTACATTGATGAATTCTTGTGGAAGCAAGAAAATGATTGGCATT  1680

Qy  2691  TATGGACACAGTCTAGATATACACTTTGATGTTTTGACAGTGAGAAGAAAATTTATCAATTTTG  2750
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  TGTCCACAGTCTAGATACACTTTGATGTTTTGACAGTGAGAAGAAAATTTATCAATTTTG  1740

Qy  2751  GCTTCAATCAAAGGGATACCAGCCGCCAACAATATAATACAAGAAGTGCAGAGAGTTTTACTA  2810
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Db  1741  GCTTCAATCAAAGGGATACCAGCCGCCAACAATATAATACAAGAAGTGCAGAGAGTTTTACTA  1800

Qy  2811  GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGTGGTGGTCAAAAA  2870
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGTGGTGGTCAAAAA  1860

Qy  2871  AGAAAGCTGTCATTAGGAATTGCTGTTCTTCGGGAACCCAAAGATACTGCTGCTAGATGAA  2930
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Db  1861  AGAAAGCTGTCATTAGGAATTGCTGTTCTTCGGGAACCCAAAGATACTGCTGCTAGATGAA  1920

Qy  2931  CCAACAGCTGGAATGGGGATCGGCTACCGCCGCTGTTCCGACATATTGTATGAATCTTTAAAATACAGA  2990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CCAACAGCTGGAATGGGGATCGGCTACCGCCGCTGTTCCGACATATTGTATGAATCTTTAAAATACAGA  1980

Qy  2991  AAAGCCAATGGGTGACAGTGTCAGTGTTCAGTAGCTCATTCGACTTCATGGATGAAGCTGCA  3050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  AAAGCCAATGGGTGACAGTGTCAGTGTTCAGTAGCTCATTCGACTTCATGGATGAAGCTGCA  2040

Qy  3051  GATAGGAAGCTGTGATATCACAAGGAATGTGAAATGTGGTCTTCAATGTCCTC  3110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  GATAGGAAGCTGTGATATCACAAGGAATGTGAAATGTGGTCTTCAATGTCCTC  2100

Qy  3111  AAAAGTAAATGGGGGATCGGCTACCGCCGCTTTCCCAAATATTGTGCCACA  3170
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  AAAAGTAAATGGGGGATCGGCTACCGCCGCTTTCCCAAATATTGTGCCACA  2160

Qy  3171  GAATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTGGACTACAACGAAT  3230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GAATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTATTACAACGAAT  2220

Qy  3231  GACCAACAACTTGTGTATAGCTTGTGTATAGCGACAAATTTCAGGTTTGTTT  3290
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GACCAACAACTTGTGTATAGCTTGTGTATAGGCAAATTTCAGGTTTGTTT  2280

Qy  3291  TCTGCCCTAGACAGTCATTCAAATTTGGGTGTCATTCTTATGGTGTTTCATGATGACT  3350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  TCTGCCCTAGACAGTCATTCAAATTTGGGTGTCATTCTTATGGTGTTTCATGATGACT  2340
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Db   121  TTTTTTTATTTGGTTAATATTAGCATGATGCATCCAAATAAGAATATGAAGAA  180
Qy  1191  GTGGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATTCTTGA  1250
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  GTGGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATTCTTGA  240

Qy  1251  TATACTCCAGTGACTAATATTACAAGCAGCATCATCGCAGAAAGTGTCTACTGATCATCTA  1310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  TATACTCCAGTGACTAATATTACAAGCAGCATCATCGCAGAAAGTGTCTACTGATCATCTA  300

Qy  1311  CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAGAAATGTTAACATCCAGTCTC  1370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAGAAATGTTAACATCCAGTCTC  360

Qy  1371  TCTAAGCCGAGCAACTTGTAGGTGTGGTTTCAAAGACTCCATGTCCTATGAACTTCGT  1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  TCTAAGCCGAGCAACTTGTAGGTGTGGTTTCAAAGACTCCATGTCCTATGAACTTCGT  420

Qy  1431  TTTTTTCCTGATATGATTCCAGTATCTTCTATTTATATGGATTCACAGAGCATCCATA  1490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  TTTTTTCCTGATATGATTCCAGTATCTTCTATTTATATGGATTCACAGAGCATCCATA  480

Qy  1491  AAATCATGTGCCATTATACAGTTGAAGACCAATGTTCTCTTGGAAGGAGCTGGAGTCAACT  1550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  AAATCATGTGCCATTATACAGTTGAAGACCAATGTTCTCTTGGAAGGAGCTGGAGTCAACT  540

Qy  1551  GATGCTGCCATTATACAGTTGAAGACTGCTTCTGTTGTAGAAATAGATACCTTTCCCCGAGGAGTA  1610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GATGCTGCCATTATACAGTTGAAGACTGCTTCTGTTGTAGAAATAGATACCTTTCCCCGAGGAGTA  1670

Qy  1611  AAAGCTGTTATTATGGGAGAAACTGCTCTGTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA  1670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  AAAGCTGTTATTATGGGAGAAACTGCTCTGTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA  660

Qy  1671  ATTTTAATAACCTAGTTATAGCATTTTCACCCTTTGGCAATTCATATC  1730
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  ATTTTAATAACCTAGTTATAGCATTTTCACCCTTTGGCAATTCATATC  720

Qy  1731  GTAGCAGAAAAGAAAGAAATTTTAAAGAAAATTTTAAAGATAAATGGGACTTCATGATACT  1790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  GTAGCAGAAAAGAAAGAAATTTTAAAGAAAATTTTAAAGATAAATGGGACTTCATGATACT  780

Qy  1791  GCCTTTGGCTTTCCTCGGGGTCTTCTATACAAGTTAATTTTTCTATGTCCCTTCTT  1850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GCCTTTGGCTTTCCTCGGGGTCTTCTATACAAGTTAATTTTTCTATGTCCCTTCTT  840

Qy  1851  ATGGCAGTCATTGGACAGCTTCTTCTTTGTTATTCTCAAAGTAGCAGCATTGTGATATTT  1910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  ATGGCAGTCATTGGACAGCTTCTTCTTTGTTATTCTCAAAGTAGCAGCATTGTGATATTT  900

Qy  1911  CTGCTTTTTTCCTTTATGGATATCATCGTATTTTTGCTTTAAATGCTGACACCTCTT  1970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CTGCTTTTTTCCTTTATGGATATCATCGTATTTTTGCTTTAAATGCTGACACCTCTT  960

Qy  1971  TTTAAAAAATCAAAACATGTGGAATAGTTGAATTTTGTTACTGTGGCTTTTGGATTT  2030
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TTTAAAAAATCAAAACATGTGGAATAGTTGAATTTTGTTACTGTGGCTTTTGGATTT  1020

Qy  2031  ATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTCATTTAGAAGATTT  2090
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  ATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTCATTTAGAAGATTT  1080

Qy  2091  CCTTTCTGTCACTGTACTTTGTTGATTGGTATGGCACAGGTCATGCAATTAGAAGATTT  2150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  CCTTTCTGTCACTGTACTTTGTTGATTGGTATGGCACAGGTCATGCAATTAGAAGATTT  1140

Qy  2151  AATGAAGGTGCTTCATTTCAAATTTGACTGCAGCGCCATATCCTCTAATTATTACAATT  2210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  AATGAAGGTGCTTCATTTCAAATTTGACTGCAGCGCCATATCCTCTAATTATTACAATT  1200

Qy  2211  ATCATGCTCACACTTAATATATTCTATGTCCCTTGGCTGTCTATCTTGATCAAGTC  2270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  ATCATGCTCACACTTAATATATTCTATGTCCCTTGGCTGTCTATCTTGATCAAGTC  1260
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Qy          3351 TTGGAAGACGTATTTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGT 3410
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2341 TTGGAAGACGTATTTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGT 2400

Qy          3411 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATGGAA 3470
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATGGAA 2460

Qy          3471 CAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG 3530
                 ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db          2461 CAGAGCTTACTTATTCTTTCTGAAACCAAGGCTGCTCTAGTGAGCACCATGAGCCTTTGG 2520

Qy          3531 AAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCTTGAAACGTGAAAGTAAA 3590
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2521 AAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCTTGAAACGTGAAAGTAAA 2580

Qy          3591 TCAGTGAGATCAGTGTTGCTTCTGCTTTTAATTTTTTTCACAGTTCAGATTTTTATGTTT 3650
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2581 TCAGTGAGATCAGTGTTGCTTCTGCTTTTAATTTTTTTCACAGTTCAGATTTTTATGTTT 2640

Qy          3651 TTGGTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTATAT 3710
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2641 TTGGTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTATAT 2700

Qy          3711 TTTCTAAAACCTGGAGACAAACCACATAAATACAAAACAAGTCTGCTTCTTCAAAATTCT 3770
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2701 TTTCTAAAACCTGGAGACAAACCACATAAATACAAAACAAGTCTGCTTCTTCAAAATTCT 2760

Qy          3771 GCT------------------GACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGC 3812
                 |||                  |||||||||||||||||||||||||||||||||||||||
Db          2761 GCTGGTGAGAGTGTNNGTGAAGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGC 2820

Qy          3813 CAGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGT 3872
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2821 CAGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGT 2880

Qy          3873 GCGGCTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGT 3932
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2881 GCGGCTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGT 2940

Qy          3933 ACTATGGTTTATTCTTTACCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCAT 3992
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2941 ACTATGGTTTATTCTTTACCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCAT 3000

Qy          3993 TTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGAT 4052
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3001 TTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGAT 3060

Qy          4053 ATAGTTTTTAAAATTGAGCTGTATTTTCAAGCAGCTTTGCTTGG-AATCATTGTTACTGC 4111
                 |||||||||||||||||||||||||||||||||||||||||||| ||||||||| |||||
Db          3061 ATAGTTTTTAAAATTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTGTAACTGC 3120

Qy          4112 AATGCCACCTTACTTTGCCATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATACTCA 4171
                 ||||||||| |||| ||||||||||||||||||||||||||
Db          3121 AATGCCACCCTACTCTGCCATGGAAAATGCAGAGAATCATA------------------- 3161

Qy          4172 ACTTAAACTTTCAGGTCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATAT 4231
                             ||||||||||||||||||||||||||||||||||||||||||||||||
Db          3162 ------------AGGTCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATAT 3209

Qy          4232 CCCCTTATTTTTATCATTCTTATTTGATGCTAGGAAGCTTACTGGCATTTCATTATGG 4291
                 ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db          3210 CCCCTTATTTTTATCATTCTTATTTGATGCTAGGAAGCTTATTGGCATTTCATTATGG 3269

Qy          4292 ATTATATTTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTTGCCTTATTGGTTATGTTCC 4351
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3270 ATTATATTTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTTGCCTTATTGGTTATGTTCC 3329

Qy          4352 ATCAGTTATTCTGTTCACTTATATTGCTTCTTTCACCTTTAAGAAAATTTTAAATACCAA 4411
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3330 ATCAGTTATTCTGTTCACTTATATTGCTTCTTTCACCTTTAAGAAAATTTTAAATACCAA 3389

Qy          4412 AGAATTTTGGTCATTTATCTATTCTGTGGCAGCGTTGNCTTGTATTGCAATCACTGAAAT 4471
                 ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db          3390 AGAATTTTGGTCATTTATCTATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAAT 3449

Qy          4472 AACTTTCTTTATGGGATACACAATTGCAACTATTCTTCATTATGCCTTTTGTATCATCAT 4531
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3450 AACTTTCTTTATGGGATACACAATTGCAACTATTCTTCATTATGCCTTTTGTATCATCAT 3509

Qy          4532 TCCAATCTATCCACTTCTAGGTTGCCTGATTTCTTTCATAAAGATTTCTTGGAAGAATGT 4591
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3510 TCCAATCTATCCACTTCTAGGTTGCCTGATTTCTTTCATAAAGATTTCTTGGAAGAATGT 3569

Qy          4592 ACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCC 4651
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Db          3570 ACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCC 3629

Qy          4652 TTACCTGCAGTGTGTACTGTGGATTTTCCTCTTACAATACTATGAGAAAAAATATGGAGG 4711
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3630 TTACCTGCAGTGTGTACTGTGGATTTTCCTCTTACAATACTATGAGAAAAAATATGGAGG 3689

Qy          4712 CAGATCAATAAGAAAAGATCCCTTTTTCAGAAACCTTTCAACGAAGTCTAAAAATAGGAA 4771
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3690 CAGATCAATAAGAAAAGATCCCTTTTTCAGAAACCTTTCAACGAAGTCTAAAAATAGGAA 3749

Qy          4772 GCTTCCAGAACCACCAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAA 4831
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3750 GCTTCCAGAACCACCAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAA 3809

Qy          4832 GGTCAAAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCATCCATTATGGTCAGCAA 4891
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3810 GGTCAAAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCATCCATTATGGTCAGCAA 3869

Qy          4892 TTTGCATAAAGAATATGATGACAAGAAAGATTTTCTTCTTTCAAGAAAAGTAAAGAAAGT 4951
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3870 TTTGCATAAAGAATATGATGACAAGAAAGATTTTCTTCTTTCAAGAAAAGTAAAGAAAGT 3929

Qy          4952 GGCAACTAAATACATCTCTTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCC 5011
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3930 GGCAACTAAATACATCTCTTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCC 3989

Qy          5012 AAATGGTGCTGGCAAAAGCACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTC 5071
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3990 AAATGGTGCTGGCAAAAGCACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTC 4049

Qy          5072 AGGCCAGGTATTTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATGATTCACTGAA 5131
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4050 AGGCCAGGTATTTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATGATTCACTGAA 4109

Qy          5132 GTGTATGGGTTACTGTCCTCAGATAAACCCTTTGTGGCCAGATACTACATTGCAGGAACA 5191
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4110 GTGTATGGGTTACTGTCCTCAGATAAACCCTTTGTGGCCAGATACTACATTGCAGGAACA 4169

Qy          5192 TTTTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAAGAAGTCATAAG 5251
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4170 TTTTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAAGAAGTCATAAG 4229

Qy          5252 TCGAATAACACATGCACTTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACC 5311
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4230 TCGAATAACACATGCACTTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACC 4289

Qy          5312 TGCAGGAATCAAACGAAAGTTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTAC 5371
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4290 TGCAGGAATCAAACGAAAGTTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTAC 4349

Qy          5372 TTTGCTAGATGAACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGC 5431
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4350 TTTGCTAGATGAACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGC 4409

Qy          5432 AATTCGAACTGCATTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGA 5491
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4410 AATTCGAACTGCATTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGA 4469

Qy          5492 GGAGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTAT 5551
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  4470  GGAGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTCTCGGCAGTTAAGAGATGTAT  4529        Qy  1251  TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGCAGAAAGTGTCTACTGATCATCTA  1310
                                                                                             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5552  CGGAACAGTACAACATCTAAAGAGTAAATTGGAAAAGGCTACTTTTTGGAAAATTAAATT  5611        Db  241   TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGCAGAAAGTGTCTACTGATCATCTA  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4530  CGGAACAGTACAACATCTAAAGAGTAAATTGGAAAAGGCTACTTTTTGGAAAATTAAATT  4589        Qy  1311  CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAAGTTAACATCCAGTCTC  1370
                                                                                             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5612  GAAGGACTGGATAGAAAACCTAGAAGTAGACCGCCTCAAAGAGAGAATTCAGTATATTTT  5671        Db  301   CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAAGTTAACATCCAGTCTC  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4590  GAAGGACTGGATAGAAAACCTAGAAGTAGACCGCCTCAAAGAGAGAATTCAGTATATTTT  4649        Qy  1371  TCTAAGCCGACCAACTTGTAGTGTGGTTTGGTTTTCAAAGACTCCATGTCCATGAACTTCGT  1430
                                                                                             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5672  CCCAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTGGCTTATAAAATTCCTAAGGA  5731        Db  361   TCTAAGCCGACCAACTTGTAGTGTGGTTTGGTTTTCAAAGACTCCATGTCCATGAACTTCGT  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4650  CCCAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTGGCTTATAAAATTCCTAAGGA  4709        Qy  1431  TTTTTTCCTGATATTATTCAGTATCTTCATTATATGGATTCAAGAGCTGGCTGTGTTCA  1490
                                                                                             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5732  AGATGTTCAGTCCCTTTCACAATCTTTTTTTAAGTGGAAGAAGCTAAACATGCTTTTGC  5791        Db  421   TTTTTTCCTGATATTATTCAGTATCTTCATTATATGGATTCAAGAGCTGGCTGTGTTCA  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4710  AGATGTTCAGTCCCTTTCACAATCTTTTTTTTAAGTGGAAGAAGCTAAACATGCTTTTGC  4769        Qy  1491  AAATCATGTGAGGCTGCTCAGTACAACATTTCACAGTTTCAGTTTTACAAGCATCCATA  1550
                                                                                             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5792  CATTGAAGAATATAGCTTTTCTCAAGCAACATTGGAACAGTTTTGTAGAACTCACTAA  5851        Db  481   AAATCATGTGAGGCTGCTCAGTACAACATTTCACAGTTTCAGTTTTACAAGCATCCATA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4770  CATTGAAGAATATAGCTTTTCTCAAGCAACATTGGAACAGTTTTGTAGAACTCACTAA  4829        Qy  1551  GATGCTGCCATTATACAGTGAAGACCAATGTTCTCTTGGAAGGAGCTGGAGTCAACT  1610
                                                                                             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5852  AGAACAAGAGAGGAAGATAATAGTTGTGGAACTTTAAACAGCACACTTTGGTGGGAACG  5911        Db  541   GATGCTGCCATTATACAGTGAAGACCAATGTTCTCTTGGAAGGAGCTGGAGTCAACT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4830  AGAACAAGAGAGGAAGATAATAGTTGTGGAACTTTAAACAGCACACTTTGGTGGGAACG  4889        Qy  1611  AAAGCTGTAATTATGGGAGAAACTGCTGTGTTGTGAGAAATAGAATAGTAACCTTTCCCGAGGAGTA  1670
                                                                                             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5912  AACACAAGAAGATAGAGTAGTATTTTGA  5939                                        Db  601   AAAGCTGTAATTATGGGAGAAACTGCTGTGTTGTGAGAAATAGAATAGTAACCTTTCCCGAGGAGTA  660
          ||||||||||||||||||||||||||||
Db  4890  AACACAAGAAGATAGAGTAGTATTTTGA  4917                                        Qy  1671  ATTTTAATATACCTAGTTATAGCATTTCACCTTTTGGATACTTTTGGCAATTCATATC  1730
                                                                                             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                                   Db  661   ATTTTAATATACCTAGTTATAGCATTTCACCTTTTGGATACTTTTGGCAATTCATATC  720
RESULT 10
AX417826                                                                           Qy  1731  GTAGCAGAAAAGAAAAAAAAAAAGAAATTTTTAAAGATAATGGGACTTCATGATACT  1790
LOCUS        AX417826        4785 bp     DNA        linear   PAT  18-JUN-2002                  |||||||||||| |||||||||||||||||||||||||||||||||||||||||||
DEFINITION   Sequence 3 from Patent WO0231147.                                      Db  721   GTAGCAGAAAAGAAAAAAAAAAAAAAATTTTTAAAGATAATGGGACTTCATGATACT  780
ACCESSION    AX417826
VERSION      AX417826.1  GI:21522943                                               Qy  1791  GCCTTTTGGCTTTCCTGGGTTCTTCCTATATACAAGTTTAATTTTTCTTATGTCCCTTCTT  1850
KEYWORDS     .                                                                               |||||||||||||||||||||||||:|||||||||||| |||||||||||||||||||
SOURCE       Homo sapiens (human)                                                  Db  781   GCCTTTTGGCTTTCCTGGGTTCTTCCTATAWACAAGTTTAATTTTTCTTATGTCCCTTCTT  840
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     Qy  1851  ATGGCAGTCATTGCGACAGCTTCTTGTATTCCTCAAAGTAGCAGCATTGTGATATTT  1910
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
REFERENCE    1                                                                     Db  841   ATGGCAGTCATTGCGACAGCTTCTTGTATTCCTCAAAGTAGCAGCATTGTGATATTT  900
  AUTHORS    Hu,Y. and Nepomnichy,B.
  TITLE      Human transporter proteins and polynucleotides encoding the same      Qy  1911  CTGCTTTTTTCCTTATGGATTATCATCTGTATTTTTGCTTAATGCTGCACACCTCTT  1970
  JOURNAL    Patent: WO 0231147-A 3 18-APR-2002;                                              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
             LEXICON GENETICS INC (US)                                             Db  901   CTGCTTTTTTCCTTATGGATTATCATCTGTATTTTTGCTTAATGCTGCACACCTCTT  960
FEATURES             Location/Qualifiers
     source          1..4785                                                       Qy  1971  TTTAAAAATCAAAACATGTGGGAATAGTTGAATTTTTGTTACTGTGGGCTTTTGGATTT  2030
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                     /mol_type="unassigned DNA"                                     Db  961   TTTAAAAATCAAAACATGTGGGAATAGTTGAATTTTTGTTACTGTGGGCTTTTGGATTT  1020
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ORIGIN                                                                             Qy  2031  ATTGGCCTTATGATAATAATCCTCATAGAAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCAGT  2090
Query Match      72.9%;    Score 4754.8;   DB 6;   Length 4785;                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Best Local Similarity   99.8%;   Pred. No. 0;   Indels   7;                         Db  1021  ATTGGCCTTATGATAATAATCCTCATAGAAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCAGT  1080
Matches  4756;   Conservative   4;   Mismatches   4;   Gaps   0;
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Qy  1011  ATGTCCACTGCATTAGGAGCGAGGAGTTTGGAGACAGAACCAGAACCTTCTACTGAAG  1070                       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||           Db  1081  CCTTTCTGTCACTGTACTTTTGTGATTGGTATTGGCACAGGTCATGCATTAGAAGATTTT  1140
Db   1    ATGTCCACTGCATTAGGAGCGAGGAGTTTGGAGACAGAACCAGAACCTTCTACTGAAG  60
                                                                                   Qy  2151  AATGAAGGTGCTCATTTGACTGCAGGCCCATATCCTCATTTTTTCCACTA  2210
Qy  1071  AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCTTTTTCTTTTCCACTA  1130                  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCTTTTTCTTTTCCACTA  120      Db  1141  AATGAAGGTGCTCATTTGACTGCAGGCCCATATCCTCAATTATTACAATT  1200
Qy  1131  TTTTTTTATTTTTTGGTTAATTAATTAGCATAGGATTCCAAATAATGAAGATGAAGAA  1190        Qy  2211  ATCATGTCCACACTTAATAGTAATTAGCATCCAAATAATAAGAAATATGAAGAA  2270
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Db  121   TTTTTTTATTTTTGGTTAATTAATTAGCATAGGATTCCAAATAATGAAGATGAAGAA  180         Db  1201  ATCATGTCCACACTTAATAGTAATTAGCATCCAAATAATAAGAAATATGAAGAA  1260
Qy  1191  GTGCCTAATATAGAACTCAATCCTCATGGACCAAGTTTACTCTTTCTAATCTTTCTTGA  1250       Qy  2271  ATTCCAGGGGAATTGGCTTACGGACGATCATCTTTATATTTTCTGAAGCCTTCATATTGG  2330
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Db  181   GTGCCTAATATAGAACTCAATCCTCATGGACCAAGTTTACTCTTTCTAATCTTTCTTGA  240         Db  1261  ATTCCAGGGGAATTGGCTTACGGACGATCATCTTTATATTTTCTGAAGCCTTCATATTGG  1320
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Qy 2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGTTAATGGAAATATTAGT 2460
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Db

Qy 3471 CAGAGCTTACTTATTCTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG 3530
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Qy 3651 TTGGTTCATCACTCTTTAAAAATGCTGTGTTCCCATCAAACTTGTTCCAGACTTATAT 3710
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Qy 3711 TTTCTAAAACCTGGAGACAAACCACATAAATACAAAACAAGCTGCTTCTTCAAAATTCT 3770
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Qy 3771 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTCACAGCCAGAACATAATGGTGACG 3830
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Qy 3891 CATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTCAACAGTACTATGGTTTATTCTTTA 3950
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Qy 3951 CCTATATTAGTGAATATCATTAGTAACTACTACTCTTATCTTACTACTACTCTTATCTTA 4010
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Qy 4011 ATCCAGATCTGAGTACCCCATTCTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCC 4070
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Qy 4131 ATGGAAAATGCAGAGAATCATCATAAGATCAAGATCAAACTTCAACTTAAACTTCAGGTCTT 4190
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Db 3121 ATGGAAAATGCAGAGAATCATCATAAGATCAAGATCAAACTTAYACTCAACTTAAACTTCAGGTCTT 3180

Qy 4191 TTGCCATCTGCATATTGGATTGGACAAGCTCGTTGATATCCCCTTATTTTTATCATT 4250
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Qy 4371 TATATTGCTTCTTCGCCAGCCGTTGNCTTGCAATAACTTCTTGGTCATTTATC 4430
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Qy 4491 ACAATTGCAACTATTCTTCATTATGCCTTTGTATCATCATTCCAATCATCCACTTCTA 4550
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Db

RESULT 11

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LOCUS       AF491842                5347 bp    mRNA      linear   ROD 25-FEB-2003
DEFINITION  Mus musculus ATP-binding cassette transporter sub-family A member 5
            (Abca5) mRNA, complete cds.
ACCESSION   AF491842
VERSION     AF491842.1  GI:2208247
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 5347)
  AUTHORS   Annilo,T., Chen,Z.Q., Shulenin,S. and Dean,M.
  TITLE     Evolutionary analysis of a cluster of ATP-binding cassette (ABC)
            genes
  JOURNAL   Mamm. Genome 14 (1), 7-20 (2003)
   MEDLINE   22419899
   PUBMED    12532264
REFERENCE   2  (bases 1 to 5347)
  AUTHORS   Annilo,T., Chen,Z.-Q., Shulenin,S. and Dean,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAR-2002) Laboratory of Genomic Diversity, National
            Cancer Institute, Frederick, MD 21702, USA
FEATURES             Location/Qualifiers
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ORIGIN

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Query Match      59.6%;  Score 3887;  DB 10;  Length 5347;
Best Local Similarity  85.0%;  Pred. No. 0;
Matches 4381;  Conservative  0;  Mismatches  751;  Indels  24;  Gaps  2;
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Right column:

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Qy  4051 ATATAGTTTTAAAAATTGAGCTGTATTTCAAGCAGCTTTGCTTGGAATCATTGTTACTG 4110
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Db  3250 ACATTGTTTTAAAAATTGAGCTATATTTTCAAGCAGCTTTGCTTGGAATCAT-GTTACTG 3309

Qy  4111 CAATGCCACCTACTTGCCATGGAAATGCAGAGAATCATCAGAGAATCAAAGCTTATACTC 4170
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Qy  4231 TCCCCTTATTTTTATCATTCTTATTTGATGCTAGGAAGCTTACTGGCATTTCATTATATG 4290
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Db  3430 TTTCCCTTGTTTTGTTTCTCGATTTGATTTGATGCTGGGAAGTTTATTTGCATTCATCATG 3489

Qy  4291 GATTATATTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTTGCCTTATTGGTTATGTTC 4350
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Qy  4351 CATCAGTTATTCTGTTCACTTATATTGCTTCTGTGGCAGCCGTTGCAATCACTACTGAAA 4410
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Db  3550 CCTCCGTCATTCTGTTCACGTACATAGCTTCGTTCACTTTCAAGAAAAATTTAAATACCA 3609

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Db  3610 AGGAATTTGGTCATTTATCTATTCTGTGGCAGCCGTGCTGGCTTGTGTGGCAATCACGGAAA 3669

Qy  4471 TAACTTTCTTTGATGGGATACACAATTGCAACTATTCTTCATTATGCCTTTGTATCATCA 4530
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Db  3670 CAACTTTCTTTCTGATTTGCTGATTTGTCTGATTTCTTCATTACACCTTCTGCATAGCCA 3729

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Qy  4711 GCAGATCAATAGAAAAGATCCCTTTTTCAGAAACCTTTCAAGCGAAGTCTAAAAATAGGA 4770
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Qy  5011 CAAAATGGTGCTGCGCAGTATTTTAGGAGATTAATTCCGTTGGTGTATATTGAACCAACTT 5070
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Qy  5131 AGTGTATGGGTTACTGTCCTCCAGATAAACCCTTTGTCGGGCCAGATACTACATTGCAGGAAC 5190
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Left column:

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Qy  2971 GGAATCTTTAAAATACAGAAAGCCAATCGGGTGACAGTGTTCAGTACTCATTCATG 3030
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Qy  3511 TGAGCACCATGAGCCTTTGGAAACAACAGAGTGTATACAATAGCAAAGTTCATTCTTTA 3570
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VERSION   AJ426052.2 GI:27368658
KEYWORDS   abca5 gene; ATP-binding cassette protein.
SOURCE   Rattus norvegicus (Norway rat)
   ORGANISM   Rattus norvegicus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
    Rattus.
REFERENCE   1
   AUTHORS   Petry,F., Kotthaus,A. and Hirsch-Ernst,K.I.
   TITLE   Cloning of human and rat ABCA5/Abca5 and detection of a human
    splice variant
   JOURNAL   Biochem. Biophys. Res. Commun. 300 (2), 343-350 (2003)
   MEDLINE   22392638
   PUBMED   12504089
REFERENCE   2 (bases 1 to 5170)
   AUTHORS   Petry,F.
   TITLE   Direct Submission
   JOURNAL   Submitted (19-DEC-2001) Petry F., Department of Toxicology,
    Georg-August-University Goettingen, Robert-Koch-Strasse 40, Lower
    Saxony, D-37075 Goettingen, GERMANY
REMARK   revised by author [27-AUG-2002]
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DEFINITION   Rattus norvegicus mRNA for Abca5 protein.
ACCESSION   AJ426052

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Best Local Similarity 85.2%; Pred. No. 0;
Matches 4384; Mismatches 736; Conservative 0; Indels 26; Gaps 4;

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Qy    991  AATAGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGA  1050
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Qy   1171  CAAATTAAGAGAAATATGAGCAAGAGTGCCTAATAAGAGAACTCAATCCATCAGT... 1230
Db    196  CAAATAAAGAAATATGAGCAAGAGTATCTGATATATAGAACTCAGCCCTATGGACAAAATCCATCC   255

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Qy   1291  AAGTGTCTACTGATCATCTACCTGATGTCATATTTACTGAAGAATATACAAATGAAAAAG  1350
Db    316  GAGTTTCTACCGATCATCTCCCGACGTTCTAGTTACTGAAGAATACGCCCAGTGAGGAGG   375

Qy   1351  AAATGTTAACATCCAGTCTCTCTAAGCCGAGCAACTTGTAGGTGTGGTTTCAAAGACT  1410
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Qy   1411  CCATGTCCTATGAACTTCGTTTTTTCCTGATATGATTCCAGTATCTTCATTTATTATATG  1470
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Qy   1711  ACTTTTTGGCAATTCATATCGTAGCAGAAAAAAAATAAAAGAAATTTTAAAGA  1770
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Qy   1771  TAATGGGACTTCATGATACTGCCCTTTGGCTTTTCCTGGGTTCTTCTATATACAAGTTAA  1830
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Qy   1831  TTTTTCTTATGTCCCTTATGGCAGTCATTGCCGTCATTGCAACGCGTCCTCCGTTATTCCCTCAAA  1890
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Qy   1891  GTAGCAGCATTGTGATATTTCTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTTG  1950
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Qy   1951  CTTTAATGCTGACACCTCTTTTAAAAATCAAAAATCATGGGAATAGTTGAATTTTG  2010
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Qy   3091  TTGGTTCTCAATGTTCCTCAAATCCTCATAGAAAGTTTCCCAAAT  3150
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Qy   3151  TAGACAAATATTGTGCCACAGAATCTCTTTCCTTCACTGGTTAAACAACATACCTGGAG  3210
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us-10-005-338b-1.rge

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         (E-mail:kubo37@sanken.osaka-u.ac.jp, Tel:81-06-6879-8546,
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ORIGIN

Query Match   59.3%; Score 3868.8; DB 10; Length 4929;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 4266; Conservative 0; Mismatches 663; Indels 0; Gaps 0;

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RESULT 13
AB097675
LOCUS   AB097675 4929 bp mRNA linear ROD 01-APR-2003
DEFINITION Mus musculus abca5 mRNA for ABC transporter subfamily A mABCA5,
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ACCESSION   AB097675
VERSION   AB097675.1 GI:29420876
KEYWORDS   .
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Kubo,Y., Satsuma,Y., Sekiya,S., Nada,S. and Yamaguchi,A.
  TITLE   Molecular cloning of mABCA5, the mouse homologue of ABCA5
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 4929)
  AUTHORS   Kubo,Y., Satsuma,Y., Sekiya,S., Nada,S. and Yamaguchi,A.
  TITLE   Direct Submission

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Qy  1911 CTGCTTTTTTCCTTTATGGATTATCATCGTATTTTTGGTTAATGCTGACCACCTCTT 1970
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Db  1971 TTTAAAAATCAAAACATGTGGAATAGTTGAATTTTTGTACTGTGGCTTTTGGATTTT 2030
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Db  1021 GTTGGCCTGCTGCTTAATGTCCTCATAGAAAGTTCCCCAGGTCGCGGTGTGTGGCTTTCAGT 1080

Db  2091 CCTTTCCGTCACTGTACTTTTGTGATTGGTATTGGCACACAGTGTCATGCATTAGAAGATTT 2150
              |||||||||||| |||||| ||||||||||| ||||||||||||| ||||||| |||||
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Db 4551 AAGAGTAAGTTTTGGTAAAGGGCTACTTTTTGGAAATTAAATTAAAGGACTGGGATAGAAAAC 4620

Qy 5631 CTAGAAGTAGACCGGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAG 5690

Qy 3471 CAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCCACCATGAGCGCCTTTGG 3530
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Db 2881 GGTTCTGAAAAAGGAGGACTATGTTTTTCTGCTGTTTTCAACAGTACTATGGTTATTGTTTG 2940

Qy 3951 CCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCATTAAATGTGACTGAAACC 4010
         ||||||||||||||||| |||||| ||||||||| |||||||||||||||||||||||
Db 2941 CCAGTCATGATGACAGCTTTGCTTGGAATCAAAGCTATATGATGCAATGTGCGAAGCC 3000

Qy 4011 ATCCAGATCTGGAGTACCCCATTCTTTCAAGAAGAAAATTAGTTTTAAAAATTGAG 4070
         |||||| |||||||||||||| |||||||||||||||||||| ||||||||||||
Db 3001 ATCCAGATCTGGAGTACCCCGTTCATTCAAGAGATCAAGAAATTACTTGTTTTAAAAATTGAG 3060

Qy 4071 CTGTATTTTCAAGCAGCTTGCTTGGAATCATTGGATTGTACTGCAATGCCACCTTACTTTGCC 4130
         |||||||||||||||||||| ||||||||||||| ||||||||| |||||||||||||||||
Db 3061 CTATATTTTCAAGCAGCTTGCTTGGAATCATTGGATATTACTGCAATGCCACCTTACTTTGCC 3120

Qy 4131 ATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATACTCAACTTTCAGGTTCTT 4190
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Db 3121 ATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATCAATGCATGATGTTATCAACTTGTTCGGGTTT 3180

Qy 4191 TTGCCATCTGCATATTGGATTGACAAGCTGTTGTTGATAATCCCCTATTTTTTATCATT 4250
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Db 3181 TTGCCATCCATTGGGTTGGACAAGCTGTTTGCCTTGGGATATTTCCCTTGTTTTTTTGTT 3240

Qy 4251 CTTATTTGATGCTAGGGAAGCTTACTCTGGCATTTCATTATGGATTATATTTTTATACTGTA 4310
         ||||||| ||||||| ||||||| |||| ||||| || || ||||| ||||||| ||||||
Db 3241 TATTCCGTGACCGGCATTGGCTTGTGTGGCAATCATCATGGAAAACACTTTTATCCTGCA 3300

Qy 4311 AAGTTCCTTGCTGTGTGGTTTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTCGTTCACT 4370
         ||||||||| ||| ||||||||| ||||| ||||| ||||| | |||||||||| ||||||
Db 3301 AAATTTCTGCTGTGTGTTTTTTGGCCTTATTGTTTTGTGCCCATCGTCATCTCGTTCACG 3360

Qy 4371 TATATTGCTTCTTTGTTTCACCTTTAAGAAAATTTAAATACCAAAGAAATTTGGTCATTATC 4430
         || | || ||||| ||| ||||||||||||||| |||||| |||||||||||||||||||
Db 3361 TACATAGCTTCGTTCACTTCTTTGTTTCACCTTTAAATACCAAGGAAATTTGGTCATTATC 3420

Qy 4431 TATTCTGTGCAGCGTTGNCTTGCAATCACTGAAATAAACTTTCTTTATGGGATAC 4490
         |||| |||| ||||||||| ||||||||||||||||||||| ||||||||||||
Db 3421 TATTCCGTGACCGGCATTGGCTTGTGTGGCAATCACTGAAACCCTTCTGCAATAT 3480

Qy 4491 ACAATTGCAACTATTCTTCATTATGCCTTTGTATCATTCCAATCATCCACTTCTA 4550
         ||| |||||||||||||||| || ||||||||||||||||||| ||||| ||||
Db 3481 GCAGTTACGGCGTGTTCTTTCATTACACCTTCTGCGATAGCCATTCCAATCCTACCCTCTCTG 3540

Qy 3481 ...

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ORIGIN

Query Match          58.5%;   Score 3816.2;   DB 10;   Length 4945;
Best Local Similarity 85.9%;   Pred. No. 0;
Matches 4249;   Conservative 0;   Mismatches 679;   Indels 16;   Gaps 1;
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Qy   1004  AGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGACACAGACCAGAACACTTCT  1063
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Db      2  AGAAAACATGGCTACTGCAATTAGGGAGGTGGGCGTTTGGACACAGACCAGAACACTTCT    61

Qy   1064  ACTGAAGAATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCTTTT  1123
                 ||||||| ||| |||||| ||||||| ||||||||||||||||||||||||||||||
Db     62  TCTGAAGAATTACCTCGTCAAATGCAGGACTAAAAAGAGTAGTGTTCAGGAAATTCTTTT   121

Qy   1124  TCCACTATTTTTTTATTTTGGTTAATATTAAATTAGCATGATGCATCAAATAAGAAATA  1183
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Db    122  TCCTCTATTTTTCTTATTTTGGCTAATATTAAATTAGCATGATGCATCAAATAAGAAATA   181

Qy   1184  TGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTACTCTTTTCCAACCTAAT  1243
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Db    182  TGAAGAAGTATCTGATATAGAACTCAGCCCTATGGACAAATCCATGTTCATGTCCTTAT   241

Qy   1244  TCTTGGATATACTCCAGTGACTAATATTACAAGCAGCATAATATTACAAGTGTCTACTGA  1303
                 | ||||  ||| ||||||||| ||| ||||||||||| ||| |||||||||||||||
Db    242  CCTGGGGTACACTCCAGTGACTAATACTACAAGCAGCGTCATGCAGAGTTTCTACCGA   301

Qy   1304  TCATCTACCTGATGTCATAATTACTGGAGATTACACAAATGAAAAGAAAAGTTAACATC  1363
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Db    302  TCATCTTCCCGACGTTCTAGTTCTGAAGAATACCGCAGTGAAGAGGAGCTGCTGGCATC   361

Qy   1364  CAGTCTCTAAGCCGAGCAACTTGTAGGTGGTTTCAAAGACTCCATGTCCATGA  1423
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Db    362  CAGTTTGTGCTAAGCCCAGCAACTTCGTCGGGTGTGGTTTTCAAAGACGTCATGTCCTTGA   421

Qy   1424  ACTTCGTTTTTTCCTGATATGATTCCAGTATCTTCATTTATATGGATTCAAGAGCTGG  1483
                 |||| | ||||||||||| || ||||||  |||||||||||  |||||||||||||||
Db    422  ACTGCGGTTTTTTTCCTGATATGGTTCCAGTGTCTTCTTCGTTTATATGGATTCAAGAGCAGG   481

Qy   1484  CTGTTCAAAATCATGTGAGGCTGCTCAGTACTGCCTCAGTTTCACAGTTTACAAGC  1543
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Db    482  CTGTTCAAAGTCATGTGATGCGTCAGTACTGCTCAGTACTGCCTCAGTTTACAGGC   541

Qy   1544  ATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGAAGGAGTGGA  1603
                 || |||||||||||||||||| |||||||| |||||||||||||||||||||||||||
Db    542  CTCAATAGATGCTGCCATTATACAGTTGAAGACCAATGTTCTTCTGTGGGAGGGAGTGGA   601

Qy   1604  GTCAACTAAAGCTGTTATTATGGGAGAACTGCTGTTGTGAGAAATAGATACCTTTCCCCG  1663
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Db    602  GTCAACCAAAGCTGTCATCATGGGAGAAGCTGCGGTCGTGAGATTGACACCTTCCCACG   661

Qy   1664  AGGAGTAATTTAATATCCAGTTATAGCAGTTCACCTTTTTGGCAAT  1723
                 |||| ||||| |||||||||| | |||||||||||||||||||||||
Db    662  AGGGGTCATCCTCATCCGTCATAGCCTCATAGCCTCCGGGTACTTTCTGCAAT   721

Qy   1724  TCATATCGTAGCAGAAAAAGAAAAGAAAAATAAAGATAATTTAAAGATAATGGACTTCA  1783
                 |||| || |||| |||||| |||||| ||||||||| |||||||||||||||||||||||
Db    722  TCACTTGTAGCAGAAAGAGAAAAGAAAGAGAGTTAAAGAGTTTAAAGATAATGGACTTCA   781

Qy   1784  TGATACTGCCTTTGGCTTCCTCGGGTTCTCTATACAAGTTTAATTTTCTTATGTC  1843
                 ||| ||||| ||||||| |||||| |||||| ||| || |||||||||||||||||
Db    782  CGACACTGCTTTTTGGGCTGTCCGGGTTCTTCTGTACCAGAGTTTGATCTTCCTTATGTC   841

Qy   1844  CCTTCTTATGGCAGTCATTGCCGACAGCTTCTTTTGTGTTATTTCCTCAAAGTAGCAGCATTGT  1903
                 ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   4621  CTGGAAATAGATGCCTTCAAAGAGGAAATTCAATATATTTCCCAAATGCAAGCAGCCGGCCAA  4680
                 |||| ||| |||||||||||||||||| ||||||||||||||||||||||||||||||
Qy   5691  GAAAGTTTTTCTTCTATTTGGCTTATAAAAATTCCTAAGGAAGATGTTCAGTCCCTTCA  5750
                 ||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   4681  GAGAGCTTTTTCTTCTTCCTTATTTGGCTTTTAAAATTCCAAAGAGAGATGTTCAGTCTCTCTCA  4740
Qy   5751  CAATCTTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTGAAGAAATATAGCTTT  5810
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Db   4741  CAATCCTTCGCTAGTTGAAGAAGAAGCAAAACGCACTTTTGCCATTGAAGAAGAATACAGCTTT  4800
Qy   5811  TCTCAAGCAACATTGGAACAGGTTTTTGTAGAACTCACTAAAGAACAAGAGGAAGGAGAT  5870
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Db   4801  TCTCAAGCAACCCCTGGAACAGGTTTTGTGAGAACTTACTAACAGAGCAAGAGGAAGAAGAT  4860
Qy   5871  AATAGTTGTGGAACTTAAACAGCACACTTGGTGGGAACGAACAGACACAGAAGATAGAGTA  5930
                 |||||| |||||||||||||||| ||||||||||||| ||| |||||||| |||||||||
Db   4861  AACAGCTGTGGGACTTTGGCCAGCACTCTCTGTGTGGGAAAGGACGAGGAGGAGGAGATAGAGTA  4920
Qy   5931  GTATTTTGA  5939
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Db   4921  GTATTTTGA  4929
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RESULT 14
RNO550165
LOCUS       RNO550165            4945 bp    mRNA      linear   ROD 24-MAR-2003
DEFINITION  Rattus norvegicus mRNA for ATP-binding cassette protein 5 (Abca5
            gene), splice variant V+16.
ACCESSION   AJ550165
VERSION     AJ550165.1  GI:29170395
KEYWORDS    Abca5 gene; alternative splicing; ATP-binding cassette protein 5.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Petry,F. and Hirsch-Ernst,K.I.
  TITLE     Identification of novel highly conserved splice variants of rat
            Abca5
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 4945)
  AUTHORS   Petry,F.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAR-2003) Petry F., Toxicology, University of
            Goettingen, Robert-Koch-Strasse 40, Goettingen, Lower Saxony,
            D-37075, GERMANY
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                     /tissue_type="testis"
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                     /gene="Abca5"
     CDS             9..2786
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                     /note="splice variant V+16"
                     /codon_start=1
                     /evidence=experimental
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                     /db_xref="GI:29170396"
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            KSCDAAQVMSGFTALQASIDAIIQLKTNVSLWRELESTKAVIMGEAAVVEIDTFPR
            GVILIYLJVIAFSPFGYFLAIHIVAEKERLKEFLKIMGLHDTAFWLSWVLLYTSLIFL
            MSLLMAVIATASSLFFPQSSSIVIFLLFFLYGLSSVFFALMLIPLFKKSKHVGVVEFFV
            TVFGFVGLLIVLVESFPRSLVWLFSPLCQCAFLIGIAQVMHLEDFNEGALFSSLITEG
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Db    842  CCTTCTTATGCCGTCATTGCAACAGCGTCCTCGTTATTCCCTCAGAGTAGCAGCAGCATCGT  901
Qy   1904  GATATTTCTGCTTTTTCCTTTATGCGGATTATCATCGTATTTTTGCTTTAATGCTGAC 1963
           || ||||||||||||||
Db    902  GATTTTTCTGCTTTTCCTCCTGCTACGGATTGTCATCGTGTTTTTGCTTTAATGTTGAC  961

Qy   1964  ACCTCTTTTTAAAAAATCAAAACATGTGGGAATGTGGGAGTCGTTGAGTTTTTGTTACTGTGGCTTT 2023
Db    962  GCCTCTTTTTAAAAAATCAAAGCACGTGGGAGTCGTTGAGTTTTTGTTCACCGTGTGTT 1021

Db   1022  TGGATTTATTGGCCTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTAGTGGCT 1081
Qy   2024  TGGATTTATTGGCCCTGTTGATAGTCCTCGTAGAAAGTTTCCCCAGGTCGCTAGTAGTGGCT 2083

Qy   2084  TTTCAGTGCCTTTCTGTCACTGTACTTTTGTGATTGTATTGCACAGGTCATGCATTTAGA 2143
Db   1082  CTTCAGTCCTTTGTGTCAGTGCGCCTTTCTGATTGGGATTGCACAGTGTCATGCATTTAGA 1141

Db   1142  AGATTTTAAATGAAGAGGTGCTTCACACTTAATAGTATATTCTATGTCCCTCTTGGCGTGTCTATCTTGA 2203
Qy   2144  AGATTTTAAATGAAGAGAGCCCTTATTTTCTAGTTTGACTGAAGGCCCCATTACCTCTAATTAT 2203

Qy   2204  TACAATTATCATGTCCACACTTAATATGCAGTGTATTCTATGTCCCTTGGCGTGTCTATCTTGA 2263
Db   1202  CACCCTTACCAGTCTCGCTCGCTCTGACAGTGTGTTCATGCGTCGGTGTGTACCTTGA 1261

Db   1262  TCAAGTCATTCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTC 2323
Qy   2264  TCAGGTCATCCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTCTGAAGCCTTC 2323

Qy   2324  ATATTGGTCAAAAGTACATTGATGAAATTCTTGTGTGGACTGCTGCCCACCTTCTGATGGGTTTGC 2383
Db   1322  ATATTGGTCAAAAGAACAAAGGAACTATAAGGAGCTATACAGAGGGGCAACATCAATGGCAA 1381

Db   1382  TATTAGTTTTAGTGAATGAAATTGTTGAGCCCGTTTCTTCAGAATTTATAGGAAAAGAAGCTAT 2443
Qy   2384  TATTAGTTCAATGAAATTGTTGAGCCCGTTTCTTCAGAATTTATAGGAAAAGAAGCTAT 2443

Qy   2444  AAGAATTAGTGTATTCAGAAGACATACAGAAGAAGGGTGAAAAATGTGGAGGCTTTGAG 2503
Db   1442  AAGAATAAGTGTATTCAGAAGACAGAGTCTCAGAAGAAGAAGAAGACCGTGGAGGCTTTGAG 1501

Db   1502  AAATTTGTCATTTGACATATATGAGGGTCAGATTACTTGCCTTACTTGCTCTGCTGGGCTCGGGAAC 2563
Qy   2504  AAATTTGTCATTTGACATATATGAGGGTCAGATTACTTGCCTTACTTGCTCTGCTGGGCTCGGGAAC 2563

Qy   2554  AGGAAAAGTACATTGATGAAATTCTTGTGTGGACTCTGCCCACCTTCTGATGGGTTTGC 2623
Db   1562  AGGAAAAAGCACAACTAAATGAATAATTCTGTGTGCCCCACCTTCTGATGGGTTTGC 1621

Db   1622  TTCTATATATGGACACACAGAGTCTCTGAAATATGAACTTGATGTTTGACAGTGCGAGAGAAATTTATC 2743
Qy   2624  ATCTATATATGGACACACAGAGTCTCTGAAATAGTGAACGAAGAAATTGAT 2683

Qy   2684  TGGCATTTGTCCAGCTTAGATATATGTCTTGTTCTTGGGAACTACAGAAGTGCAGAGGT 2803
Db   1682  TGGCATATGTCCAGCTTAGATATAGAAAGTTGACTGAGAAGAAAAAAATTTATC 1741

Db   1742  AATTTTGGCTTCAATCAAAGGGATACCAGCCAACAATAATAAATTCAGGAAGTACAGAAAGT 2803
Qy   2744  TCAAAAAGAGAAAGCTGTCAATCAAAGGGATACCAGCCAACAATAATAAATAACCTAAGTGGTGG 2803

Qy   2804  TTTTACTAGATTTAGACATGCAAGCCATCAAAGATAACCAAGCTAAAAAAATTAAGTGGTGG 2863
Db   1802  TTTTACTGGATTTGGACATGCAAGCCATCAAAGAAGCTAAAAAAATTAAGTGGTGG 1861

Db   1862  TCAAAAAGAGAAAGCTGTCAATCAAAGGGATACCAGCCAACAATAATAAATTCAGGAAGT 1921
Qy   2864  CCAAAAGAGAAAGCTGTCTTTAGGAATTCTTGGGAATCCAGAATCCTCCTGCT 2923

Qy   2924  AGATGAACCAACAGCTGAAATGGGAAATGGCACAGCCGACACCCCCGCTCCGCCACCATGTTTGCTT 2983
Db   1922  AGATGAGCCGACAGCCAGCAGAATGGACAGTAGGAATGGCACCCCCGCTCCGCCACCATGTTTGGAATTTCTCCA 1981
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Qy   2984  ATACAGAAAGCCAATCGGGTGACAGTGTTCAGTACTCATTCATGGATGAAGCTGACAT 3043
Db   1982  GTACAGGAGGCTAACCGAGTGACCAGTGCTCCAGCAGTCCTCAGCGATGAGGCCGACAT 2041

Db   3044  TCTTGCAGATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTGGTTCTTCAAT 3103
Qy   2042  TCTTGCCGACGAGAAGCTCTCATATCACAAGGAATGCTGAAATGTGTTGGTTCTTCAAT 2101

Qy   3104  GTTCCTCAAAAGTAAATGGGGGGATCGGCTACCGCGTCTGAGCGCTGAGCATCGACAGAACAAATATTG 3163
Db   2102  TTTCCTGAAAAGTAAATGGGGGAATCGGCTACCGTCTGAGCATGCATCGACAGCAGGTACTG 2161

Db   3164  TGCCACAGAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACA 3223
Qy   2162  TGCCACAGAGTCGCTCTGCGCTGTGTTAGCACAGTCCTCCTGCTGC 2221

Qy   3224  ACAGAATGACCAACAACTGTGTATGCAGTCATCAAATTGGGTGTCATTCTATGTGTTTCCAT 3283
Db   2222  GCAGAATGACCAGCAGATTGTCATAGCTTGCCCTTCAAAGACATGACAAATTTTCAGG 2281

Db   3284  TTTGTTTTCTGCCCTAGACAGTCATTCAAATTCTATGTCCCTTGGCGTGTCTTTCCAT 3343
Qy   2282  CTTGTTTTCTGCTCTAGACATTCATTCATTCAAAGCGGGTGTAATTTCTTATGTGTTTTCCAT 2341

Qy   3344  GACGACTTTGGAAGACGTATTTTAAAGCTAGAGTGAAGCAGAAATCTTTTGATGA 3403
Db   2342  GACGACATTGGAAGACGTGTTTTAAAGCTAGAGTGAAGCAGAAATTGACCAAGCAGA 2401

Db   3404  TTATAGTGTATTTACTCAGCAGCCACTGGAGGAGGGCAATGTTGGGAGTGGAGCAGAAATCTTTTGATGA 3463
Qy   2402  TTATAGTGTATTTACCCAGCAGCCACGGGAGGAGGGAGAAACAGATTCAAAGTCTTTTGATGA 2461

Qy   3464  AATGGAACAAGAGATTCTTACTTATTCTTGAAACCAAGTTCATTCTTTCATTTCTCATGAG 3523
Db   2462  AATGGAACAAGAGTTACTTATTCTTGAAACCAAGTTCATTCTTTCATTCTCTCGAGAG 2521

Db   3524  CCTTTGGAAACAACAGATGTATACAGATAGACAATAGCAAAGTTCATTTCTTCATTTCTCCTCACTGAACGTGA 3583
Qy   2522  TCTCTGGAAGCAGCAAGTATCTCACAATATGCACAATAGCAAAGTTTCATTTCCCTCACTGAAGCGAGA 2581

Qy   3584  AAGTAAATCAGTGAGATCAGTGTCGTTGCTTCAGTTGTGTTTAATTTTTTCACAGTTCAGATTTT 3643
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Db   3644  TATGTTTTTGGTTCATCACTCTTTAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGA 3703
Qy   2642  TATGTTTTTTGGTCCATCATTCTTTTAAAATGTGTGGTTCCCATCAAGCTGTGGTTCCAGA 2701

Qy   3704  CTTTATATTTTCTAAAACCTGGAGACAAAACCACCATCAAAAACAAGTCTGCTTCCTTCA 3763
Db   2702  CCTTGTATTTTCTAAAACCTGGAGATAAACCTCATAAATAACAAAACAAGCCTGCTGCTTCA 2761

Qy   3764  AAATTCTGCT----------GACTCAGATATCAGTGATCTTATTAGTCTTTTCA 3807
Db   2762  AAATTCTACTGGTACGGCGTGTGAAGACTTCGAGATTATCAATGATCTTATTATTGACTTTTTCA 2821

Db   3808  CAAGCCAGAACATAATGTACGATGATTAATGACAGTGACTATGTTTTTGAGCTCCC 3867
Qy   2822  CACAGCCAGAACATAATTAATGTTTAAATGACAGTGACTAGTGTGTCTGCTCCTC 2881

Qy   3868  ATAGTGTGCGGCTTTAAATGTGATGCAGTTGCAGTTCTTAAAAAATTAAGTGGTGG 3927
Db   2882  ATAGTGCGGCTCTCAATGTGGTGCAGTCAGTGCGAGAAAGGACTATGTTTTTTACTGTGTTTTCA 2941

Qy   3928  ACAGTACATGGTTTATTCTTTACCTATATCATTAGTAACTACTATCTTT 3987
Db   2942  ACAGTACTATGGTTTATTCTTTGCCAGTAATGATAACATACTACTAGTACTACTATCTCT 3001

Db   3988  ATCATTTAAATGTGACTGACTGACTACACTCATCCAGATCTGAGTACCCCGTTCATTCAAGAAATTA 4047
Qy   3002  ATCATTTAAAATGTGACTGACTACACTCATCCAGATCTGAGTACCCCGTTCATTCAGGAAATTA 3061
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Qy   4048 CTGATATAGTTTTAAAATTGAGCTGTATTTCAAGCAGCTTGCTTGGAATCATTGTTA 4107
          |||| ||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3062 CTGACATTGTTTTAAAGTTGAGCTATATTTCAAGCAGCTTGCTTGGAATCATTGTTA 3121

Qy   4108 CTGCAATGCCACCTTACTTTGCCATGGAAATGCAGAGAATCATAAGATCAAAGCTTATA 4167
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Qy   4168 CTCAACTAAAACTTTCAGTGTCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTG 4227
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Db   3182 CTCAGCTTAAACTTTCAGTGTCTTTTGCCATCCGCCTACTGGATTGGACAGGCTGTGGTGG 3241

Qy   4228 ATATCCCCTATTTTATCATTCTTATTTGATGCTAGGAAGCTTACTGCGCATTCATT 4287
          | ||||||| || |||| |||||||||||||||||||||||||||||||||||||||
Db   3242 ACATTCCCCTGTTTTTGTTTGTCGACTTGATGCTGGGAAGTTTATTTGCCTTTCATC 3301

Qy   4288 ATGGATTATATTTTTATACTGTAAAGTTCCTTGCTGTGTTTTTGCCTTATTGGTTATG 4347
          |||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||
Db   3302 ACGGACTGTATTTTTATCCTGTAAAGTTCTTGCTGTGTTTTTGCCTCATTGCTTATG 3361

Qy   4348 TTCCATCAGTTATTCTGTTCATTATAATTGCTTCTTCTCACCTTTAAGAAAATTTAAATA 4407
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3362 TGCCCTCGGTTATTCTGTTCATTATATAGCTTCGTTCTTCACCTTTAAGAAAATTTAAATA 3421

Qy   4408 CCAAAGAATTTGGTCATTTATCCATTCTCGTGGCAGCGTTGNCTTGTGATTGCAATCACTG 4467
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3422 CCAAGGAATTTGGTCATTTATCCATTCTGTGCAGCATTGGCTTGCCTTGTGTCCGCAGTCACGG 3481

Qy   4468 AAATAACTTTCTTTATGGGATACACAAATTGCACAATTGCTTCTTCATTATGCCTTTGTATCA 4527
          |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   3482 AAATAACTTTCTTTTCTCGGGTATGGCAGTGTTTTCATTACCTTTCTGCATAG 3541

Qy   4528 TCATTCCAATCTATCCACTTCTAGGTTGCCTGATTTTCTGATTTCATAAAGATTTCTTGGAAGA 4587
          |||||||||||||||||||| ||  ||||||||||||||||||||||||||||||||||||||
Db   3542 CCATCCCAATCTACCCGCTCGGTTGCGCCTGATTTTCTCGATTTCATAAAGATAAATTCAATATA 3601

Qy   4588 ATGTACGAAAAATGGACACCTATAATCCATGGACAGAGCTTCAGTAGCTGTTATAT 4647
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DEFINITION Homo sapiens mRNA; cDNA DKFZp686K07118 (from clone DKFZp686K07118).
ACCESSION   BX640746
VERSION   BX640746.1 GI:34364843
KEYWORDS   .
SOURCE   Homo sapiens (human)
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REFERENCE   1 (bases 1 to 4078)
  AUTHORS   Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  CONSRTM   The German Human cDNA Consortium
  TITLE   Direct Submission

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JOURNAL    Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
           Neuherberg, GERMANY
COMMENT    Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
           Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
           sequenced by DKFZ (German Cancer Research Center,
           Heidelberg/Germany) within the cDNA sequencing consortium of the
           German Genome Project.
           This clone (DKFZp686K07118) is available at the RZPD in Berlin.
           Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
           Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
           information about the clone and the sequencing project is available
           at http://mips.gsf.de/proj/cDNA/.
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ORIGIN
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Matches 4013;     Conservative    0;     Mismatches     5;   Indels  169;   Gaps    3;
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Qy   1998 GTTGAATTTTTGTTACTGTGGCTTTGGCTTTCAGTCCTTATTGGCCTTATGATAATCCTCATAGAA 2057
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Qy   2058 AGTTTCCCAAATCGTTAGTGTGGCTTTTCAGTCCTTTCTGTCACTGTACTTTTGTGATT 2117
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Qy   2118 GGTATTGCACAGGTCATCGCATTAGAAGATTTAAATGAAGGTGCTTCATTTTCAAAATTG 2177
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Qy   3705 TTATATTTTCTAAAACCTGGAGACAAACCACATAAAATACAAAAACAAGTCTGCTTCTTCAA 3764
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 TTATATTTTCTAAAACCTGGAGACAAACCACATAAAATACAAAAACAAGTCTGCTTCTTCAA 1800

Qy   3765 AATTCTGCT--------GACTCAGATATCAGTGATCTTATTAGCTTTTTCAC 3808
          ||||||||||        |||||||||||||||||||||||||||||||||
Db   1801 AATTCTGCTGGTGGTGAGAGTGACTCAGATATCAGTGATCTTATTAGCTTTTTCAC 1860

Qy   3809 AAGCCAGAACATAATGGTGACGATGATTAATGACAGTGATCTCGGTGGCTCCCCA 3868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AAGCCAGAACATAATGGTGACGATGATTAATGACAGTGATCTCGGTGGCTCCCCA 1920

Qy   3869 TAGTGCGGCTTAAAATGTGATGCATTCAGAAAAGGACTATGTTTTGCAGCTGTTTTCAA 3928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TAGTGCGGCTTAAAATGTGATGCATTCAGAAAAGGACTATGTTTTGCAGCTGTTTTCAA 1980

Qy   3929 CAGTACTATGGTTTATTCTTTACCTATATTAGTGAATATCATTAGTAACTACTACATCTTTA 3988
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Db   1981 CAGTACTATGGTTTATTCTTTACCTATATTAGTGAATATCATTAGTAACTACTACATCTTTA 2040

Qy   3989 TCATTTAAATGTGACTGAAACCATCCAGATCTGAGTCGTACCCCATTCTTTCAAGAAAATTAC 4048
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Db   2041 TCATTTAAATGTGACTGAAACCATCCAGATCTGAGTCGTACCCCATTCTTTCAAGAAAATTAC 2100

Qy   4049 TGATATAGTTTTTAAAAATGAGCTGTATTTTCAAGCAGTTTGCTTGGAATCATTGTTAC 4108
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Qy   4109 TGCAATGCCACCTTGCTTGCCATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATAC 4168
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Db   2161 TGCAATGCCACCTTGCTTGCCATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATAC 2220

Qy   4169 TCAACTTAAACTTTCAGGTTCTTCAGGTTCTATATTGCCATCGTGATATTGGATTGGACAAGCTGTTGTTGA 4228
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCAACTTAAACTTTCAGGTTCTTCAGGTTCTATATTGCCATCGTGATATTGGATTGGACAAGCTGTTGTTGA 2280

Qy   4229 TATCCCCTATTTTTATCATTCTTATTTTGATGCTGGAAGCTTACTGCGATTCATTA 4288
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Db   2281 TATCCCCTATTTTTATCATTCTTATTTTGATGCTGGAAGCTTACTGCGATTTCATTA 2340

Qy   4289 TGGATTATATTTTTATATACTGTAAAGTTCCTTGGTGGTTTTTTTGCCTTATTGGTTATGT 4348
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Db   2341 TGGATTATATTTTTATATACTGTAAAGTTCCTTGGTGGTTTTTTTGCCTTATTGGTTATGT 2400

Qy   4349 TCCATCAGTTATTCTGTTCACTTATATTGCTTCTTCACCTTTAAGAAAATTTAAAATAC 4408
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Db   2401 TCCATCAGTTATTCTGTTCACTTATATTGCTTCTTCACCTTTAAGAAAATTTAAAATAC 2460

Qy   4409 CAAAGAATTTTGGTCATTCATTATCATTCTGTGGCAGCCGTTGNCCATTGGCTTGCAATCACTGA 4468
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CAAAGAATTTTGGTCATTCATTATCATTCTGTGGCAGCCGTTGGCTTGCAATCACTGA 2520
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Db   3481  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
           TATCGGAACAGTACAACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTTGGAAATTAA  3540

Qy   5609  ATTGAAGGACTGGATAGAAACCTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATAT  5668
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Db   3541  ATTGAAGGACTGGATAGAAAACCTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATAT  3600

Qy   5669  TTTCCCAAATGCAAGCCGTCAGGAAAGTTTTCTTCTATTTGGCTTATAAAATTCCTAA  5728
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Db   3601  TTTCCCAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTGGCTTATAAAATTCCTAA  3660

Qy   5729  GGAAGATGTTCAGTCCCTTCACAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTT  5788
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Db   3661  GGAAGATGTTCAGTCCCTTTCACAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTT  3720

Qy   5789  TGCCATTGAAGAATATAGCTTTTCTCAAGCAACATGGAACAGGTTTTTGTAGAACTCAC  5848
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Db   3721  TGCCATTGAAGAATATAGCTTTTCTCAAGCAACATGGAACAGGTTTTTGTAGAACTCAC  3780

Qy   5849  TAAAGAACAAGAGGAGGAAGATAAATAGTTGTGAACTTAAACAGCACACTTTGGTGGGA  5908
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Db   3781  TAAAGAACAAGAGGAGGAAGATAATAGTTGTGAACTTAAACAGCACACTTTGGTGGGA  3840

Qy   5909  ACGAACACAAGAAGATAGAGTATTTGAATTTGTATTGTTCGGTCTGCTTACTGGGA  5968
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   5969  CTTCTTTCTTTTCACTTAATTTAACTTGGTTTAAAAAGTTTTTATTGGAATGGTAA  6028
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Qy   6029  CTGGAGACCAAGAACGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTCGTT  6088
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Qy   6089  GTGTGTTTTGCTTTTCTTTAAATAAAACGTATGTATAATTAAGTGAA  6135
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Db   4021  GTGTGTTTTGCTTTTCTTTAAATAAAACGTATGTATAATTAAAAAAA  4067
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Search completed: December 4, 2004, 14:34:47
Job time : 26285 secs

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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:       December  4, 2004, 04:56:06 ; Search time 2739 Seconds
                                         (without alignments)
                              12505.466 Million cell updates/sec

Title:           US-10-005-338B-1
Perfect score:   6525
Sequence:        1 aaaatgttgatattttcct.........ttgatcataataagtgaaat 6525

Scoring table:   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:        4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters:      8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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         3:   geneseqn2000s:*
         4:   geneseqn2001as:*
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         7:   geneseqn2002bs:*
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         9:   geneseqn2003bs:*
        10:   geneseqn2003cs:*
        11:   geneseqn2003ds:*
        12:   geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                    SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	6524	100.0	6525	6	ABN89594	Abn89594 Human ATP
2	6524	100.0	6525	12	ADN06076	Adn06076 Antipsori
3	6122.8	93.8	6369	6	AAD33648	Aad33648 Human TRI
4	5708.8	87.5	6170	12	ADH22577	Adh22577 cDNA enco
5	5373.2	82.3	5475	10	ABS57751	Abs57751 cDNA enco
6	5255.8	80.5	5463	10	ABS57749	Abs57749 cDNA enco
7	5247.4	80.4	5262	6	AAD37620	Aad37620 Human tra
8	4918.4	75.4	4929	10	AAD37618	Aad37618 Human tra
9	4807.4	73.7	4917	10	ABS57750	Abs57750 Coding se
10	4754.8	72.9	4785	6	AAD37619	Aad37619 Human tra
11	3258.2	49.9	3347	11	ADM01475	Adm01475 Human cDN
12	3178	48.7	3268	10	ADA53416	Ada53416 Human cod
13	2934.4	45.0	3950	10	ADF74739	Adf74739 Murine dn
14	2807	43.0	3831	10	ADF74738	Adf74738 Murine dn
15	2683.8	41.1	2723	10	ADC51606	Adc51606 Human mac
16	2378.8	36.5	2481	8	ABZ35938	Abz35938 Human sec
17	1809.4	27.7	2325	10	ADF81819	Adf81819 Leukaemia
18	1789.4	27.4	3928	6	ABK35707	Abk35707 cDNA sequ
19	1731.8	26.5	1943	11	ADM02739	Adm02739 Human cDN
20	1722.8	26.4	1818	5	AAS63176	Aas63176 Human pur
21	1543.8	23.7	1548	6	ABK35706	Abk35706 cDNA sequ
22			1319	20.2	1506	3 AAC81717 Aac81717 Human sec
23			1182	18.1	1346	6 ABL64459 Abl64459 Stomach c
24			1182	18.1	1346	6 ABL63763 Abl63763 Breast ca
25			1182	18.1	1346	10 ABN96909 Abn96909 Gene #340
26			1182	18.1	1346	6 ADH29065 Adh29065 Human chr
27			1150.4	17.6	6181	6 ABN89597 Abn89597 Human ATP
28			1149.8	17.6	5722	8 ABZ22923 Abz22923 Human ABC
29			1123.6	17.2	6112	12 ADM67036 Adm67036 Human hom
30			1122.4	17.2	5966	11 ADL33372 Adl33372 Human tra
31			1118.8	17.1	5981	6 ABN89596 Abn89596 Human ATP
32			1117.2	17.1	4875	8 ABS57519 Abs57519 Human ABC
33			1117.2	17.1	5018	8 ABS57518 Abs57518 Human ABC
34			1090.8	16.7	5296	9 ABN89595 Abn89595 Human ATP
35			1090.4	16.7	5797	9 ADA20300 Ada20300 Human ATP
36			1089.2	16.7	5211	8 AAD47363 Aad47363 Human tra
37			1086	16.6	5332	8 ABQ77736 Abq77736 Human ABC
38			1084.6	16.6	5680	8 ABZ22922 Abz22922 Human ABC
39			1030.6	15.8	5125	12 ADJ27227 Adj27227 Human TRI
40			1020.2	15.6	6268	12 ADM67035 Adm67035 Murine ad
41			982.2	15.1	1632	8 ABZ35926 Abz35926 Human sec
42			979	15.0	5311	10 ADD29639 Add29639 Mouse tum
43			933.2	14.3	5846	8 AAD49503 Aad49503 Human TRI
44			930.6	14.3	4727	6 AAL44690 Aal44690 Human tra
45			930.6	14.3	5149	6 AAD33675 Aad33675 Human TRI

```
                                    ALIGNMENTS

RESULT 1
ABN89594
ID   ABN89594 standard; cDNA; 6525 BP.
XX
AC   ABN89594;
XX
DT   18-SEP-2002  (first entry)
XX
DE   Human ATP-binding cassette transporter ABCA5 cDNA SEQ ID NO:1.
XX
KW   Human; ABCA5; ABCA6; ABCA9; ABCA10; ATP-binding cassette transporter;
KW   chromosome 17; chromosome 17q; chromosome 17q24; antiarteriosclerotic;
KW   gene therapy; cholesterol; cholesterol; lipophilic molecule; inflammation;
KW   prostaglandin; prostacyclin; arteriosclerosis; transport; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200246458-A2.
XX
PD   13-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-EP015401.
XX
PR   07-DEC-2000; 2000EP-00403440.
PR   23-JAN-2001; 2001US-0263231P.
XX
PA   (AVET ) AVENTIS PHARMA SA.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Denefle P,   Rosier-Montus M,  Prades  C,   Arnould-Reguigne I;
PI   Duverger N,   Allikmets R,   Dean M;
XX
DR   WPI; 2002-557584/59.
DR   P-PSDB; ABB81574.
XX
PT   A novel nucleic acid corresponding to ATP-binding cassette transporter
PT   genes and the encoded polypeptide, useful for preventing or treating a
PT   dysfunction in reverse transport of cholesterol.
XX
PS   Claim 1; Page 151-153; 216pp; English.
XX
CC   The present invention describes the human ATP-binding cassette transporters
CC   (ABC). Specifically described are the human ABCA5, ABCA6, ABCA9 and
CC   ABCA10 genes (see ABN89594 to ABN89597) which encode the proteins given
```

CC   in ABB81574 to ABB81577). ABN89598 to ABN89715 represent ABCA5, ABCA6,
CC   ABCA9 and ABCA10 nucleotide fragments; and ABN89716 to ABN89806 represent
CC   primers for ABCA5, ABCA6, ABCA9 and ABCA10 genes which are used in the
CC   exemplification of the present invention. The ABC sequences have
CC   antiarteriosclerotic activities and can be used in gene therapy. ABC
CC   sequences can be used in the manufacture of a medicament intended for the
CC   prevention and/or treatment of a subject affected by a dysfunction in the
CC   reverse transport of cholesterol. The ABC proteins are involved in the
CC   reverse transport of cholesterol, in membrane transport of lipophilic
CC   molecules, in particular inflammation mediting substance such as
CC   prostaglandins and prostacyclins, or in any pathology whose candidate
CC   chromosomal region is situated on chromosome 17. They are also useful for
CC   the manufacture of a medicament intended for prevention of
CC   arteriosclerosis in various forms. The ABCA5, ABCA6, ABCA9 and ABCA10
CC   genes are located to chromosome 17, more specifically to the 17q24 locus
XX
SQ   Sequence 6525 BP; 1973 A; 1108 C; 1258 G; 2185 T; 0 U; 1 Other;

Query Match   100.0%;   Score 6524;   DB 6;   Length 6525;
Best Local Similarity   100.0%;   Pred. No.0;
Matches 6525;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 AAAATGTGATATTTCTCTTAGCAGGTTGTCAACCAGGTTAGGTTCAGGTCATAAGTT 60
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Db   1 AAAATGTGATATTTCTCTTAGCAGGTTGTCAACCAGGTTAGGTTCAGGTCATAAGTT 60

Qy   61 CTACCCACATTCTTTGAACTGTAGTTGTCATTTTAGTTTATTTTCAAAAACTTTGCAG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CTACCCACATTCTTTGAACTGTAGTTGTCATTTTAGTTTATTTTCAAAAACTTTGCAG 120

Qy   121 TACTTTTTGGTCTGTCTGTGTGTGCCTTGCAGTGAACAGTCTGGATTTGGACAGTGGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TACTTTTTGGTCTGTCTGTGTGTGCCTTGCAGTGAACAGTCTGGATTTGGACAGTGGT 180

Qy   181 CTGTCTGTAGTTCAGTTTCTCAAGCCTTTGTCACACTAATAGGATTGGATTTATGTATG 240
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Db   181 CTGTCTGTAGTTCAGTTTCTCAAGCCTTTGTCACACTAATAGGATTGGATTTATGTATG 240

Qy   241 TCCAGCTTGGGAATTATTACAGGAATTAAAAACAACTTTTAGAGTGCTTTCCTGAGCTC 300
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Db   241 TCCAGCTTGGGAATTATTACAGGAATTAAAAACAACTTTTAGAGTGCTTTCCTGAGCTC 300

Qy   301 TCTTTCTATTTGTTCCCCCTCTACTTTTGCTTCCCCTGTGGCTGCTTGTTTCTATCCTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TCTTTCTATTTGTTCCCCCTCTACTTTTGCTTCCCCTGTGGCTGCTTGTTTCTATCCTCC 360

Qy   361 AGCCAGAGAGCTAGTGTTTATTTTCTCCATTGTTGTTACACACTTGTGCAGCTGCAACCAC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AGCCAGAGAGCTAGTGTTTATTTTCTCCATTGTTGTTACACACTTGTGCAGCTGCAACCAC 420

Qy   421 CATATCCAGGGCCCAATGGTAGAGGTAGAGAAGCAAAGGGATTGGCCTCATCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CATATCCAGGGCCCAATGGTAGAGGTAGAGAAGCAAAGGGATTGGCCTCATCC 480

Qy   481 TCTTACAACGATAGTTCCATTGGATAGAGAAGAAGGTTTCTGCCTTCAGAGTGTTGCT 540
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Db   481 TCTTACAACGATAGTTCCATTGGATAGAGAAGAAGGTTTCTGCCTTCAGAGTGTTGCT 540

Qy   541 GCACTAGGCTTTGTTACTGTAGTCGGCCCTGTTACCATGGAGATTGCTTGCATGTGGGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCACTAGGCTTTGTTACTGTAGTCGGCCCTGTTACCATGGAGATTGCTTGCATGTGGGG 600

Qy   601 ATACAGGAGAATTCAGAAGAAAGAGATTTGCTATTTCTACATTCCCCTGAGCATT 660
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Db   601 ATACAGGAGAATTCAGAAGAAAGAGATTTGCTATTTCTACATTCCCCTGAGCATT 660

Qy   661 AAGACCTCCCTTGCCCATTCCTCAAAGCTAAGGCTTCTTCTGAGCTTGCTCCTCGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AAGACCTCCCTTGCCCATTCCTCAAAGCTAAGGCTTCTTCTGAGCTTGCTCCTCGT 720

Qy   721 GGGCGGTTCGGGAGATACCAAAGGAGAAAAAGTACCACTGTTGATAATGGTGTATTTCAA 780
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Db   721 GGGCGGTTCGGGAGATACCAAAGGAGAAAAAGTACCACTGTTGATAATGGTGTATTTCAA 780

Qy   781 ATTCTGGTCTACCCATTTCACATGCCTTGTTACTTTCAGAGCTGACAGAGATTGCTGCT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ATTCTGGTCTACCCATTTCACATGCCTTGTTACTTTCAGAGCTGACAGAGATTGCTGCT 840

Qy   841 CCATGCATTCGTGTCCAGTTCCTAAGAGAGCAGCTTGGAGTATGTTAATCCATCTTAC 900
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Db   841 CCATGCATTCGTGTCCAGTTCCTAAGAGAGCAGCTTGGAGTATGTTAATCCATCTTAC 900

Qy   901 CTGGGACTGAAACAGCTGCTTATTTTGCCGTTAAAAATTACATGCAGTTTACTGCGTGGC 960
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Db   901 CTGGGACTGAAACAGCTGCTTATTTTGCCGTTAAAAATTACATGCAGTTTACTGCGTGGC 960

Qy   961 TCCGGGTTGTTGTTGTTTGTTTGTTTCCCTTAATAGTTTATTCAGAAAAACATGTCCACTG 1020
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Db   961 TCCGGGTTGTTGTTGTTTGTTTGTTTCCCTTAATAGTTTATTCAGAAAAACATGTCCACTG 1020

Qy   1021 CAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAATTACTTAA 1080
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Db   1021 CAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAATTACTTAA 1080

Qy   1081 TTAAATGCAGAACCAAAAAGTAGTGTTCAGGAATTCTTTTTCCACTATTTTTTTAT 1140
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Db   1261 TGACTAATATTACAAGCAGCATCATGCAGAGAAGTGTCTACTGACTCATCCTGATGTCA 1320

Qy   1321 TAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAACATCCAGTCTCTCTAAGCCGA 1380
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Db   1321 TAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAACATCCAGTCTCTCTAAGCCGA 1380

Qy   1381 GCAACTTGTAGGTGTGGTTTCAAAGACTCCATGTCCATGAACTTCGTTTTTTTTCCTG 1440
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Db   1381 GCAACTTGTAGGTGTGGTTTCAAAGACTCCATGTCCATGAACTTCGTTTTTTTTCCTG 1440

Qy   1441 ATATGATTCCAGTACTTCTCATTTATATGGATTCAAGAGCTGGCTGTGTTCAAAATCATGTG 1500
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Db   1441 ATATGATTCCAGTATCTTCATTTATATGGATTCAAGAGCTGGCTGTGTTCAAAATCATGTG 1500

Qy   1501 AGGCTGCTCAGTACTGTCCTCAGTTTCACAGTTTACAGCATCCATAGATGCTGCCA 1560
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGCTGCTCAGTACTGTCCTCAGTTTCACAGTTTACAGCATCCATAGATGCTGCCA 1560

Qy   1561 TTATACAGTTGAAGACCAATGTTCTTCTTTGGAAGGAGCTCGAGTCAACTAAAGCTGTTA 1620
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              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TTTCCTGGGTTCTTCTATATACAAGTTAATTTTTCTTATGGTGTATTTCAA 1860

us-10-005-338b-1.rng

Mon Dec 6 10:08:08 2004

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Qy  1861 TTGCGACAGCTTCTTGTTATTCCTCAAAGTAGCAGCATTGTGATATTCTGCTTTTTT 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 TTGCGACAGCTTCTTGTTATTCCTCAAAGTAGCAGCATTGTGATATTCTGCTTTTTT 1920

Qy  1921 TCCTTTATGGATTAATCATCTGTATTTTTGCTTTAATGCTGACACCCTCTTTTAAAAAAT 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 TCCTTTATGGATTAATCATCTGTATTTTTGCTTTAATGCTGACACCCTCTTTTAAAAAAT 1980
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(DNA sequence alignment — Qy/Db paired rows, positions 1861–4080)

us-10-005-338b-1.rng

Mon Dec 6 10:08:08 2004

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Db  4021 GGAGTACCCATCTTTCAAGAAATTACTGATATAGTTTTAAAATGAGCTGTATTTC          4080
Qy  4081 AAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCAATGAAAATG     4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081 AAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCAATGAAAATG     4140
Qy  4141 CAGAGAATCATAAGATCAAAGCTTATACTCAACTTAAACTTTCAGTGTCTTTTGCCATCTG   4200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141 CAGAGAATCATAAGATCAAAGCTTATACTCAACTTAAACTTTCAGTGTCTTTTGCCATCTG   4200
Qy  4201 CATATTGGATTGGACAAGCTGTTGTGATATCCCCTATTTTTATCATTCTTATTTTGA       4260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201 CATATTGGATTGGACAAGCTGTTGTGATATCCCCTATTTTTATCATTCTTATTTTGA       4260
Qy  4261 TGCTAGGAGAGCTTACTGGCATTTCATTATGGATTATATTTTATACTGTAAAGTTCCTTG    4320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4261 TGCTAGGAGAGCTTACTGGCATTTCATTATGGATTATATTTTATACTGTAAAGTTCCTTG    4320
Qy  4321 CTGTGGTTTTTGCCTTATTGGTATGTTCCATCAGTTATTCTGTTCACTTATATTGCTT      4380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4321 CTGTGGTTTTTGCCTTATTGGTATGTTCCATCAGTTATTCTGTTCACTTATATTGCTT      4380
Qy  4381 CTTTCACCTTTAAGAAAATTTAAATACCAAAGAATTTGGTCATTTATCTTATTCTTCTGG    4440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4381 CTTTCACCTTTAAGAAAATTTAAATACCAAAGAATTTGGTCATTTATCTTATTCTTCTGG    4440
Qy  4441 CAGCCGTTGNCTTGTATTGCAATCACTACTGAAATAACTTCTTATGGGATACACAATTGCAA 4500
         ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  4441 CAGCCGTTGNCTTGTATTGCAATCACTACTGAAATAACTTCTTATGGGATACACAATTGCAA 4500
Qy  4501 CTATTCTTCATTATGCCTTTTGTATCATCATTCCAATCATCCTATTAGGTTGCCTGA       4560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4501 CTATTCTTCATTATGCCTTTTGTATCATCATTCCAATCATCCTATTAGGTTGCCTGA       4560
Qy  4561 TTTCTTCATAAAGATTTCTTGGAAGAATGTACGAAAAAATGTGGACACCTATAATCCAT    4620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4561 TTTCTTCATAAAGATTTCTTGGAAGAATGTACGAAAAAATGTGGACACCTATAATCCAT    4620
Qy  4621 GGGATAGGCTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTACTGTGTGATTTTCC     4680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4621 GGGATAGGCTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTACTGTGTGATTTTCC     4680
Qy  4681 TCTTACAATACTATCGAGAAAAAAATATGAGAAATCAATAAGAAGTCCCTTTTTCA        4740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4681 TCTTACAATACTATCGAGAAAAAAATATGAGAAATCAATAAGAAGTCCCTTTTTCA        4740
Qy  4741 GAAACCTTTCAACGAAGTCTAAAATGATGGTTCAGCAATTGCATAAAGAATATGACAAGAAAG 4800
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Db  4741 GAAACCTTTCAACGAAGTCTAAAATGATGGTTCAGCAATTGCATAAAGAATATGACAAGAAAG 4800
Qy  4801 AAGATGAAGAGTGAAGATGTCAAAGGTCAAAGCTAAAGGTCAAGAGCTGATGGGTTGCCAGTGTT 4860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4801 AAGATGAAGAGTGAAGATGTCAAAGGTCAAAGCTAAAGGTCAAGAGCTGATGGGTTGCCAGTGTT 4860
Qy  4861 GTGAGGAGAAAACCATCCATTATGTGTCAAGAAAGTAAAGATAAAATACATCTCTTTCTGTGA   4920
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Db  4861 GTGAGGAGAAAACCATCCATTATGTGTCAAGAAAGTAAAGATAAAATACATCTCTTTCTGTGA   4920
Qy  4921 ATTTTCTTCTTCAAGAGATCTTAGGACTATTGGTGATATTGAACCAACTCAGGCCAAAATGT    4980
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Db  4921 ATTTTCTTCTTCAAGAGATCTTAGGACTATTGGTGATATTGAACCAACTCAGGCCAAAATGT    4980
Qy  4981 AAAAAGGAGAGATCTTAGGACTTGGTGCTCGGCAAAAGCACACAATTATTA             5040
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Db  4981 AAAAAGGAGAGATCTTAGGACTTGGTGCTCGGCAAAAGCACACAATTATTA             5040
Qy  5041 ATATTCTCGGTGGTGATATTGAACCAACTCAGGTATTTTTAGGAGATTATTCTT          5100
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Db  5041 ATATTCTCGGTGGTGATATTGAACCAACTCAGGTATTTTTAGGAGATTATTCTT          5100
Qy  5101 CAGAGACAAGTGAAGATGATGAGTCACTGAAGTGTATGGGTTACTGTCCTCCAGATAAACC   5160
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Db  5101 CAGAGACAAGTGAAGATGATGAGTCACTGAAGTGTATGGGTTACTGTCCTCCAGATAAACC   5160
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Qy  5161 CTTTGTTGGCCAGATACTACATTGCAGGAACATTTGAAATTTATGGAGCTGTCAAAGGAA    5220
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Db  5161 CTTTGTTGGCCAGATACTACATTGCAGGAACATTTGAAATTTATGGAGCTGTCAAAGGAA    5220
Qy  5221 TGAGTGCAAGTGACATGAAAGAAGTCATAAGTCGAATAACAACATGCGAATCTG          5280
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Db  5221 TGAGTGCAAGTGACATGAAAGAAGTCATAAGTCGAATAACAACATGCGAATCTG          5280
Qy  5281 AACATCTTCAGAGACTGTAAAGAAATCACCTGCAGGAATCAGGAATCAAACGAAAGTGTGTTTTG 5340
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Db  5281 AACATCTTCAGAGACTGTAAAGAAATCACCTGCAGGAATCAGGAATCAAACGAAAGTGTGTTTTG 5340
Qy  5341 CTCTAAGTATGTCTAGGGAATCCTCAGATTACTTGCTAGATAACCATCTACAGGTATGG     5400
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Db  5341 CTCTAAGTATGTCTAGGGAATCCTCAGATTACTTGCTAGATAACCATCTACAGGTATGG     5400
Qy  5401 ATCCCAAAGCCAAACAGCACATGGCGAGCAATTGCATTTAAAAAACAGAAAGC           5460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5401 ATCCCAAAGCCAAACAGCACATGGCGAGCAATTGCATTTAAAAAACAGAAAGC           5460
Qy  5461 GGGCTGCTATTCTGACCACTCACTATGAGGAGGCAGAGGCTGTCTGTGATCGCAGTAG     5520
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Db  5461 GGGCTGCTATTCTGACCACTCACTATGAGGAGGCAGAGGCTGTCTGTGATCGCAGTAG     5520
Qy  5521 CTATCATGTGTCTCGGCAGTTAAGATGTATCGGACACAGTACAACATCTAAAGAGTAAAT   5580
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Db  5521 CTATCATGTGTCTCGGCAGTTAAGATGTATCGGACACAGTACAACATCTAAAGAGTAAAT   5580
Qy  5581 TTGGAAAAGGCTACTTTTTGGAAAATTAAATTGAAATTAAATTCCCAAATGAGTTCAGTCCTTTCACAATCTTTT 5640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5581 TTGGAAAAGGCTACTTTTTGGAAAATTAAATTGAAATTAAATTCCCAAATGAGTTCAGTCCTTTCACAATCTTTT 5640
Qy  5641 ACCGCCTTCAAAGAGAAATTCAGTATATATTTCCCAAATGCAAGCCGTCCCTTTCACCAATCTTTT          5700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5641 ACCGCCTTCAAAGAGAAATTCAGTATATATTTCCCAAATGCAAGCCGTCCCTTTCACCAATCTTTT          5700
Qy  5701 CTTCTATTTTGGCTTATAAATTCCTAAGGAAGATGTTCAGTCCTGTGTACTGTGGATTTCC              5760
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Db  5701 CTTCTATTTTGGCTTATAAATTCCTAAGGAAGATGTTCAGTCCTGTGTACTGTGGATTTCC              5760
Qy  5761 TTAAGCTGGAAGAAGCTAAACATGCTTTGCCATTGAAGATATAGCTTTTCTCAAGCAA                  5820
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Db  5761 TTAAGCTGGAAGAAGCTAAACATGCTTTGCCATTGAAGATATAGCTTTTCTCAAGCAA                  5820
Qy  5821 CATTGGAACACAGTTTTTGTAGAACTCACTCAAAGAACCAAGAACAACAAGAGGATG                   5880
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Db  5821 CATTGGAACACAGTTTTTGTAGAACTCACTCAAAGAACCAAGAACAACAAGAGGATG                   5880
Qy  5881 GAACTTAAACAGCAACTTTGTGGGAAGCTAAACATGCTTTGCCATTGAAGATTTTGAA                  5940
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Db  5881 GAACTTAAACAGCAACTTTGTGGGAAGCTAAACATGCTTTGCCATTGAAGATTTTGAA                  5940
Qy  5941 TTTGTATTGTTCGGTCGTACTGGACTTCTTCTTTTTCACTTAATTTGGAACTTTGG                    6000
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Db  5941 TTTGTATTGTTCGGTCGTACTGGACTTCTTCTTTTTCACTTAATTTGGAACTTTGG                    6000
Qy  6001 TTTAAAAGTTTTTTATTGGAATGGTAACTGACGTTTGGAGTATATTGAACTTGAAATTTTTC              6060
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Db  6001 TTTAAAAGTTTTTTATTGGAATGGTAACTGACGTTTGGAGTATATTGAACTTGAAATTTTTC              6060
Qy  6061 TAAGCTTCCTTAATTGAAATGCGTGTGGTTATTGAAGTATATTAACTTGTTTGTATG                   6120
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Db  6061 TAAGCTTCCTTAATTGAAATGCGTGTGGTTATTGAAGTATATTAACTTGTTTGTATG                   6120
Qy  6121 GTATAATTAAGTGAAGCTGCATGTTTGTATTGAAGTAGTATATATAGTTTGTGATG                    6180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6121 GTATAATTAAGTGAAGCTGCATGTTTGTATTGAAGTAGTATATATAGTTTGTGATG                    6180
Qy  6181 TCATCTTTTCACCATTCAGAAACAGTGCTTCTGAATTTGTGATTTGAATTTAAAGGAATTGTAAT          6240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6181 TCATCTTTTCACCATTCAGAAACAGTGCTTCTGAATTTGTGATTTGAATTTAAAGGAATTGTAAT          6240
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Qy 6241 AGAATAGTAGTTTATTTTTAAGTATCTTTAAGTTATGCCATCTTCTTAAATAAGTACGTA 6300
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Db 6241 AGAATAGTAGTTTATTTTTAAGTATCTTTAAGTTATGCCATCTTCTTAAATAAGTACGTA 6300

Qy 6301 ATGTTCCAATCTAAATAAAAAACTAATACACTAATACACTAATACACTAGAAAAGATACATAAAGC 6360
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Db 6301 ATGTTCCAATCTAAATAAAAAACTAATACACTAATACACTAGAAAAGATACATAAAGC 6360

Qy 6361 AATGTGAAAGTTTCTTGCTTCCTTTTTAATTTCTAAAAAAGCCACTTTGAATGGAAGT 6420
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Db 6361 AATGTGAAAGTTTCTTGCTTCCTTTTTAATTTCTAAAAAAGCCACTTTGAATGGAAGT 6420

Qy 6421 TGTCATCCGTAAAAGCTGAAGTGTAAGCACTAGGAAATCTCAATATAGAGATTTGAGGAA 6480
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Db 6421 TGTCATCCGTAAAAGCTGAAGTGTAAGCACTAGGAAATCTCAATATAGAGATTTGAGGAA 6480

Qy 6481 AGTTATATCCACTAGGTGGCAGTCATTGATCATAATAAGTGAAAT 6525
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Db 6481 AGTTATATCCACTAGGTGGCAGTCATTGATCATAATAAGTGAAAT 6525
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RESULT 2
ADN06076
ID ADN06076 standard; cDNA; 6525 BP.
XX
AC ADN06076;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antipsoriatic cDNA sequence #1280.
XX
KW ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
OS Homo sapiens.
XX
PN WO2004028479-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030907.
PR 25-SEP-2002; 2002US-0414006P.
XX
PA (GETH) GENENTECH INC.
XX
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-305105/28.
DR P-PSDB; ADN06077.
XX
PT New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
PS Claim 1; SEQ ID NO 2471; 3069pp; English.
XX
CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polynucleotides of the invention.
XX
SQ Sequence 6525 BP; 1973 A; 1108 C; 1258 G; 2185 T; 0 U; 1 Other;

Query Match 100.0%;   Score 6524;   DB 12;   Length 6525;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 6525;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy    1 AAAATGTTGATATTTTCTCTTAGCAGGCTGTCAACCAGTTAGTTCAGTTCATAAGTT 60
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Db    1 AAAATGTTGATATTTTCTCTTAGCAGGCTGTCAACCAGTTAGTTCAGTTCATAAGTT 60
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Qy   61 CTACCCACATTCTTTGAACGTAGTGTCATTTAGTTTATTTTCAAAAACTTTGCAG 120
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Db   61 CTACCCACATTCTTTGAACGTAGTGTCATTTAGTTTATTTTCAAAAACTTTGCAG 120

Qy  121 TACTTTTTGGTCTGTCTGTGTGTGCCTGCAGTGAACAGTCTGGATTTGGACAGTGGT 180
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Db  121 TACTTTTTGGTCTGTCTGTGTGTGCCTGCAGTGAACAGTCTGGATTTGGACAGTGGT 180

Qy  181 CTGTCTGTAGTTCAGTTCTCAAGCCTTGTCACACTAATAGGATTGGATTTATGTATG 240
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Db  181 CTGTCTGTAGTTCAGTTCTCAAGCCTTGTCACACTAATAGGATTGGATTTATGTATG 240

Qy  241 TCCAGCTTGGGAATTATTACAGGAGTTAAAAACAACTTTTTAGAGTGCTTCCTGAGCTC 300
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Db  241 TCCAGCTTGGGAATTATTACAGGAGTTAAAAACAACTTTTTAGAGTGCTTCCTGAGCTC 300

Qy  301 TCTTTCTATTTGTTCCCCTTCTACTTTTTGCTTCCCGTGGCTGCTGTTTCTATCCTCC 360
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Db  301 TCTTTCTATTTGTTCCCCTTCTACTTTTTGCTTCCCGTGGCTGCTGTTTCTATCCTCC 360

Qy  361 AGCCAGAGAGCTAGTGTTTATTTTCTCCATTGTGTACACACTTGTGCAGCTGCAACCAC 420
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Db  361 AGCCAGAGAGCTAGTGTTTATTTTCTCCATTGTGTACACACTTGTGCAGCTGCAACCAC 420

Qy  421 CATATCCAGGGCCCAATGGTAGGAGTAGAACAAAAGCAAAGGGATTGGCCTCATCC 480
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Db  421 CATATCCAGGGCCCAATGGTAGGAGTAGAACAAAAGCAAAGGGATTGGCCTCATCC 480

Qy  481 TCTTACAACGATAGTTCCATTGAATGAATAGAGAGAGAAAGGTTTCCTGCCTCAGAGTGTTGGCT 540
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Db  481 TCTTACAACGATAGTTCCATTGAATGAATAGAGAGAGAAAGGTTTCCTGCCTCAGAGTGTTGGCT 540

Qy  541 GCACTAGGCTTTGTACTGTAGTCTGGCCCGTTACCATGGAGTTGCTTGCATGTGGGG 600
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Db  541 GCACTAGGCTTTGTACTGTAGTCTGGCCCGTTACCATGGAGTTGCTTGCATGTGGGG 600

Qy  601 ATACAGGAGAATTCAGAAAGAAAGAAAGATTTGCTATTTCTACATTCTCCCTGAGCATT 660
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Db  601 ATACAGGAGAATTCAGAAAGAAAGAAAGATTTGCTATTTCTACATTCTCCCTGAGCATT 660

Qy  661 AAGACCCTCCCTTGCCCATTCCTCAATTCAAAGCTTCTTCTTCTGGAGCGCTTGCCTCTGT 720
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Db  661 AAGACCCTCCCTTGCCCATTCCTCAATTCAAAGCTTCTTCTTCTGGAGCGCTTGCCTCTGT 720

Qy  721 GGGCGGTTCGGGAGATACCAAAGAGAGAAAAAGTACCACTGTTGATATGGTTGTATTCAA 780
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Db  721 GGGCGGTTCGGGAGATACCAAAGAGAGAAAAAGTACCACTGTTGATATGGTTGTATTCAA 780

Qy  781 ATTCTGGTCTACCCTATTTCACATGCCTTGTTTACTTTGACGAGCTGACAGATTGCTGCT 840
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Db  781 ATTCTGGTCTACCCTATTTCACATGCCTTGTTTACTTTGACGAGCTGACAGATTGCTGCT 840

Qy  841 CCATGCATTCGTCCAGTTCCTAAGAGAGACAGCTTGGAGTATGCTAATCCATCTTAC 900
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Db  841 CCATGCATTCGTCCAGTTCCTAAGAGAGACAGCTTGGAGTATGCTAATCCATCTTAC 900

Qy  901 CTGGGACTGAAACAGCTGCTTATTTTGCCGTTAAATTACATGGCAGTTTACTGCGTGGC 960
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Db  901 CTGGGACTGAAACAGCTGCTTATTTTGCCGTTAAATTACATGGCAGTTTACTGCGTGGC 960

Qy  961 TCCGGGTTGTTGTTGTTTCCTCTTAATAGGTTTATTCAGAAAAACATGTCCACTG 1020
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Db  961 TCCGGGTTGTTGTTGTTTCCTCTTAATAGGTTTATTCAGAAAAACATGTCCACTG 1020

Qy 1021 CAATTAGGAGGTAGGAGTTTGGAGACAGAGAACCAGAACACTTCTACTGGAATTACTTAA 1080
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Db 1021 CAATTAGGAGGTAGGAGTTTGGAGACAGAGAACCAGAACACTTCTACTGGAATTACTTAA 1080

Qy 1081 TTAAATCCAGAACCAAAAAGTAGTGTTCAGGAAATTCTTTTCCACTATTTTTTTTAT 1140
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Db 1081 TTAAATGCAGAACCAAAAAGTAGTGTTCAGAAAATTCTTTTCCACTATTTTTTTTAT 1140

Qy 1141 TTTGTTAATATTAATTAGCATGATGATGCATCCAAATAGAAAATATGAGAAGTGCCTAATA 1200
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Db  2221  CACTTAATAGTATATTCTATGTCCCTGCTGTCTATCTTGATCAAGTCATTCCAGGGG  2280

Db  2281  AATTTGGCTTACGGAGGATCATCTTTATATTTCTGAAGCCTTCATATTGGTCAAAGAGTA  2340
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Qy  2281  AATTTGGCTTACGGAGGATCATCTTTATATTTCTGAAGCCTTCATATTGGTCAAAGAGTA  2340

Db  2341  AAAGAAATTATGAGAGAGTTATCAGAGGGCAATGTAATGAAATATTAGTTTAGTGAAA  2400
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Qy  2341  AAAGAAATTATGAGAGAGTTATCAGAGGGCAATGTAATGAAATATTAGTTTAGTGAAA  2400

Db  2401  TTATTGAGCCAGTTTCTTCAGAATTGTAGGAAAAGAGCCATAAGAATTAGTGGTATTC  2460
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Qy  2401  TTATTGAGCCAGTTTCTTCAGAATTGTAGGAAAAGAGCCATAAGAATTAGTGGTATTC  2460

Db  2461  AGAAGACATACAGAAAGAAGGGTGAAAATGGGAGGCTTGGAGGCTTTGAGAAATTGTCATTTGACA  2520
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Qy  2461  AGAAGACATACAGAAAGAAGGGTGAAAATGGGAGGCTTTGAGGAAATTGTCATTTGACA  2520

Db  2521  TATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAACAGGAAGAGTACATTGA  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2521  TATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAACAGGAAGAGTACATTGA  2580

Db  2581  TGAATATTCTTTGTGGACTCTGCCCACCTTCGATCGGTTTGCATCTATATATGGACACA  2640
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Qy  2581  TGAATATTCTTTGTGGACTCTGCCCACCTTCGATGGGTTTGCATCTATATATGGACACA  2640

Db  2641  GAGTCTTCAGAAATAGATGAAAGTGTTGAAGCAAGAAAAATGATTGGCATTTGTCCACAGT  2700
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Qy  2641  GAGTCTTCAGAAATAGATGAAAGTGTTGAAGCAAGAAAAATGATTGGCATTTGTCCACAGT  2700

Db  2701  TAGATATACACTTGATGTTTTGACAGTAGAGAAGAAAATTTATCAATTTTGGCTTCAATCA  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2701  TAGATATACACTTGATGTTTTGACAGTAGAGAAGAAAATTTATCAATTTTGGCTTCAATCA  2760

Db  2761  AAGGGATACCAGCCAACAATAATAATACAAGAAGTGCAGAAGGTTTACTAGATTTAGACA  2820
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Qy  2761  AAGGGATACCAGCCAACAATAATAATACAAGAAGTGCAGAAGGTTTACTAGATTTAGACA  2820

Db  2821  TGCAGACTATCAAAGATAACCAAGTAAAAAATTAAGTGGTGGTCAAAAAGAAGAAGCTGT  2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2821  TGCAGACTATCAAAGATAACCAAGTAAAAAATTAAGTGGTGGTCAAAAAGAAGAAGCTGT  2880

Db  2881  CATTAGGAATTGCTGTTCTGGAACCCAAAGATACTGCTGCTAGATGAACCAACAGCTG  2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2881  CATTAGGAATTGCTGTTCTGGAACCCAAAGATACTGCTGCTAGATGAACCAACAGCTG  2940

Db  2941  GAATGACCCCGTGTTCTCGACATATGTATGGAATCTTTTAAAATACAGAAAAGCCAATC  3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2941  GAATGACCCCGTGTTCTCGACATATGTATGGAATCTTTTAAAATACAGAAAAGCCAATC  3000

Db  3001  GGGTGACAGTGTTCAGTGCTCAGTTCATTCATGGATGAGCTGACATTCCTGCAGATAGGAAAG  3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3001  GGGTGACAGTGTTCAGTGCTCAGTTCATTCATGATGAGCTGACATTCCTGCAGATAGGAAAG  3060

Db  3061  CTGTGATATCACAAGGAATGCTGAAATGTGTTGGTTCTTCCTCAAAGTTCCTCAAAGTAAAT  3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3061  CTGTGATATCACAAGGAATGCTGAAATGTGTTGGTTCTTCCTCAAAGTTCCTCAAAGTAAAT  3120

Db  3121  GGGGGATCGGCTACCGCCTGAGCATGTACATAGAGCAATTTCTTATTACAACAGAATGACCAACAAC  3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3121  GGGGGATCGGCTACCGCCTGAGCATGTACATAGAGCAATTTCTTATTACAACAGAATGACCAACAAC  3180

Db  3181  CTTCACTGGTAAACACATATACCTGGAGCTACTTATTCAACAGAATCTCTTT  3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3181  TTGTGTATAGCTGCTTTTGCCTTTCAGGTTGTTTTCTGCCCTAG  3240

Db  3241  TTGTGTATAGCTGCTTTTGCCTTTCAGGACATGGACATGTACATAGACTACTTATTTCAGGTTGTTTTCTGCCCTAG  3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3241  TTGTGTATAGCTGCTTTTGCCTTTCAGGACATGGACATGTACATAGACTACTTATTTCAGGTTGTTTTCTGCCCTAG  3300

Db  3301  ACAGTCATTCAATTTGGGTGTCATTTCTTATGGTGTTTCCATGACGACTTTGGAAGACG  3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3301  ACAGTCATTCAATTTGGGTGTCATTTCTTATGGTGTTTCCATGACGACTTTGGAAGACG  3360
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Db  1141  TTTGGTTAATATTAATTAATTAGAGCATGATGCATAATATGAAGAAGTGCCTAATA  1200

Db  1201  TAGAACTCAATCCTATGGACAAGTTACTCTTCTAATCTAAATCTTGGATAATACTCCAG  1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1201  TAGAACTCAATCCTATGGACAAGTTACTCTTTCTAATCTAAATCTTGGATAATACTCCAG  1260

Db  1261  TGACTAATATTACAAGCAGCATCATGCAGAAGTGTCTACTCACTGATCATCACCTGATGTCA  1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1261  TGACTAATATTACAAGCAGCATCATGCAGAAGTGTCTACTCACTGATCATCACCTGATGTCA  1320

Db  1321  TAATTACTGAAGAATACAAATGAAAAGAAATGTTAACATCCAGTCTCTCTAAGCCGA  1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1321  TAATTACTGAAGAATACAAATGAAAAGAAATGTTAACATCCAGTCTCTCTAAGCCGA  1380

Db  1381  GCAACTTTGTAGGTGTGGTTTCAAAGACTCCATGTCCTATGAACTTCGTTTTTTTCCTG  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1381  GCAACTTTGTAGGTGTGGTTTCAAAGACTCCATGTCCTATGAACTTCGTTTTTTTCCTG  1440

Db  1441  ATATGATTCCAGTATCTTCTATTTATATGGATTCAAGAGCTGCTGTGTTCAAAATCATGTG  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1441  ATATGATTCCAGTATCTTCTATTTATATGGATTCAAGAGCTGCTGTGTTCAAAATCATGTG  1500

Db  1501  AGGCTGCTCAGTACTGGTCCTCAGGTTTCACAGTTTTACAAGCATCCATAGATGCTGCCA  1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1501  AGGCTGCTCAGTACTGGTCCTCAGGTTTCACAGTTTTACAAGCATCCATAGATGCTGCCA  1560

Db  1561  TTATACAGTTGAAGACCAATGTTTCTCTTGGAAGGAGCTGAGTCAACTAAAGCTGTTA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1561  TTATACAGTTGAAGACCAATGTTTCTCTTGGAAGGAGCTGAGTCAACTAAAGCTGTTA  1620

Db  1621  TTATGGGAGAAACTGCTGTGTAGAAATAGATACCTTTCCCCGAGGAGTAATTTTAATAT  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1621  TTATGGGAGAAACTGCTGTGTAGAAATAGATACCTTTCCCCGAGGAGTAATTTTAATAT  1680

Db  1681  ACCTAGTTATAGACATTTCACCTTTTGATACTTTTTGCAATTCATATCGTAGCAGAAA  1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1681  ACCTAGTTATAGACATTTCACCTTTTGATACTTTTTGCAATTCATATCGTAGCAGAAA  1740

Db  1741  AAGAAAAAAATAAAAGAATTTTAAAGATAATGGGACTTCATGATACTGCCTTTTGGC  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1741  AAGAAAAAAATAAAAGAATTTTAAAGATAATGGGACTTCATGATACTGCCTTTTGGC  1800

Db  1801  TTTCCTGGGTTCTTCTATACAAGTTAATTTTCTTATGTCCCTTCTTATGGCAGTCA  1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1801  TTTCCTGGGTTCTTCTATACAAGTTAATTTTCTTATGTCCCTTCTTATGGCAGTCA  1860

Db  1861  TTGGCACAGCTTCTTTGTATTCCCAAAGTAGCAGCATTGTGATATTTCTGCTTTTT  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1861  TTGGCACAGCTTCTTTGTATTCCCAAAGTAGCAGCATTGTGATATTTCTGCTTTTT  1920

Db  1921  TCCTTATGGTATTATCATCTGTATTTTTGCTTTAATCTGACACCTCTTTTTAAAAAT  1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1921  TCCTTATGGTATTATCATCTGTATTTTTGCTTTAATCTGACACCTCTTTTTAAAAAT  1980

Db  1981  CAAAACATGTGGGAATAGTTGAATTTTTTGTTACTGTGGCTTTTGGATTTATTGGCCTTA  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1981  CAAAACATGTGGGAATAGTTGAATTTTTTGTTACTGTGGCTTTTGGATTTATTGGCCTTA  2040

Db  2041  TGATAATCCTCATAGAAAGTTTTTCCCAAATCGTTAGTGTGGCTTTTTCAGTCCTTCTGTC  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2041  TGATAATCCTCATAGAAAGTTTTTCCCAAATCGTTAGTGTGGCTTTTTCAGTCCTTCTGTC  2100

Db  2101  ACTGTACTTTTGTGATTGGAATAGTTGAATTTTGTGGTGCTTTTTGGTGGCTTTAATGGCCTTA  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2101  ACTGTACTTTTGTGATTGGAATAGTTGAATTTTGTGGTGCTTTTTGGTGGCTTTAATGGCCTTA  2160

Db  2161  CTTCATTTTCAAATTTGACTGCAGGCCCATATCCCTCTCAATTATTCAATTATCATGCTCA  2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2161  CTTCATTTTCAAATTTGACTGCAGGCCCATATCCCTCTCAATTATTCAATTATCATGCTCA  2220

Db  2221  CACTTAATAGTATATTCTATGTCCCTGCTGTCTATCTTGATCAAGTCATTCCAGGGG  2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2221  CACTTAATAGTATATTCTATGTCCCTGCTGTCTATCTTGATCAAGTCATTCCAGGGG  2280
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Qy  4441  CAGGCGTTGCNTGTATTGCAATCACTGAAATAACTTCTTTATGGGATACACAATTGCAA  4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4441  CAGGCGTTGCNTGTATTGCAATCACTGAAATAACTTCTTTATGGGATACACAATTGCAA  4500

Qy  4501  CTATTCTTCATTATGCCTTTGTATCATCATTCCAATCATCATCCACTTCTCAGGTTGCCTGA  4560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4501  CTATTCTTCATTATGCCTTTGTATCATCATTCCAATCATCATCCACTTCTCAGGTTGCCTGA  4560

Qy  4561  TTTCTTTCATAAAGATTCTTGGAAGAATGTACGAAAAAATGTGACACCTATAATCCAT  4620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4561  TTTCTTTCATAAAGATTCTTGGAAGAATGTACGAAAAAATGTGACACCTATAATCCAT  4620

Qy  4621  GGGATAGGCTTCAGTAGCTGTTATATCCCCTTACCTGCAGTGTGTACTGTGGATTTTCC  4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4621  GGGATAGGCTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTACTGTGGATTTTCC  4680

Qy  4681  TCTTACAATACTATGAGAAAAATATGGAGGCAGCATCAATAAGAAAAGATCCCTTTTTCA  4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4681  TCTTACAATACTATGAGAAAAATATGGAGGCAGCATCAATAAGAAAAGATCCCTTTTTCA  4740

Qy  4741  GAAACCTTTCAACGAAGCTTAAAAATAGGAAGCTTCCAGAACCACCAGAACAATGAGGATG  4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4741  GAAACCTTTCAACGAAGCTTAAAAATAGGAAGCTTCCAGAACCACCAGAACAATGAGGATG  4800

Qy  4801  AAGATGAAGATGTCAAAGCTGAAAGCTAAAGGTCAAAGCTGATGATGGGTTGCCAGTGTT  4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4801  AAGATGAAGATGTCAAAGCTGAAAGCTAAAGGTCAAAGCTGATGATGGGTTGCCAGTGTT  4860

Qy  4861  GTGAGAGAAACCATCCATTATGGTCAGCAATTGCATAAAGAATTGCATGATGACAGAAAG  4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4861  GTGAGAGAAACCATCCATTATGGTCAGCAATTGCATAAAGAATTGCATGATGACAGAAAG  4920

Qy  4921  ATTTCTTCTTCAAGAAAGTGGCAACTAAATAACATCTCTTTCTGTGTGA  4980
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  4921  ATTTCTTCTTCAAGAAAGTGGCAACTAAATAACATCTCTTTCTGTGTGA  4980

Qy  4981  AAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGTGCTGGCAAAAGCACAATTATTA  5040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4981  AAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGTGCTGGCAAAAGCACAATTATTA  5040

Qy  5041  ATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGTATTTTAGGAGATTATTCTT  5100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5041  ATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGTATTTTAGGAGATTATTCTT  5100

Qy  5101  CAGAGACAAGTGATGAAGATGATTCACTGAAGTGTATGGTTACTGTCCTCAGATAAACC  5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5101  CAGAGACAAGTGATGAAGATGATTCACTGAAGTGTATGGTTACTGTCCTCAGATAAACC  5160

Qy  5161  CTTTGTGTGGCCAGATACATCAGATTGCAGCACACTACACCTGCGATGAGCGTCAAAGGAA  5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5161  CTTTGTGTGGCCAGATACATCAGATTGCAGCACACTACACCTGCGATGAGCGTCAAAGGAA  5220

Qy  5221  TGAGTGCAAGTGACATGCACACAGCACATGGGCAGCAATTCGAATAACACATGCGATTAAAAG  5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5221  TGAGTGCAAGTGACATGCACACAGCACATGGGCAGCAATTCGAATAACACATGCGATTAAAAG  5280

Qy  5281  AACATCTTCAGAAGACTGTAAAGAAATCGCAGGAATCAGGAATCCAGAATCAAACGAAAGTTGTGTTTTG  5340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5281  AACATCTTCAGAAGACTGTAAAGAAATCGCAGGAATCAGGAATCCAGAATCAAACGAAAGTTGTGTTTTG  5340

Qy  5341  CTCTAAGTATGTGCTAGGGAATCCTCGATTATTGCCTAGATGTTGCTAGATGGAAGAGC  5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5341  CTCTAAGTATGTGCTAGGGAATCCTCGATTATTGCCTAGATGTTGCTAGATGGAAGAGC  5400

Qy  5401  ATCCCAAAGCCAAACAGCACAGCACATGCGGCGAGCAATTCGAATCGCATTTAAAAACAGAAAGC  5460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5401  ATCCCAAAGCCAAACAGCACAGCACATGCGGCGAGCAATTCGAATCGCATTTAAAAACAGAAAGC  5460

Qy  5461  GGGCTGCTATTCTGACCACTCCACTCCGATCGTGTCTGTCGAGTCGATCGAGTAG  5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5461  GGGCTGCTATTCTGACCACTCCACTCCGATCGTGTCTGTCGAGTCGATCGAGTAG  5520

Qy  5521  CTATCATGTGTCTGTGGCAGTTAAGATGTATCGGAACAGTATCACACATCTAAAGAGTAAAT  5580
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Qy  3361  TATTTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGTGTATTTACTC  3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361  TATTTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGTGTATTTACTC  3420

Qy  3421  AGCAGCCACTGAGGAGGAAGAAATGGATTCAAAATCTTTGATGAAATGGAACGAGAGCTTAC  3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  AGCAGCCACTGAGGAGGAAGAAATGGATTCAAAATCTTTGATGAAATGGAACGAGAGCTTAC  3480

Qy  3481  TTATTCTTTCTGAAAACCAAGGCTTCTCTAGTGAGCACCATGAGCGCCTTTGGAAACAACAGA  3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  TTATTCTTTCTGAAAACCAAGGCTTCTCTAGTGAGCACCATGAGCGCCTTTGGAAACAACAGA  3540

Qy  3541  TGTATACAATAGCAAAGTTCATTCTTTACCTTGAAACGTGAAAATCAGTGAGAT  3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  TGTATACAATAGCAAAGTTCATTCTTTACCTTGAAACGTGAAAATCAGTGAGAT  3600

Qy  3601  CAGTGTTGCTTCGCTTCTGCTTTTAATTTTTTTCACAGTTCCAGATTTTTGGTTCATC  3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  CAGTGTTGCTTCGCTTCTGCTTTTAATTTTTTTCACAGTTCCAGATTTTTGGTTCATC  3660

Qy  3661  ACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTATATTTCTAAAAC  3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  ACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTATATTTCTAAAAC  3720

Qy  3721  CTGGAGACAAACCACCATCAAATCAAAACAAGTCCTGCTTCTTCAAAATTCTGCTGACTCAG  3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  CTGGAGACAAACCACCATCAAATCAAAACAAGTCCTGCTTCTTCAAAATTCTGCTGACTCAG  3780

Qy  3781  ATATCAGTGAACATCTTATTAGCTTTTTCACAAGCCAGAACAATAATGGTGACGATGATTAATG  3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  ATATCAGTGAACATCTTATTAGCTTTTTCACAAGCCAGAACAATAATGGTGACGATGATTAATG  3840

Qy  3841  ACAGTGACTATGTATCCGTGGCTGCGGCTTAAAGTGTGATGCATTCAGAAA  3900
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  ACAGTGACTATGTATCCGTGGCTGCGGCTTAAAGTGTGATGCATTCAGAAA  3900

Qy  3901  AGGACTATGTTTTGCAGCTGTTTCAACAGTACTATGGTTTATTCTTACCTATATTAG  3960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901  AGGACTATGTTTTGCAGCTGTTTCAACAGTACTATGGTTTATTCTTACCTATATTAG  3960

Qy  3961  TGAATATCATTAGTAACTACTATCTTTATCATTTAAATGTGACTGAAACCATCCAGATCT  4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961  TGAATATCATTAGTAACTACTATCTTTATCATTTAAATGTGACTGAAACCATCCAGATCT  4020

Qy  4021  GGAGTACCCCATTCTTCAAGAATCTTTTTATATAGTTTTAAAATTGAGTCGTATTTTC  4080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021  GGAGTACCCCATTCTTCAAGAATCTTTTTATATAGTTTTAAAATTGAGTCGTATTTTC  4080

Qy  4081  AAGCAGCTTGCTTGGAATCATTGTTACTGCAATGCAATGGAAAATG  4140
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  4081  AAGCAGCTTGCTTGGAATCATTGTTACTGCAATGCAATGGAAAATG  4140

Qy  4141  CAGAGAATCATAAGATCAAAAGCTTATATCTCAACTAAACTTCAGGTCTTTTGCCATCTG  4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141  CAGAGAATCATAAGATCAAAAGCTTATATCTCAACTAAACTTCAGGTCTTTTGCCATCTG  4200

Qy  4201  CATATTGGATTGGACAAGCTGTTGTTGTTGTTGGTGATAATCCCCTTATTTTATCATTCTTATTTTGA  4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201  CATATTGGATTGGACAAGCTGTTGTTGTTGTTGGTGATAATCCCCTTATTTTATCATTCTTATTTTGA  4260

Qy  4261  TGCTAGGAAGCTTACTGCCATTCCATCAGTTATTGTTCCATCTTAAAGTTCCTTG  4320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4261  TGCTAGGAAGCTTACTGCCATTCCATCAGTTATTGTTCCATCTTAAAGTTCCTTG  4320

Qy  4321  CTGTTGGTTTTTGCCTTATGTTCCTCATCAGTTATTCTGTTCACTTATATTGCTT  4380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4321  CTGTTGGTTTTTGCCTTATGTTCCTCATCAGTTATTCTGTTCACTTATATTGCTT  4380

Qy  4381  CTTTCACCTTAAGAAGAATTTAAATACCAAAGAATTTGGTCATTAATCTATTCTGTGG  4440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4381  CTTTCACCTTAAGAAGAATTTAAATACCAAAGAATTTGGTCATTAATCTATTCTGTGG  4440
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Qy  5521                                                                  5580
Db  5521 CTATCATGGTGTCGGGCAGTTAAGATGTATCGGAACAGTACAACATCTAAAGAGTAAAT 5580

Qy  5581 TTGGAAAAGGCTACTTTTTGGAAATAAATTGAAGGACTGGATAGAAAACCTAGAAGTAG 5640
Db  5581 TTGGAAAAGGCTACTTTTTGGAAATAAATTGAAGGACTGGATAGAAAACCTAGAAGTAG 5640

Qy  5641 ACCGCCTTCAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGGAAAGTTTTT 5700
Db  5641 ACCGCCTTCAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGGAAAGTTTTT 5700

Qy  5701 CTTCTATTTTGGCTATAAAAATTCCTAAGGAAGATGTTCAGTCCCTTCACAATCTTTTT 5760
Db  5701 CTTCTATTTTGGCTATAAAAATTCCTAAGGAAGATGTTCAGTCCCTTCACAATCTTTTT 5760

Qy  5761 TTAAGCTGGAAGAAGCTAAACATGCTTTGCCATTGAGAATATAGCTTTTCCAAGCAA 5820
Db  5761 TTAAGCTGGAAGAAGCTAAACATGCTTTGCCATTGAGAATATAGCTTTTCCAAGCAA 5820

Qy  5821 CATTGGAACCAGGTTTTTGTAGAACTCACTAAAGAACAAGAGGAGGAAGATAATAGTGTG 5880
Db  5821 CATTGGAACCAGGTTTTTGTAGAACTCACTAAAGAACAAGAGGAGGAAGATAATAGTGTG 5880

Qy  5881 GAACTTAAACAGCACACTTGGTGGGAACGAACACAAGAGTAGTATTTTGAA 5940
Db  5881 GAACTTAAACAGCACACTTGGTGGGAACGAACACAAGAGTAGTATTTTGAA 5940

Qy  5941 TTTGTATTGTTCGGTCTGCTCACTGGGACTTCTTTCTTTTCACTTAATTTTAACTTTGG 6000
Db  5941 TTTGTATTGTTCGGTCTGCTCACTGGGACTTCTTTCTTTTCACTTAATTTTAACTTTGG 6000

Qy  6001 TTTAAAAAGTTTTTTATTGGAATGGTAACTGGAACGCGACACTTGAAATTTTTC 6060
Db  6001 TTTAAAAAGTTTTTTATTGGAATGGTAACTGGAACGCGACACTTGAAATTTTTC 6060

Qy  6061 TAAGCTCCTTAATTGAAATGCTGTGGGTTGTGTTTTGCTTTTCTTTAAATAAAACGTAT 6120
Db  6061 TAAGCTCCTTAATTGAAATGCTGTGGGTTGTGTTTTGCTTTTCTTTAAATAAAACGTAT 6120

Qy  6121 GTATAATAAGTGAAGCTGCATGTTGTATTGAAGTATATTGAACTATATAGTTTGTATG 6180
Db  6121 GTATAATAAGTGAAGCTGCATGTTGTATTGAAGTATATTGAACTATATAGTTTGTATG 6180

Qy  6181 TCATCTTTTTTCACCATTCAGAAACAGTGCTTCTGAATTTGTGTGATTTAAAGGAATTGTAAT 6240
Db  6181 TCATCTTTTTTCACCATTCAGAAACAGTGCTTCTGAATTTGTGTGATTTAAAGGAATTGTAAT 6240

Qy  6241 AGATAGTTTTATTTTAAGTTTATGCCATCTTCTTAAATAAGTAAGTACGTA 6300
Db  6241 AGATAGTTTTATTTTAAGTTTATGCCATCTTCTTAAATAAGTAAGTACGTA 6300

Qy  6301 ATGTTCCAATCTAAATAAAAAAACTAATAACTAATGCATAGAAAAGAGTACATAAAGC 6360
Db  6301 ATGTTCCAATCTAAATAAAAAAACTAATAACTAATGCATAGAAAAGAGTACATAAAGC 6360

Qy  6361 AATGTGAAAGTTTCTTGCTTCTTCCTTTTAATTTCTAAAAAAGCCACTTGAATGGAAGT 6420
Db  6361 AATGTGAAAGTTTCTTGCTTCTTCCTTTTAATTTCTAAAAAAGCCACTTGAATGGAAGT 6420

Qy  6421 TGTCATCCGTAAAGCTGAAGTGTAAGCACTAGGAAATCTCAATATAGAGATTTGAGGAA 6480
Db  6421 TGTCATCCGTAAAGCTGAAGTGTAAGCACTAGGAAATCTCAATATAGAGATTTGAGGAA 6480

Qy  6481 AGTTATATCCACTAGGTGGCAGTCATTGATCATAATAAGTGAAAT 6525
Db  6481 AGTTATATCCACTAGGTGGCAGTCATTGATCATAATAAGTGAAAT 6525
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XX
DT   01-JUL-2002 (first entry)
XX
DE   Human TRICH-3 cDNA.
XX
KW   Human; transporter and ion channel; TRICH-3; transport disorder; angina;
KW   amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder;
KW   cardiac disorder; polymyositis; diabetes; neurological disorder; cancer;
KW   depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease;
KW   cell proliferated disorder; infertility; arteriosclerosis; gene therapy;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy;
KW   myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension;
KW   acquired immune deficiency syndrome; immunological disorder; scleroderma;
KW   endocrine disorder; autoimmune thyroiditis; rheumatoid arthritis; goitre;
KW   cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection;
KW   epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease;
KW   muscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirrhosis;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1238..6166
FT   /*tag= a
FT   /product= "Human TRICH-3 protein"
XX
PN   WO200212340-A2.
XX
PD   14-FEB-2002.
XX
PF   01-AUG-2001; 2001WO-US024217.
XX
PR   03-AUG-2000; 2000US-0223369P.
PR   10-AUG-2000; 2000US-0224456P.
PR   18-AUG-2000; 2000US-0226410P.
PR   25-AUG-2000; 2000US-0228140P.
PR   31-AUG-2000; 2000US-0230067P.
PR   08-SEP-2000; 2000US-0231434P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yue H, Thornton M, Ramkumar J, Tang YT, Azimzai Y, Baughn MR;
PI   Yang J, Yao MG, Lal P, Walia NK, Gandhi AR, Hafalia AJA, Nguyen DB;
PI   Patterson C, Elliott VS, Tribouley CM, Lu DAM, Xu Y, Reddy R;
PI   Hernandez R, Borowsky ML, Lo TP, Lu Y, Policky JL, Greene BD;
PI   Sanjanwala MS, Raumann BE, Burford N, Ison CH, Lee EA, Ding L;
PI   Das D, Kallick DA, Khan FA, Seilhamer JJ;
XX
DR   WPI; 2002-206330/26.
DR   P-PSDB; AAB21159.
XX
PT   New human transporters and ion channels polypeptides and polynucleotides
PT   for diagnosing, preventing or treating transport, neurological, muscle,
PT   immunological and cell proliferative disorders.
XX
PS   Claim 77; Page 203-205; 230pp; English.
XX
CC   The invention relates to human transporter and ion channel polypeptides
CC   designated TRICH and nucleic acid molecules encoding such polypeptides.
CC   TRICH sequences are useful for diagnosis, treatment and prevention of
CC   transport, muscle, neurological, immunological and cell proliferative
CC   disorders. Transport disorders include akinesia, amyotrophic lateral
CC   sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular
CC   dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis,
CC   myocarditis, prostate cancer, cardiac disorders associated with transport
CC   e.g. polymyositis, bradyarrythmia, dermatomyositis, angina, neurological
CC   disorders associated with transport e.g. amnesia, bipolar disorder,
CC   depression, Tourette's disorder, schizophrenia, other disorders
CC   associated with transport e.g. neurofibromatosis, sickle cell anaemia,
CC   Wilson's disease, cataracts, infertility, hyperglycaemia, hypoglycaemia,
CC   goitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell
CC   proliferated disorders include cancer, actinic keratosis, cirrhosis,
CC   arteriosclerosis, atherosclerosis, bursitis, hepatitis and psoriasis.

RESULT 3
AAD33648
ID   AAD33648 standard; cDNA; 6369 BP.
XX
AC   AAD33648;

CC Neurological disorders include Alzheimer's, Pick's and Parkinson's
CC disease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's
CC disease, multiple sclerosis, dementia and other extrapyramidal disorder,
CC motor neuron disorder, prion disease, metabolic disease of the nervous
CC system and other developmental disorders of the central nervous system,
CC neuromuscular disorders, metabolic, endocrine and toxic myopathies,
CC periodic paralysis, mental disorders including mood, anxiety; and
CC immunological disorders include acquired immune deficiency syndrome
CC (AIDS), adult respiratory distress syndrome, Addison's disease,
CC allergies, asthma, atherosclerosis, osteporosis, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis,
CC Grave's disease, glomerulonephritis, rheumatoid arthritis, scleroderma,
CC systemic lupus erythematosus, systemic sclerosis, ulcerative colitis,
CC haemodialysis, uveitis; viral, bacterial, fungal, parasitic, protozoal,
CC helminthic infections and trauma; and muscle disorders include cardiac
CC myopathy, myocarditis, polymyositis, arrhythmias and hypertension. The
CC TRICH polynucleotides are used in gene therapy. The present sequence is
XX human TRICH-3 cDNA

SQ Sequence 6369 BP; 1893 A; 1112 C; 1246 G; 2118 T; 0 U; 0 Other;

Query Match   93.8%;   Score 6122.8;   DB 6;   Length 6369;
Best Local Similarity   99.9%;
Matches 6127;   Conservative   0; Mismatches   8; Indels   0; Gaps   0;

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Db 2028  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TTTCCTGGGTTCTTCTACATACAAGTTAATTTTCTTATGTCCCTTCTTATGGCAGTCA   2087
Qy 1861  TTGGCGACAGCTTCTTGTATTCCTCAAAGTAGCAGCATTGTGATATTCTGCTTTTT      1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2088  TTGGCGACAGCTTCTTGTATTCCTCAAAGTAGCAGCATTGTGATATTCTGCTTTTT      2147
Qy 1921  TCCTTTATGGATTATCATCGTATTTTTGCTTAATGCTGACACCTCTTTTAAAAAAT      1980
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Db 2148  TCCTTTATGGATTATCATCGTATTTTTGCTTAATGCTGACACCTCTTTTAAAAAAT      2207
Qy 1981  CAAAACATGGGGAATAGTTGAATTTTTGTTACTGTGGCTTTTGGATTTATTGGCCTTA    2040
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Db 2208  CAAAACATGGGGAATAGTTGAATTTTTGTTACTGTGGCTTTTGGATTTATTGGCCTTA    2267
Qy 2041  TGATAATCCTCATAGAAAGTTTCCCAAATCGTAGTGTGGCTTTCAGTCCTTTCTGTC     2100
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Db 2268  TGATAATCCTCATAGAAAGTTTCCCAAATCGTAGTGTGGCTTTCAGTCCTTTCTGTC     2327
Qy 2101  ACTGTACTTTTGTGATTGGTATTGGCACAGTTGCACAGGTCATGCATGATTAGAAGATTTAATGAAGTG   2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2328  ACTGTACTTTTGTGATTGGTATTGGCACAGTTGCACAGGTCATGCATGATTAGAAGATTTAATGAAGTG   2387
Qy 2161  CTTCATTTTCAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAATTATCATGCTCA   2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2388  CTTCATTTTCAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAATTATCATGCTCA   2447
Qy 2221  CACTTAATAGTATATTCTATGTCCTCTGGCTGTCTATCTTGATCAAGTCATTCCAGGGG   2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2448  CACTTAATAGTATATTCTATGTCCTCTGGCTGTCTATCTTGATCAAGTCATTCCAGGGG   2507
Qy 2281  AATTTGGCTTACGGAGATCATCTTTATATTTCTGAAGCCTTCATATTGGTCAAAGAGTA   2340
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Db 2508  AATTTGGCTTACGGAGATCATCTTTATATTTCTGAAGCCTTCATATTGGTCAAAGAGCA   2567
Qy 2341  AAAGAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGTTTTAGTGAAA  2400
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Db 2568  AAAGAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGTTTTAGTGAAA  2627
Qy 2401  TTATTGAGCCAGTTCTTCAGAATTGTAGGAGAAGAGAGCCATAGAAGAATTAGTGGTATTC  2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2628  TTATTGAGCCAGTTCTTCAGAATTGTAGGAGAAGAGAGCCATAGAAGAATTAGTGGTATTC  2687
Qy 2461  AGAAGACATACAGAAGAGAAGGGTGAAAATGTTGGAGGCTTGAGAAATGTGTCATTGACA   2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2688  AGAAGACATACAGAAGAGAAGGGTGAAAATGTTGGAGGCTTGAGAAATGTGTCATTGACA   2747
Qy 2521  TATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAACAGGAGAGTACATTGA    2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2748  TATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAACAGGAGAGTACATTGA    2807
Qy 2581  TGAATATTCTTGTGGACTTTGGGACTTCTGCCCACCTTCTGATGGGTTGCATCTATATG   2640
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Db 2808  TGAATATTCTTGTGGACTTTGGGACTTCTGCCCACCTTCTGATGGGTTGCATCTATATG   2867
Qy 2641  GAGTCTCAGAAATACTTTGACAGTGATGAAATGTTGAGCAAGAAATAGATTGGCATTTG   2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2868  GAGTCTCAGAAATACTTTGACAGTGATGAAATGTTGAGCAAGAAATAGATTGGCATTTG   2927
Qy 2701  TAGATATACACTTTGATGTTTGACAGTAGAAGAATTTATCAATTTGGGCTTCAATCA     2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2928  TAGATATACACTTTGATGTTTGACAGTAGAAGAATTTATCAATTTGGGCTTCAATCA     2987
Qy 2761  AAGGGATACCAGCCAACATAATACAGAAGTTGCAGAAGGTTTTACTAGATTTAGACA     2820
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Db 2988  AAGGGATACCAGCCAACATAATACAGAAGTTGCAGAAGGTTTTACTAGATTTAGACA     3047
Qy 2821  TGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAAAGAAAGCTGT  2880
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Db 3048  TGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAAAGAAAGCTGT  3107
Qy 2881  CATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGTGAACCAACAGCTG   2940
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Db 3108  CATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGTGAACCAACAGCTG   3167
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Qy 2941  GAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTAAAATACAGAAAAGCCAATC   3000
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Db 3168  GAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTAAAATACAGAAAAGCCAATC   3227
Qy 3001  GGGTGACAGTGTTCAGTACTCATTCATGGATGAAGCTGACATTCTGCAGATAGGAGAAAG  3060
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Db 3228  GGGTGACAGTGTTCAGTACTCATTCATGGATGAAGCTGACATTCTGCAGATAGGAGAAAG  3287
Qy 3061  CTGTGATATCACAAGGAATGCTGGAAATGTGTGGTGGTCTTCAATGTTCCTCAAAAGTAAAT  3120
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Db 3288  CTGTGATATCACAAGGAATGCTGGAAATGTGTGGTGGTCTTCAATGTTCCTCAAAAGTAAAT  3347
Qy 3121  GGGGGATCGGCTACCGCCTGAGCACGTGCACATAGACAATATTGCCCACAGAATATTGTGCCACAGAAATCTCTTT  3180
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Db 3348  GGGGGATCGGCTACCGCCTGAGCACGTGCACATAGACAATATTGCCCACAGAATATTGTGCCACAGAAATCTCTTT  3407
Qy 3181  CTTCACTGGTAAACAACATATACCTGGAGCTACTTTATTCACAACAGAATGACCAACAAC  3240
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Db 3408  CTTCACTGGTAAACAACATATACCTGGAGCTACTTTATTCACAACAGAATGACCAACAAC  3467
Qy 3241  TTGTGTATAGCTGCCTTCAAGGACATGGACACAAATTTCAGGTTGTTGTTTCTGCCCTAG  3300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3468  TTGTGTATAGCTGCCTTCAAGGACATGGACACAAATTTCAGGTTGTTGTTTCTGCCCTAG  3527
Qy 3301  ACAGTCATTCAAATTTGGGTGTCATTCTTATGGTGTTCCATGACGACTTGGAAGACG     3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3528  ACAGTCATTCAAATTTGGGTGTCATTCTTATGGTGTTCCATGACGACTTGGAAGACG     3587
Qy 3361  TATTTTAAAGCTAGAAGTGAAGCAGCAGAAATTGACCAAGACAGATTATAGTGTATTACTC  3420
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Db 3588  TATTTTAAAGCTAGAAGTGAAGCAGCAGAAATTGACCAAGACAGATTATAGTGTATTACTC  3647
Qy 3421  AGCAGCCACTGAGGAGAAGAAATGGATTCAAAATCTTTGATGAAATGGAACAGAGCTTAC  3480
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Db 3648  AGCAGCCACTGAGGAGAAGAAATGGATTCAAAATCTTTGATGAAATGGAACAGAGCTTAC  3707
Qy 3481  TTATTCTTTCTGAAACCAAGGCTTCTCCTAGTGAGCACCATGAGCCTTTGGAAACAACAGA  3540
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Db 3708  TTATTCTTTCTGAAACCAAGGCTTCTCCTAGTGAGCACCATGAGCCTTTGGAAACAACAGA  3767
Qy 3541  TGTATACAATAGCAAAGTTCATTTCATTCTTCTTACCTTGAAACGTAAATCAGTGAGAT   3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3768  TGTATACAATAGCAAAGTTCATTTCATTCTTCTTACCTTGAAACGTAAATCAGTGAGAT   3827
Qy 3601  CAGTGTTGCTTCTGCTTTAATTTTTTCACAGTCAGATTTTTATGTTTTTGGTTCATC     3660
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Db 3828  CAGTGTTGCTTCTGCTTTAATTTTTTCACAGTCAGATTTTTATGTTTTTGGTTCATC     3887
Qy 3661  ACTCTTTAAAAATGTCGTGGTTCCCATCAAACTGTTCCATCAAACTTGTCAAAATTTCAAAAC  3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3888  ACTCTTTAAAAATGTCGTGGTTCCCATCAAACTGTTCCATCAAACTTGTCAAAATTTCAAAAC  3947
Qy 3721  CTGGAGACAAACCACATACAAAACAAGTCTGCTCTTCAAAATTCTGCTGACTCAG       3780
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Db 3948  CTGGAGACAAACCACATACAAAACAAGTCTGCTCTTCAAAATTCTGCTGACTCAG       4007
Qy 3781  ATATCAGTGATCTTATTAGCTTTACCATGAGTGCATTGATGATAATG             3840
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 4008  ATATCAGTGATCTTATTAGCTTTACCATGAGTGCATTGATGATAATG             4067
Qy 3841  ACAGTGACTATGTATCCGTGCGGCTTCCCCATAGTGCGGCTTAAATGGTCATTCAGAAA   3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4068  ACAGTGACTATGTATCCGTGCGGCTTCCCCATAGTGCGGCTTAAATGGTCATTCAGAAA   4127
Qy 3901  AGGACTATGTTTTGCAGCTGTTTCAACAGTTTATTCTTACCTATATTAG           3960
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 4128  AGGACTATGTTTTGCAGCTGTTTCAACAGTTTATTCTTACCTATATTAG           4187
Qy 3961  TGAATATCATTAGTAACTACTATCTTTATCATTTAAATGTGACTGAAATGTGACTCCAGATCT  4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4188  TGAATATCATTAGTAACTACTATCTTTATCATTTAAATGTGACTGAAATGTGACTCCAGATCT  4247
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Qy   5101 CAGAGACAAGTGAAGATGATGATTCACTGAAGTGTATGGGTACTGTCCTCAGATAAACC 5160
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Db   5328 CAGAGACAAGTGAAGATGATGATTCACTGAAGTGTATGGGTACTGTCCTCAGATAAACC 5387

Qy   5161 CTTTGTGGCCAGATCACTACATTGCAGGAGAATTTGAAGTTTGAAATTTATGGAGCTGTGTCAAAGGAA 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5388 CTTTGTGGGCCAGATACTACATTGCAGGAGAATTTGAAGTTTGAAATTTATGGAGCTGTGTCAAAGGAA 5447

Qy   5221 TGAGTGCAAGTGACATGAAAGAAGTCATAAGTGCAATAACACATGCCACTTGATTTAAAAG 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5448 TGAGTGCAAGTGACATGAAAGAAGTCATAAGTGCAATAACACATGCCACTTGATTTAAAAG 5507

Qy   5281 AACACTTCAGAAGACTGTAAAGAAACACTACCTGCAGGAATCAAACGAAAGTGTGTTTTG 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5508 AACACTTCAGAAGACTGTAAAGAAACACTACCTGCAGGAATCAAACGAAAGTGTGTTTTG 5567

Qy   5341 CTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGAGTGAACCATCTACAGGTATGG 5400
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Db   5568 CCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGAGTGAACCATCTACAGGTATGG 5627

Qy   5401 ATCCCAAAGCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTTAAAAACAGAAAGC 5460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5628 ATCCCAAAGCAAACAGCCACATGTGGCGAGCAATTCGAACTGCATTTAAAAACAGAAAGC 5687

Qy   5461 GGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCTGTCTGTGATCGAGTAG 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5688 GGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCTGTCTGTGATCGAGTAG 5747

Qy   5521 CTATCATGGTGTCTCGGCAGTTAAGATGTATCGGACACAGTACAACATCTAAAGAGTAAAT 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5748 CTATCATGGTGTCTCGGCAGTTAAGATGTATCGGACACAGTACAACATCTAAAGAGTAAAT 5807

Qy   5581 TTGGAAAAGGTACTTTTTGGAAATTAAATTGAAGGACTGATAGAAAAACCTAGAAGTAG 5640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5808 TTGGAAAAGGTACTTTTTGGAAATTTGGAAATTAAATTGAAGGACTGATAGAAAAACCTAGAAGTAG 5867

Qy   5641 ACCGCCTCAAAGAGAAATTCAGTACATATATTTTCCCAAATGCAAGCCGGTCAGGAAAGTTTTT 5700
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Db   5868 ACCGCCTTCAAAGAGAAATTCAGTATTATTTTTCCCAAATGCAAGCCGGTCAGGAAAGTTTTT 5927

Qy   5701 CTTCTATTTGGCTTATAAAAATTCCTAAGGAAGATGTTCAGTCGTCCCTTTTTCACCAATCTTTTT 5760
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Db   5928 CCTTCTATTTGGCTTATAAAAATTCCTAAGGAAGATGTTCAGTCGTCCCTTTTCACAATCTTTTT 5987

Qy   5761 TTAAGCTGGAAGAAGTCAACATGCTTTGTAGAACTCACTAAAGAACAAGAGAGGAAGATATAGTGTG 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5988 TTAAGCTGGAAGAAGTCAACATGCTTTGTAGAACTCACTAAAGAACAAGAGGAAGAGATATAGTTGTG 6047

Qy   5821 CATTGGAACAGGTTTTGTAGAACTGGAATGGTAACTGACTAAAGAACATCTCTTTCTCTGTGA 5880
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Db   6048 CATTGGAACAGGTTTTGTAGAACTGGAATGGTAACTGACTAAAGAACATCTCTTTCTCTGTGA 6107

Qy   5881 GAACTTTAAACAGCACACTTTGGTGGAACGAACTGATGGGTTGCCAGTGTT 5940
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6108 GAACTTTAAACAGCACACTTTGGTGGAACGAACTGATGGGTTGCCAGTGTT 6167

Qy   5941 TTTGTATTGTTCCGGTCGTTCTTACTGGAGCACTTCTTTCTCTGGAGATTATTCTT 6000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6168 TTTGTATTGTTCCGGTCGTTCTTACTGGAGCACTTCTTTCTCTGGAGATTATTCTT 6227

Qy   6001 TTTAAAAGTTTTTATTGGAATGGTAACTGGAATGGTAACGCACTTGAAATTTTTC 6060
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Db   6228 TTTAAAAGTTTTTATTGGAATGGTAACTGGAATGGTAACGCACTTGAAATTTTTC 6287

Qy   6061 TAAGCTCCTTAATTGAAATGCTGTGTGTTGTGTTCTTTTGCTTTTCTTTTCTTTAAATAAAACGTAT 6120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6288 TAAGCTCCTTAATTGAAATGCTGTGTGTTGTGTTCTTTTGCTTTTCTTTTCTTTAAATAAAACGTAT 6347

Qy   6121 GTATAATTAAGTGAA 6135
          |||||||||||||||
Db   6348 GTATAATTAAAAAA 6362
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Qy   4021 GGAGTACCCCATTCTTCTTCAAGAAATTACTGATATAGTTTTAAAATTGAGCTGTATTTTC 4080
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Db   4248 GGAGTACCCCATTCTTCTTCAAGAAATTACTGATATAGTTTTAAAATTGAGCTGTATTTTC 4307

Qy   4081 AAGCAGCTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCCATGGAAAATG 4140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4308 AAGCAGCTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCCATGGAAAATG 4367

Qy   4141 CAGAGAATCATAAGATCAAAGATCTATACTCAACTAAACTTCAGGTCTTTTGCCATCTG 4200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4368 CAGAGAATCATAAGATCAAAGCTTATACTCAACTAAACTTCAGGTCTTTTGCCATCTG 4427

Qy   4201 CATATTGGATTGGACAAGCTGTGTTGTGATATCCCCTATTTTTATCATTCTTATTTTGA 4260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4428 CATATTGGATTGGACAAGCTGTGTTGTGATATCCCCTATTTTTATCATTCTTATTTTGA 4487

Qy   4261 TGCTAGGAAGCTTACTGCATTCATTATGGATTATATATTTTATACTGTAAAGTTCCTTG 4320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4488 TGCTAGGAAGCTTATTGCATTCATTATGGATTATATATTTTATACTGTAAAGTTCCTTG 4547

Qy   4321 CTGTGGTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACTTATATTGCTT 4380
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Db   4548 CTGTGGTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACTTATATTGCTT 4607

Qy   4381 CTTTCACCTTTAAGAAAATTTAAATACCAAAGAATTTGGTCATTTATCTATTCTTGTGG 4440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4608 CTTTCACCTTTAAGAAAATTTAAATACCAAAGAATTTGGTCATTTATCTATTCTTGTGG 4667

Qy   4441 CAGCGTTGCNCTTGTATTGCAATCACTGAAATAACTTCTTTATGGGATACACAAATTGCAA 4500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4668 CAGGCGTTGGCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGATACACAAATTGCAA 4727

Qy   4501 CTATTCTTCATTATGCCTTTGTATCATCATCTCCAATCTATCCACCTTCTAGGTTGCCTGA 4560
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Db   4728 CCATTCTTCATTATGCCTTTGTATCATCATCTCCAATCTATCCACCTTCTAGGTTGCCTGA 4787

Qy   4561 TTTCTTTCATAAAGATTTCTTGGAAGAATGTACGAAAAAAATGTGAACACCTATAATCCAT 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4621 GGGATAGGCTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTTGTACTGTCACTGGATTTTCC 4680
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Qy   4741 GAAACCTTTCAACGAAGTCTAAAATAGGAGGCAGATCTTCCAGCAACAATTGCAGCTTGTTCC 4800
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RESULT 4:
ADH22577
ID   ADH22577 standard; cDNA; 6170 BP.
XX
AC   ADH22577;
XX
DT   11-MAR-2004  (first entry)
XX
DE   cDNA encoding a human transporter & ion channel (TRICH) protein SeqID75.
XX
KW   gene; ss; human; transporters and ion channel; TRICH; cell proliferative;
KW   arteriosclerosis; cancer; autoimmune/inflammatory; AIDS; asthma;
KW   neurological; epilepsy; stroke; developmental; Cushing's syndrome;
KW   hypothyroidism; infection; gene therapy; cytostatic; antiinflammatory;
KW   immunosuppressive; antiasthmatic; anticonvulsant; nootropic;
KW   neuroprotective; single nucleotide polymorphism; SNP.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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PD   13-NOV-2003.
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PF   02-MAY-2003; 2003WO-US014026.
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PR   03-MAY-2002; 2002US-0377444P.
PR   05-JUN-2002; 2002US-0386497P.
PR   11-JUN-2002; 2002US-0388180P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Baughn MR, Becha SD, Bulloch SA, Chang H, Elliott VS;
PI   Emerling BM, Griffin JA, Hafalia AJA, Ison CH, Jackson AA, Jiang X;
PI   Jin P, Kable AZ, Khare R, Lee SY, Lee S, Mason PM, Marquis JP;
PI   Ramkumar J, Richardson TW, Swarnakar A, Tran UK, Chawla NK;
PI   Wilson AD;
XX
DR   WPI; 2004-022655/02.
DR   P-PSDB; ADH22511.
XX
PT   New human transporters and ion channels (TRICH), useful for diagnosing,
PT   treating and preventing diseases or conditions associated with the
PT   aberrant TRICH expression e.g. cancer, AIDS, atherosclerosis, epilepsy,
PT   or infections.
XX
PS   Claim 12; SEQ ID NO 75; 448pp; English.
XX
CC   This invention relates to novel isolated polynucleotides identified as
CC   human transporters and ion channels (TRICH), and the encoded polypeptides
CC   thereof. Specifically, it describes using these TRICH molecules, as well
CC   as agonists, antagonists, antibodies, expression vectors and host cells,
CC   in appropriate screening and toxicity assays to assess the effects of
CC   exogenous compounds on TRICH expression. The present invention describes
CC   TRICH compositions that are useful in the diagnosis, treatment and
CC   prevention of various disorders such as cell proliferative (e.g.
CC   arteriosclerosis, cancer), autoimmune/inflammatory (e.g. AIDS, asthma),
CC   neurological (e.g. epilepsy, stroke) and developmental (e.g. Cushing's
CC   syndrome hypothyroidism) and for infections. Accordingly, these TRICH
CC   molecules can be used for gene therapy purposes and exhibit various
CC   activities such as cytostatic, antiinflammatory, immunosuppressive,
CC   antiasthmatic, anticonvulsant, nootropic and neuroprotective.
CC   Furthermore, a microarray is useful in monitoring or measuring protein-
CC   protein interactions, drug-target interactions and gene expression
CC   profiles. This polynucleotide sequence is a human TRICH cDNA of the
CC   invention.
XX
SQ   Sequence 6170 BP; 1825 A; 1078 C; 1209 G; 2058 T; 0 U; 0 Other;

Query Match             87.5%;  Score 5708.8;  DB 12;  Length 6170;
Best Local Similarity   96.6%;  Pred. No. 0;
Matches  5925;  Conservative    0;  Mismatches    8;  Indels 202;  Gaps    1;

Qy        1 AAAATGTTGATATTTCTTAGCAGGCTGTCAACCAGGTTAGGTTCAGGTTCATTAAGTTT 60
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Db      228 AAAATGTTGATATTTCTTAGCAGGCTGTCAACCAGGTTAGGTTCAGGTTCATTAAGTTT 287

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Left column

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Qy    181  CTGTCTGTTAGTTCAGTTCTCAAGCCTTTGTCACACTAATAGGATTGGATTATGTATG  240
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Qy    421  CATATCCAGGGCCCAATGGTAGGAGTAGAAGAAAAGCAAAAGGGATTGGCCTCATCC  480
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Db    648  CATATCCAGGGCCCAATGGTAGGAGTAGAAGAAAAGCAAAAGGGATTGGCCTCATCC  707

Qy    481  TCTTACAACGATAGTTCCATTGAATAGAGAGAAAGGTTTTCTGCCTCAGAGTGTTGGCT  540
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Qy    541  GCACTAGGCTTTTGTTACTGGTCTCGGCCCGTGTACCCTGTTACCATGGGATTGCTTGCATTCTCCCCTGAGCATT  600
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Qy    601  ATACAGGAGGAATTCAGAAAGAAAAAGATTTGCTATTTCTACATTCTCCCTGAGCATT  660
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Qy    901  CTGGGACTGAAACAGCTGCTTATTTGCCGTAAAAATTACATGCAGTTACTGCGTGGTGGC  960
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Qy    961  TCCGGGTTGTTGTTTGTTTCTCCTCTTTAATAGGTTTATTCAGAAAACATGTCCACTG  1020
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Qy    1021 CAATTAGGGAGGAGGTTGGAGACAGAGTAGTGTTCAGGAAATTCTTTTTCCACTTTTTTAT  1080
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Right column

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Qy    1261 TGACTAATATTACAGCAGCATCATGCAGAAAGTGTCTACTGATCATCCTGATGTCA  1320
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Qy 2401 TTAATTGAGCCAGTTCTTCGAGAATTTGTAGGAAAAGAGAGCCATAAGAATTAGTGGTATTC 2460
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Db 3288 CTGTGTGATATCACAAGGAATGCTGAAATGTGTTGGTTGGTTCTTCAATGTTCCTCAAAAGTAAAT 3347

Qy 3121 GGGGGGATCGGCTACCGCCGCCGGAGCATGCATGGCATCATAGAGCTACTTTATTACAACAGAATGACCAACAAC 3180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3348 GGGGGGATCGGCTACCGCCGCCGGAGCATGCATGGCATCATAGAGCTACTTTATTACAACAGAATGACCAACAAC 3407

Qy 3181 CTTCACTGGTTAAACAACATATACCGGAGCTACCTTTATTACACAACAGAATGACCAACAAC 3240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3408 CTTCACTGGTTAAACAACATATACCGGAGCTACCTTTATTACACAACAGAATGACCAACAAC 3467

Qy 3241 TTGTGTATAGCTGCCTTGGGTGTCATTTCTTATGGGTGTTGTTCCAGGTTGTTGTTCTGCCCTTGG 3300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3468 TTGTGTATAGCTGCCTTGGGTGTCATTTCTTATGGGTGTTGTTCCAGGTTGTTGTTCTGCCCTAG 3527

Qy 3301 ACAGTCATTCAAATTTGGGTGTCAAGTTGAAGCTAGTAGGACCAAGCAGAATTGACCAAGCTTATTACTC 3360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3528 ACAGTCATTCAAATTTGGGTGTCAAGTTGAAGCTAGTAGGACCAAGCAGAATTGACCAAGCAG 3587

Qy 3361 TATTTTTAAAGCTAGAAGTTGAAGCTAGAAGTGAAGCAGAAATTGAAGCAGAAATTGACCAAGCAG 3420
        ||||||||||||||||||||||||||||||||||||||||||||||||||------
Db 3588 TATTTTTAAAGCTAGAAGTTGAAGCTAGAAGTGAAGCAGAAATTGAAGCAGAAATC 3629

Qy 3421 AGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGGAAATGGAACAGAGCTTAC 3480
        |||||||||||||
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Db 3630 ------------------------------------------------------ 3629
Qy 3481 TTATTCTTCTTGAAACCAAGGCTTCTCTAGTGAGCACCATGGCCTTTGGAAACAACAGA 3540

Db 3630 ------------------------------------------------------ 3629
Qy 3541 TGTATACAAATGCAAAGTTCATTCTTCTTACCTTGAAACGTGAAAGTAATCAGTGAGAT 3600

Db 3630 ------------------------------------------------------ 3629
Qy 3601 CAGTGTTGCTTCGCTTTAATTTTTTCACAGTCAGATTTTATGTTTTTGGTTCATC 3660

Db 3630 ----GTTGCTTCGCTTTAATTTTTTCACAGTCAGATTTTATGTTTTTGGTTCATC 3685

Qy 3661 ACTCTTTTAAAAATGTGTTCCATCAAACTTGTTCCAGACTTATATTTTCTAAAAC 3720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3686 ACTCTTTTAAAAATGTGTTCCATCAAACTTGTTCCAGACTTATATTTTCTAAAAC 3745

Qy 3721 CTGGAGACAAACCACCACAATACAAACAACAGTCTGCTTCTTCAAAATTCTGCTGACTCAG 3780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3746 CTGGAGACAAACCACCACAATACAAACAAACAAGTCTGCTTCTTCAAAATTCTGCTGACTCAG 3805

Qy 3781 ATATCAGTGATCTTATTAGCTTTTTCACAGCCAGAACATAATGTGACGATGATTAATG 3840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3806 ATATCAGTGATCTTATTAGCTTTTTCACAGCCAGAACATAATGTGACGATGATTAATG 3865

Qy 3841 ACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGGCTTAAAATGTGGTGCATTCAGAAA 3900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3866 ACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGGCTTAAAATGTGGTGCATTCAGAAA 3925

Qy 3901 AGGACTATGTTTTGCAGCTGTTTCAACAGTTCATGGTTCTTACCTATTAG 3960
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3926 AGGACTATGTTTTGCAGCTGTTTCAACAGTTCATGGTTCTTACCTATTAG 3985

Qy 3961 TGAAATCATTAGTAACTAACTCTTTATCATTAAATGTGACTGAAACCATCCAGATCT 4020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3986 TGAAATCATTAGTAACTAACTCTTTATCATTAAATGTGACTGAAACCATCCAGATCT 4045

Qy 4021 GGAGTACCCCATTCTTCAAGAAATTACTGATATAGTTTTAAAATTGAGCTGTATTTTC 4080
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4046 GGAGTACCCCATTCTTCAAGAAATTACTGATATAGTTTTAAAATTGAGCTGTATTTTC 4105

Qy 4081 AAGCAGCTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTGCCATGGAAAATG 4140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4106 AAGCAGCTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTGCCATGGAAAATG 4165

Qy 4141 CAGAGAATCATAAGATCAAAGCTTATACTGACTCAACTTAAAAACCATCCAGATCT 4200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4166 CAGAGAATCATAAGATCAAAGCTTATACTGACTCAACTTAAAACTTCCAGATCT 4225

Qy 4201 CATATTGGATTGGACAGCTGTGTTGTGATATCCCCTTATTTTTATCATTCTATTTGA 4260
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4226 CATATTGGATTGGACAGCTGTGTTGTGATATCCCCTTATTTTTATCATTCTATTTGA 4285

Qy 4261 TGCTAGGAAGCTTACTGGCATTCATTGGCATTCATTATGGCATTATATACTGTAAAGTCCATCTG 4320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4286 TGCTAGGAAGCTTACTGGCATTCATTGGCATTCATTATGGCATTATATACTGTAAAGTTCCTTG 4345

Qy 4321 CTGTGGTTTTTGCCTTTATGTTAATGTTCCATCAGTAGTTCGTTCATTCTTATTGCTT 4380
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4346 CTGTGGTTTTTGCCTTTATGTTAATGTTCCATCAGTAGTTCGTTCATTCTTATTGCTT 4405

Qy 4381 CTTTCACCTTGNCTTGGCTGTATTGCAATCACTGAAATAACCAAAGAAAATTTTATCTCGTTCATTCTGTGG 4440
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4406 CTTTCACCTTGGCTGTATTGCAATCACTGAAATAACCAAAGAAAATTTTATCTCGTTCATTCTGTGG 4465

Qy 4441 CAGCGGTTGNCTTGGCTGTTGGTTGCAATCACTGAAATAACTTTCTTTATGGGATACACAAATTGCAA 4500
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4466 CAGCGGTTGGCTGTTGGTTGCAATCACTGAAATAACTTTCTTTATGGGATACACAAATTGCAA 4525

Qy 4501 CTATTCTTCATTATGCCTTTTGTATCATCATCCAATCATCATCCAATCATCTTAGGTTGCCTGA 4560
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Db 4526 CTATTCTTCATTATGCCTTTTGTATCATCATCCAATCATCATCCAATCATCTTAGGTTGCCTGA 4585
```

Qy 5641 ACCGCCTTCAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGGAAAGTTTTT 5700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5666 ACCGCCTTCAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGGAAAGTTTTT 5725

Qy 5701 CTTCTATTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTCACAATCTTTTT 5760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5726 CTTCTATTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTCACAATCTTTTT 5785

Qy 5761 TTAAGCTGGAAGAAGCTAAACATGCTTTGCCATTGAAGAATAGCTTTTCTCAAGCAA 5820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5786 TTAAGCTGGAAGAAGCTAAACATGCTTTGCCATTGAAGAATAGCTTTTCTCAAGCAA 5845

Qy 5821 CATTGGAACAGGTTTTTGTAGAACTCACTAAAGAACAAGAGGAGGAAGATAATAGTTGTG 5880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5846 CATTGGAACAGGTTTTTGTAGAACTCACTAAAGAACAAGAGGAGGAAGATAATAGTTGTG 5905

Qy 5881 GAACTTAAACAGCACACTTGGTGGGAACGAACACAAGAAGATAGAGTAGTATTTTGAA 5940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5906 GAACTTAAACAGCACACTTGGTGGGAACGAACACAAGAAGATAGAGTAGTATTTTGAA 5965

Qy 5941 TTTGTATTGTTCGGTCTGCTGCTTACTGGGACTTCTTTCTTTCTTTTCACTTAATTTAACTTTGG 6000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5966 TTTGTATTGTTCGGTCTGCTGCTTACTGGGACTTCTTTCTTTCTTTTCACTTAATTTAACTTTGG 6025

Qy 6001 TTTAAAAGTTTTTTATTGGAATGTAACTGGAGAACCAGAAGAACGCACTTGAAATTTTTC 6060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 6026 TTTAAAAGTTTTTTATTGGAATGTAACTGGAGAACCAGAAGAACGCACTTGAAATTTTTC 6085

Qy 6061 TAAGCTCCTTAATTGAAATGCTGTGTGTTGCTTTTCTTTCTTTAAATAAAACGTAT 6120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 6086 TAAGCTCCTTAATTGAAATGCTGTGTGTTGCTTTTCTTTCTTTAAATAAAACGTAT 6145

Qy 6121 GTATAATTAAGTGAA 6135
         |||||||||||||||
Db 6146 GTATAATTAAAAAAA 6160

RESULT 5
ABS57751
ID   ABS57751 standard; cDNA; 5475 BP.
XX
AC   ABS57751;
XX
DT   04-FEB-2003 (first entry)
XX
DE   cDNA encoding novel human ATP binding cassette ABCA5 transporter #2.
XX
KW   Human; ATP binding cassette; ABC; ABCA5; transporter;
KW   neurotoxin transport; beta-amyloid peptide; chromosome mapping;
KW   blood brain barrier transport; tissue typing; predictive medicine;
KW   ABCA5 mediated disorder; ABCA5 related disorder; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   114..5042
FT   /tag= a
FT   /product= "ABCA5"
FT   /note= "ATP binding cassette (ABC) A5 transporter"
XX
PN   US2002123107-A1.
XX
PD   05-SEP-2002.
XX
PF   01-MAR-2002; 2002US-00090458.
XX
PR   02-MAR-2001; 2001US-0272885P.
XX
PA   (ACTI-) ACTIVE PASS PHARM INC.
XX
PI   Chen H, Kilinski L, Le Bihan S;
XX
DR   WPI; 2003-066798/06.

Qy 4561 TTTCTTTCATAAAGATTCTTGGAAGAAAAATGTGGACACCTATAATCCAT 4620
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4586 TTTCTTTCATAAAGATTCTTGGAAGAAAAATGTGGACACCTATAATCCAT 4645

Qy 4621 GGGATAGGCTTTCAGTAGCTGTTGTTATATCGCCTACCTGCAGTGTGTACTGTGGATTTCC 4680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4646 GGGATAGGCTTTCAGTAGCTGTTGTTATATCGCCTACCTGCAGTGTGTACTGTGGATTTCC 4705

Qy 4681 TCTTACAATACTATGAGAAAAAAAAAATATTGGAGGCAGATCAATAGAAAGAATCCCTTTTCA 4740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4706 TCTTACAATACTATGAGAAAAAAAAAATATTGGAGGCAGATCAATAGAAAGAATCCCTTTTCA 4765

Qy 4741 GAAACCTTTCAACGAGGTCTAAAAATAGGAAGCTTCCAGAACCACCAGACAATGAGGATG 4800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4766 GAAACCTTTCAACGAGGTCTAAAAATAGGAAGCTTCCAGAACCACCAGACAATGAGGATG 4825

Qy 4801 AAGATGAAGATGTCAAAGCTAAAGGTCAAAAGTGATGGGTTGCCAGTGTT 4860
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4826 AAGATGAAGATGTCAAAGCTAAAGGTCAAAAGTGATGGGTTGCCAGTGTT 4885

Qy 4861 GTGAGGAGAAACCATCCATTATGGTCAGCAATTGCATAAAGAATATGATGACAAGAAAG 4920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4886 GTGAGGAGAAACCATCCATTATGGTCAGCAATTGCATAAAGAATATGATGACAAGAAAG 4945

Qy 4921 ATTTTCTTTCTTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTGTGTGA 4980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4946 ATTTTCTTTCTTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTGTGTGA 5005

Qy 4981 AAAAAGGAGAGATCTTAGGACTATTGGTGCTGCCAAATGCACAATTATTA 5040
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Db 5006 AAAAAGGAGAGATCTTAGGACTATTGGTGCTGCCAAATGCACAATTATTA 5065

Qy 5041 ATATTCTGGTTGTGATATTGAACCACTTCAGGCCAGTGTATTTTTAGGAGATTATTCTT 5100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5066 ATATTCTGGTTGTGATATTGAACCACTTCAGGCCAGTGTATTTTTAGGAGATTATTCTT 5125

Qy 5101 CAGAGACAAGTGAAGATGAAGATGATTCACTGAAGTGTATGGGTTACTGTCCTCCAGATAAACC 5160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5126 CAGAGACAAGTGAAGATGAAGATGATTCACTGAAGTGTATGGGTTACTGTCCTCCAGATAAACC 5185

Qy 5161 CTTTGTGTGGCCAGATACTACTAGGCCAGGAACACATTTGAAATTTATGGAGCTGTCAAAGGAA 5220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5186 CTTTGTGTGGCCAGATACTACTAGGCCAGGAACACATTTGAAATTTATGGAGCTGTCAAAGGAA 5245

Qy 5221 TGAGTGCAAGTGCAAGTGACAGAAGAGTCATAAGTCAATAACAACATGCACTTGATTTAAAAG 5280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5246 TGAGTGCAAGTGCAAGTGACAGAAGAGTCATAAGTCAATAACAACATGCACTTGATTTAAAAG 5305

Qy 5281 AACATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAGTGTGTTTG 5340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5306 AACATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAGTGTGTTTG 5365

Qy 5341 CTCTAAGATGCTAGGGAATCCTCGAGATTACTTCTGCTAGATGAACCATCCACAGGTATGG 5400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5366 CTCTAAGATGCTAGGGAATCCTCGAGATTACTTCTGCTAGATGAACCATCCACAGGTATGG 5425

Qy 5401 ATCCCAAAGCCAAACAGCACACATGTGGCGAGCAATTCGAACTGCATTTAAAAACAGAAAGC 5460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5426 ATCCCAAAGCCAAACAGCACACATGTGGCGAGCAATTCGAACTGCATTTAAAAACAGAAAGC 5485

Qy 5461 GGGCTGCTATTCTGACCACTCACTCATCTATATGGAGGAGGCAGAGGCTGTCTGTGATCGAGTAG 5520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5486 GGGCTGCTATTCTGACCACTCACTCATCTATATGGAGGAGGCAGAGGCTGTCTGTGATCGAGTAG 5545

Qy 5521 CTATCATGGTGTCTGGGCAGTTAAGATATCGGAACAGTACAACATCTAAAGAGTAAAT 5580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5546 CTATCATGGTGTCTGGGCAGTTAAGATATCGGAACAGTACAACATCTAAAGAGTAAAT 5605

Qy 5581 TTGGAAAAGGCTACTTTTTGGAAATTAAATTGAAGGAGGACTGGAATAGAAAACCTAGAAGTAG 5640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5606 TTGGAAAAGGCTACTTTTTGGAAATTAAATTGAAGGAGGACTGGAATAGAAAACCTAGAAGTAG 5665

DR   P-PSDB; ABG72424.
XX
PT   Novel isolated ATP binding cassette transporter family polypeptide,
PT   ABCA5, useful for treating disorders associated with aberrant or unwanted
PT   ABCA5 transporter expression or activity.
XX
PS   Claim 2; Page 39-42; 52pp; English.
XX
CC   The invention describes an isolated ATP binding cassette (ABC)
CC   transporter family polypeptide (I), designated ABCA5. (I) or the
CC   polynucleotide encoding it (II) are useful as targets for developing
CC   modulating agents to regulate a variety of cellular processes,
CC   particularly the transport of neurotoxic molecules, e.g., beta-amyloid
CC   peptide (Abeta), across cell membranes or, e.g., the blood brain barrier
CC   (BBB), as targets for developing modulating agents of multi-drug
CC   resistance, as diagnostic and therapeutic tools, or to treat disorders
CC   associated with aberrant or unwanted ABCA5 transporter expression or
CC   activity. (I), (II) or a host cell (III) expressing (II) are useful in
CC   screening assays, detection assays (e.g. chromosomal mapping, tissue
CC   typing, forensic biology), predictive medicine (e.g., diagnostic assays,
CC   prognostic assays, monitoring clinical trials and pharmacogenomics), and
CC   in methods of treatment (e.g., therapeutic and prophylactic). (I) or
CC   (III) are useful as reagents or targets in assays applicable to treatment
CC   and diagnosis of ABCA5-mediated or related disorders. (I) is useful to
CC   screen for naturally occurring ABCA5 substrates; to screen for drugs or
CC   compounds which modulate ABCA5 activity; as a bait protein in a yeast two
CC   -hybrid or three-hybrid assay; and to identify other proteins which bind
CC   to or interact with ABCA5. (II) is useful in: gene therapy; to detect
CC   ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5
CC   activity; to locate gene regions associated with genetic disease or to
CC   associate ABCA5 with the disease, to identify an individual from a minute
CC   biological sample (tissue typing), and to aid in forensic identification
CC   of the biological sample. This sequence encodes a novel human ATP binding
CC   cassette (ABC) A5 transporter
XX
SQ   Sequence 5475 BP; 1705 A; 917 C; 1048 G; 1804 T; 0 U; 1 Other;

Query Match   82.3%; Score 5373.2; DB 10; Length 5475;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 5375; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   994 AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGAGGTAGGAGTTGGAGACAGACCA 1053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97 AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGAGGTAGGAGTTGGAGACAGACCA 156

Qy   1054 GAACACTTCTACTGAAGAATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGG 1113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   157 GAACACTTCTACTGAAGAATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGG 216

Qy   1114 AAATTCTTTTTCCACTATTTTTTTATTTGGTTAATATTAATTAGCATGATGCATCCAA 1173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   217 AAATTCTTTTTCCACTATTTTTTTATTTGGTTAATATTAATTAGCATGATGCATCCAA 276

Qy   1174 ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTC 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   277 ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 336

Qy   1234 CTAATCTAATTCTTGGATATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAG 1293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   337 CTAATCTAATTCTTGGATATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAG 396

Qy   1294 TGTCTACTGATCATCTCGATGTCATATGATGTCATATAATCTTCTATTTATATGAAA 1353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   397 TGTCTACTGATCATCTCGATGTCATATGATGTCATATAATCTTCTATTTATATGAAA 456

Qy   1354 TGTTAACATCCAGTCTCTTAAGCCGAGCAACTTTGTAGGTGTTGTTTTCAAAGACTTCCA 1413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   457 TGTTAACATCCAGTCTCTTAAGCCGAGCAACTTTGTAGGTGTTGTTTTCAAAGACTTCCA 516

Qy   1414 TGTCCTATGGAACTTCGTTTTTTTCCTGATATGATTCCAGTATCTTCTATTTATATGGATT 1473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   517 TGTCCTATGGAACTTCGTTTTTTTCCTGATATGATTCCAGTATCTTCTATTTATATGGATT 576

Qy   1474 CAAGAGCTGGCTGTTCAAATCATGTGAGGCTGCTCAGTACTGGCTCCTCAGGTTTCACAG 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   577 CAAGAGCTGGCTGTTCAAATCATGTGAGGCTGCTCAGTACTGGCTCCTCAGGTTTCACAG 636

Qy   1534 TTTTACAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGA 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   637 TTTTACAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGA 696

Qy   1594 AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGGAAAACTGCTGTTGTAGAAATAGATA 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   697 AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGGAAAACTGCTGTTGTAGAAATAGATA 756

Qy   1654 CCTTTCCCGAGGAGTAATTTAATATACCTAGTTATAGCATTTCACCTTTTGGATACT 1713
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   757 CCTTTCCCCGAGGAGTAATTTAATATACCTAGTTATAGCATTTCACCTTTTGGATACT 816

Qy   1714 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAGAAAAATAAAAGAATTTTAAAGATAA 1773
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   817 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAGAAAAAGAAAAATAAAAGAATTTTAAAGATAA 876

Qy   1774 TGGGACTTCATGATACTGCCTTTGGCTTTCCTGGGTCTTCCTGGGTCTTCTCTATATACAAGTTTAATT 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   877 TGGGACTTCATGATACTGCCTTTGGCTTTCCTGGGTCTTCCTGGGTCTTCTCTATATACAAGTTTAATT 936

Qy   1834 TTCTTATGTCCCTCTTATGGCAGTCATTGGACAGCTTCTTGTATTCCTCAAGTA 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   937 TTCTTATGTCCCTCTTATGGCAGTCATTGGACAGCTTCTTGTATTCCTCAAGTA 996

Qy   1894 GCAGCATTGTGATATTCTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTTGCTT 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   997 GCAGCATTGTGATATTCTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTTGCTT 1056

Qy   1954 TAAATGCTGACACCTCTTTTAAAAAATCAAAAAATCAAAACATGTGGAATAGTTGAATTTTTGTTA 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1057 TAAATGCTGACACCTCTTTTAAAAAATCAAAAAATCAAAACATGTGGAATAGTTGAATTTTTGTTA 1116

Qy   2014 CTGTGGCTTTTGGATTTATTGGCCTTATGGCCTTATGATAATCCTCATAGAAAGTTTTCCCAAATCGT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1117 CTGTGGCTTTTGGATTTATTGGCCTTATGGCCTTATGATAATCCTCATAGAAAGTTTTCCCAAATCGT 1176

Qy   2074 TAGTGTGCCTTTCAGTCCTTTCTGTCACTGTACTTTGTATTGGTATTGCACAGGTCA 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1177 TAGTGTGCCTTTCAGTCCTTTCTGTCACTGTACTTTGTATTGGTATTGCACAGGTCA 1236

Qy   2134 TGCATTGGAGAGATTTAATGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCCATATC 2193
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1237 TGCATTTAGAGAGATTTAATGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCCATATC 1296

Qy   2194 CTCTAATTATTACAATTATCATGCTCACACTTAATAGTATATTCTATGTCCTCTTGGCTG 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1297 CTCTAATTATTACAATTATCATGCTCACACTTAATAGTATATTCTATGTCCTCTTGGCTG 1356

Qy   2254 TCTATCTTGATCAAGTCATTCCCAGGGGAATTGGCTTACCAGGGGATCATCTTTATATTTC 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1357 TCTATCTTGATCAAGTCATTCCCAGGGGAATTGGCTTACCAGGGGATCATCTTTATATTTC 1416

Qy   2314 TGAAGCCTTCATATTGTCAAGAGTAAAGAAAGCAAAAGAAATTATGAGGAGGCAATG 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1417 TGAAGCCTTCATATTGTCAAGAGTAAAGAAAGCAAAAGAAATTATGAGGAGGCAATG 1476

Qy   2374 TTAATGAAATATTAGTTTAGTTTAGTAAGAATTGAACTTGAACTTCAGAATTTGTTAGGAA 2433
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   1477 TTAATGAAATATTAGTTTAGTTTAGTAAGAATTGAACTTGAACTTCAGAATTTGTTAGAA 1536

Qy   2434 AAGAAGCCATAGAAGAAGATAGTAGTAGTAGTTATTCAGAGACATACAGAAGAGGGTGAAAATGTGG 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1537 AAGAAGCCATAGAAGAAGATAGTAGTAGTAGTTATTCAGAGACATACAGAAGAGGGTGAAAATGTGG 1596

Qy   2494 AGGCTTTGAGAAATTTGTCATTTGACATATATGAGGGTCAGATTACTTGCCTTACTTGGCC 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1597 AGGCTTTGAGAAATTTGTCATTTGACATATATGAGGGTCAGATTACTTGCCTTACTTGGCC 1656

Qy   2554 ACAGTGGAACAGGAAAGAGTACATTGTTGTGACTGTAATATTCTTTGTTGGACTTCTGCGACTCGCCACCTTCTG 2613

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Qy   4774 TTCCAGAACCACCAGACAATGAGGATGAAGATGAGATGTCAAAGACTGAAAGACTAAAGG 4833
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3877 TTCCAGAACCACCAGACAATGAGGATGAAGATGAGATGTCAAAGACTGAAAGACTAAAGG 3936

Qy   4834 TCAAAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCATCCATTATGGTCAGCAATT 4893
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3937 TCAAAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCATCCATTATGGTCAGCAATT 3996

Qy   4894 TGCATAAAGAATATGATGACAAGAAAGATTTCTTCTTCAGAAAGTAAAGAAAGTGG 4953
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3997 TGCATAAAGAATATGATGACAAGAAAGATTTCTTCTTCAGAAAGTAAAGAAAGTGG 4056

Qy   4954 CAACTAAATACATCTCTTTCTGTGTGAAAAAAGGAGATCTTAGGACTATTGGGTCCAA 5013
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4057 CAACTAAATACATCTCTTTCTGTGTGAAAAAAGGAGATCTTAGGACTATTGGGTCCAA 4116

Qy   5014 ATGGTGCTGCAAAAGCACAATTATTAATATTCGGTTGGTGATATTGAACCAACTTCAG 5073
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4117 ATGGTGCTGCAAAAGCACAATTATTAATATTCGGTTGGTGATATTGAACCAACTTCAG 4176

Qy   5074 GCCAGGTATTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATTCACTGAAGT 5133
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4177 GCCAGGTATTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATTCACTGAAGT 4236

Qy   5134 GTATAGGGTTACTGTCCTCCAGATAAACCCTTGTGCCCAGATACTACATTGCAGGAACATT 5193
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4237 GTATGGGTTACTGTCCTCCAGATAAACCCTTGTGCCCAGATACTACATTGCAGGAACATT 4296

Qy   5194 TTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGCATGAAAGAGTCATAAGTC 5253
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4297 TTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGCATGAAAGAGTCATAAGTC 4356

Qy   5254 GAATAACACATGCACTTGATTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTG 5313
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4357 GAATAACACATGCACTTGATTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTG 4416

Qy   5314 CAGGAATCAAACGAAAGTTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCCAGATTACTT 5373
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4417 CAGGAATCAAACGAAAGTTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCCAGATTACTT 4476

Qy   5374 TGCTAGAATGAACCATCTACAGGTATGAGTCCCAAAGCCAAAGCAGCACATGTGGCGAGCAA 5433
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4477 TGCTAGAATGAACCATCTACAGGTATGAGTCCCAAAGCCAAAGCAGCACATGTGGCGAGCAA 4536

Qy   5434 TTCGAACTGCATTTAAAAAACAGAAACGGGCCGTATTCTGACCACTCACTATATGGAGG 5493
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4537 TTCGAACTGCATTTAAAAAACAGAAACGGGCCGTATTCTGACCACTCACTATATGGAGG 4596

Qy   5494 AGGCAGAGCGTGTCTGATCGAGTAGCTATCATGGTGTCGGGCAGTTAAGATGTATCG 5553
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4597 AGGCAGAGCGTGTCTGATCGAGTAGCTATCATGGTGTCGGGCAGTTAAGATGTATCG 4656

Qy   5554 GAACAGTACAACATCTAAAGAGTAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTGA 5613
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4657 GAACAGTACAACATCTAAAGAGTAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTGA 4716

Qy   5614 AGGACTGGATAGAAACCTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCC 5673
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4717 AGGACTGGATAGAAACCTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCC 4776

Qy   5674 CAAATGCAAGCCGTCAGGAAAGTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAG 5733
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4777 CAAATGCAAGCCGTCAGGAAAGTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAG 4836

Qy   5734 ATGTTCAGTCCCTTCACAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCA 5793
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4837 ATGTTCAGTCCCTTCACAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCA 4896

Qy   5794 TTGAAGAATATAGCTTTTGTGCAACATTGGAACAGTTTTTGTAGAACTCACTAAAG 5853
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4897 TTGAAGAATATAGCTTTTGTGCAACATTGGAACAGTTTTTGTAGAACTCACTAAAG 4956
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Qy   5854 AACAAGAGGAGGAAGAGATAATAGTTGTGGAACTTTAAACAGCACACTTGGTGGGAACGAA 5913
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4957 AACAAGAGGAGGAAGAGATAATAGTTGTGGAACTTTAAACAGCACACTTGGTGGGAACGAA 5016

Qy   5914 CACAAGAAGATAGAGTAGTATTTGAATTGTATTTGAATTGTATTGTTCGGTCGCTTACTGGGACTTCT 5973
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5017 CACAAGAAGATAGAGTAGTATTTGAATTGTATTTGAATTGTATTGTTCGGTCGCTTACTGGGACTTCT 5076

Qy   5974 TTCTTTTCACTTAATTTAACTTTGGTTTAAAAAGTTTTTATTGGAATGGTAACTGGA 6033
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5077 TTCTTTTCACTTAATTTAACTTTGGTTTAAAAAGTTTTTATTGGAATGGTAACTGGA 5136

Qy   6034 GAACCAAGAAGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTGTGTGTG 6093
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5137 GAACCAAGAAGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTGTGTGTG 5196

Qy   6094 TTTTGCTTTCTTAAATAAAACGTATGTATAATTAAGTGAAGCTGCATGTTGTATTGA 6153
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5197 TTTTGCTTTCTTAAATAAAACGTATGTATAATTAAGTGAAGCTGCATGTTGTATTGA 5256

Qy   6154 AGTATATTGAACTATATAGTTGTATGTCATCTTTTCACCATTCAGAAACAGTGCTTCT 6213
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5257 AGTATATTGAACTATATAGTTGTATGTCATCTTTTCACCATTCAGAAACAGTGCTTCT 5316

Qy   6214 GAATTTGTGATTTAAAGGAATTGTAATAGAATAGTTTATTTTATTCTTTAAGTTATCTTTAAGTT 6273
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5317 GAATTTGTGATTTAAAGGAATTGTAATAGAATAGTTTATTTTATTCTTTAAGTTATCTTTAAGTT 5376

Qy   6274 TATGCCATCTTCTTAAATAAGTACGTAATGTTCCAATCTAAATAAAAAACTAATACATAA 6333
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5377 TATGCCATCTTCTTAAATAAGTACGTAATGTTCCAATCTAAATAAAAAACTAATTCATAA 5436

Qy   6334 CTAAATGCATAGAAAAGATACATAAAGCAATGTGAAAGTT 6372
               |||||||||||||||||||||||||||||||||||||||
Db   5437 CTAAATGCATAGAAAAGATACATAAAGCAATGTGAAAGTT 5475
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DR   WPI; 2003-066798/05.
DR   P-PSDB; ABG72423.
XX
PT   Novel isolated ATP binding cassette transporter family polypeptide,
PT   ABCA5, useful for treating disorders associated with aberrant or unwanted
PT   ABCA5 transporter expression or activity.
XX
PS   Claim 2; Fig 1; 52pp; English.
XX
CC   The invention describes an isolated ATP binding cassette (ABC)
CC   transporter family polypeptide (I), designated ABCA5. (I) or the
CC   polynucleotide encoding it (II) are useful as targets for developing
CC   modulating agents to regulate a variety of cellular processes,
CC   particularly the transport of neurotoxic molecules, e.g., beta-amyloid
CC   peptide (Abeta), across cell membranes or, e.g., the blood brain barrier
CC   (BBB), as targets for developing modulating agents of multi-drug
CC   resistance, as diagnostic and therapeutic tools, or to treat disorders
CC   associated with aberrant or unwanted ABCA5 transporter expression or
CC   activity. (I), (II) or a host cell (III) expressing (II) are useful in
CC   screening assays, detection assays (e.g., chromosomal mapping, tissue
CC   typing, forensic biology), predictive medicine (e.g., diagnostic assays,
CC   prognostic assays, monitoring clinical trials and pharmacogenomics), and
CC   in methods of treatment (e.g., therapeutic and prophylactic). (I) or
CC   (III) are useful as reagents or targets in assays applicable to treatment
CC   and diagnosis of ABCA5-mediated or related disorders. (I) is useful to
CC   screen for naturally occurring ABCA5 substrates; to screen for drugs or
CC   compounds which modulate ABCA5 activity; as a bait protein in a yeast two
CC   -hybrid or three-hybrid assay; and to identify other proteins which bind
CC   to or interact with ABCA5. (II) is useful in: gene therapy; to detect
CC   ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5
CC   activity; to locate gene regions associated with genetic disease or to
CC   associate ABCA5 with the disease, to identify an individual from a minute
CC   biological sample (tissue typing), and to aid in forensic identification
CC   of the biological sample. This sequence encodes a novel human ATP binding
CC   cassette (ABC) A5 transporter
XX
SQ   Sequence 5463 BP; 1699 A; 912 C; 1055 G; 1794 T; 0 U; 3 Other;

Query Match             80.5%;  Score 5255.8;  DB 10;  Length 5463;
Best Local Similarity   98.9%;  Pred. No. 0;
Matches  5340;  Conservative   0;  Mismatches   0;  Indels   8;  Gaps   3;

Qy    994  AGGTTATTCAGAAAACAACATGTCCACTGCAATTGCCAATTAGGGAGGTAGGAGTTGGAGACAGACCA  1053
            |||||||||||||||| ||||||||||||||||||||   ||||||||||||||||| ||||||||||
Db     97  AGGTTTATTCAGAAAACA-CATGTCCACTGCAATT---AGGGAGGTAGGAGTTTGGAGACAGACCA   156

Qy   1054  GAACACTTCTACTGAAGAATTACTTAATTAAATCAGAACCAAAAAGAGTAGTGTTCAGG  1113
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    157  GAACACTTCTACTGAAGAATTACTTAATTAAATCAGAACCAAAAAGAGTAGTGTTCAGG   216

Qy   1114  AAATTCTTTTTCCACTATTTTT-TATTTTGGTTAATATTAATTAGCCATGATGCATCCAA  1173
            |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    217  AAATTCTTTTTCCACTATTTTTTTATTTTTGGTTAATATTAATTAGCCATGATGCATCCAA   276

Qy   1174  ATAAGAAATATGAAGAAGTGCCTAATATAGACTCAATCCTATGGACCAAGTTACTCCTTT  1233
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    277  ATAAGAAATATGAAGAAGTGCCTAATATAGACTCAATCCTATGGACCAAGTTTACTCTTT   336

Qy   1234  CTAATCTAATTCTTGGATATACTCCAGTGACTAATAATTACAAGCAGCATCATGCGAAAG  1293
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    337  CTAATCTAATTCTTGGATATACTCCAGTGACTAATAATTACAAGCAGCATCATGCAGAAAG   396

Qy   1294  TGTTAACATCCAGTCTCTGATCATCTACCTGACTCATAATCAGTCATAATTAATCAGAAG  1353
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    397  TGTTAACATCCAGTCTCTGATCATCTACCTGACTCATAATCAGTCATAATTAATCAGAAG   456

Qy   1354  TGTTAACATCCAGTCCTCTAAGCCGGCAACTTGTAGGTGTTGTTTCAAAGACTCCA  1413
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457  TGTTAACATCCAGTCCTCTAAGCCGAGCAACTTGTAGGTGTTGTTTCAAAGACTCCA   516

Qy   1414  TGTCCTATGAACTTCGTTTTTTCCTGATATGATCTTTCATTTATATATGATT  1473
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    517  TGTCCTATGAACTTCGTTTTTTCCTGATATGATCTTTCATTTATATATGATT   576

Qy   1474  CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTCACAG  1533
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    577  CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTCACAG   636

Qy   1534  TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGA  1593
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    637  TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGA   696

Qy   1594  AGGAGCTGGAGTCAACTAAAGCTGTTATATGGGAGAAACTGCTGTGTGTAGAAATAGATA  1653
            |||||||||||||||||||||||||||||||||||||| ||||||||| |||||||||||
Db    697  AGGAGCTGGAGTCAACTAAAGCTGTTATATGGGAGAAATGCTGTGTTGTAGAAATAGATA   756

Qy   1654  CCTTTCCCGAGGAGTAATTTAATATACCTAGTATAGCATTTCACCTTTGGATACT  1713
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    757  CCTTTCCCGAGGAGTAATTTAATATACCTAGTATAGCATTTCACCTTTGGATACT   816

Qy   1714  TTTTGGCAATTCATATCGTAGCAGAAAAGAAAAAAATAAAAGAATTTTAAAGATAA  1773
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    817  TTTTGGCAATTCATATCGTAGCAGAAAAGAAAAAAATAAAAGAATTTTAAAGATAA   876

Qy   1774  TGGGACTTCATGATACTGCCTTTGGCTTCCTGGGTTCTTCTATATACAAGTTAATT  1833
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    877  TGGGACTTCATGATACTGCCTTTGGCTTCCTGGGTTCTTCTATATACAAGTTAATTT   936

Qy   1834  TCCTTATGTCCCTCTTATGGCAGTCATTGCGACAGCTTCTTGTATTCCTCAAAGTA  1893
            ||||||||||| ||||||||||||||||||||||||||||||| |||||||||||||
Db    937  TCTTATGTCCCTTCTTATGGCAGTCATTGCGACAGCTTCTTGTTATTCCTCAAAGTA   996

Qy   1894  GCAGCATTGTGATATTTCTGCTTTTTCCTTTATGATTATCATCGTATTTTTGCTT  1953
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    997  GCAGCATTGTGATATTTCTGCTTTTTTCCTTTATGATTATCATCGTATTTTTGCTT  1056

Qy   1954  TAATGCTGCACCTCTTTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTTGTTA  2013
            ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   1057  TAATGCTGCACCCTCTTTTTAAAAAAATCAAAACATGTGGGAATAGTTGAATTTTTGTTA  1116

Qy   2014  CTGTGGCTTTTGGATTTATTGGCCTTATGATAATCCTCATAGAAAAGTTTCCCAAAATCGT  2073
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1117  CTGTGGCTTTTGGATTTATTGGCCTTATGATAATCCTCATAGAAAAGTTTCCCAAAATCGT  1176

Qy   2074  TAGTGTGGCTTTCAGTCCTTCTGTCACTGTACTTTGTGATTGGTATTGGCACAGGTCA  2133
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1177  TAGTGTGGCTTTCAGTCCTTCTGTCACTGTACTTTGTGATTGGTATTGGCACAGGTCA  1236

Qy   2134  TGCATTGGAAGATTTAATGAAGTGCTTCATTTCAAATTTGACTGCAGGCCCATATC  2193
            ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1237  TGCATTTAGAAGATTTAATGAAGTGCTTCATTTCAAATTTGACTGCAGGCCCATATC  1296

Qy   2194  CCTAATTATTACAATTATCATGCTCACACTTAATAGTATTAGTGCCTTCTTGGCTG  2253
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   1297  CCTAATTATTACAATTATCATGCTCACACTTAATAGTATTAGTGTCCCTCCTTGGCTG  1356

Qy   2254  TCTATCTTGATCAAGTCATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC  2313
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1357  TCTATCTTGATCAAGTCATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC  1416

Qy   2314  TGAAGCCTTCATATTGGTCAAAGAAATTATTGAGCCAGTTCTTCAGAAATTGTAGGAA  2373
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1417  TGAAGCCTTCATATTGGTCAAAGAAATTATTGAGCCAGTTCTTCAGAAATTGTAGGAA  1476

Qy   2374  TTAATGGAAATAATAGTTAGTTTGGAAATTATTGAGCCAGTTCTTCAGAATTGTAGGAA  2433
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1477  TTAATGGAAATAATAGTTAGTTTGGAAATTATTGAGCCAGTTCTTCAGAATTGTAGGAA  1536

Qy   2434  AAGAAGCCATAAGAATTAGTGTATTCAGAAGACATACAGAAAGAAGGGTGAAAATGTGG  2493
            ||||||||| |||||||||||||||||||| |||||||||||||||||||||||||||
Db   1537  AAGAAGCCATAAGAATTAGTGGTATTCAGAAGACATACAGAAAGAAGGGTGAAAATGTGG  1596

Qy   2494  AGGCTTTGAGAAATTTGTCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCC  2553
            ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   1597  AGGCTTTGAGAAATTTGTCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCC  1656
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Qy  2554  ACAGTGGAACAGGAAAGAGTACATTGATGAATATTCTTGTGGACTCTGCCCACCTTCTG  2613
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1657  ACAGTGGAACAGGAAAGAGTACATTGATGAATATTCTTGTGGACTCTGCCCACCTTCTG  1716

Qy  2614  ATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA  2673
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1717  ATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA  1776

Qy  2674  GAAAAATGATTGGGCATTGTCCACAGTTAGATATACACTTTGATGTTTGACAGTAGAAG  2733
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1777  GAAAAATGATTGGGCATTGTCCACAGTTAGATATACACTTTGATGTTTGACAGTAGAAG  1836

Qy  2734  AAAAATTATCAATTTGGCTTCAATCAAAGGATACCAGCCAACAATATAATACAAGAGAAG  2793
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1837  AAAAATTATCAATTTGGCTTCAATCAAAGGATACCAGCCAACAATATAATACAAGAGAAG  1896

Qy  2794  TGCAGAAGGTTTTACTACAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAT  2853
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1897  TGCAGAAGGTTTTACTACAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAT  1956

Qy  2854  TAAGTGGTGGTCAAAAAAGAAAGCTGTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGA  2913
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1957  TAAGTGGTGGTCAAAAAAGAAAGCTGTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGA  2016

Qy  2914  TACTGCTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGA  2973
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2017  TACTGCTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGA  2076

Qy  2974  ATCTTTTAAAATACAGAAAAGCCAATCGGTGACAGTTCAGTACTCATTCATTCATGGATG  3033
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2077  ATCTTTTAAAATACAGAAAAGCCAATCGGTGACAGTTCAGTACTCATTCATTCATGGATG  2136

Qy  3034  AAGCTGACATTCTTGCAGATAGGAAAGCTGTGATATCACAAGGAAGTGCTGAAATGTGTTG  3093
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2137  AAGCTGACATTCTTGCAGATAGGAAAGCTGTGATATCACAAGGAAGTGCTGAAATGTGTTG  2196

Qy  3094  GTTCTTCAATGTTCCTCAAAAGTAAATGGGGATCGGCTACCCCCTGAGCCATGTACATAG  3153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2197  GTTCTTCAATGTTCCTCAAAAGTAAATGGGGATCGGCTACCCCCTGAGCCATGTACATAG  2256

Qy  3154  ACAAATATTGTGCCACAGAATCTCTTTCTTCCACTGGTTAAACAACATACCTGGGAGCTA  3213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2257  ACAAATATTGTGCCACAGAATCTCTTTCTTCCACTGGTTAAACAACATACCTGGGAGCTA  2316

Qy  3214  CTTTATTACAACAGAATGACCAACAACTTGTATAGCTTGCCTTTCAAGGACATGGACA  3273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2317  CTTTATTACAACAGAATGACCAACAACTTGTATAGCTTGCCTTTCAAGGACATGGACA  2376

Qy  3274  AATTTTCAGGTTTGTTTTCTGCCCTAGACAGTCATTCAAATTGGGTGTCATTTCTTATG  3333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2377  AATTTTCAGGTTTGTTTTCTGCCCTAGACAGTCATTCAAATTGGGTGTCATTTCTTATG  2436

Qy  3334  GTGTTCCATGAGGACTTTGGAAGACGACTTGGAGAAGTTGAAGCAGAATTGAAGCAGAAATTG  3393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2437  GTGTTCCATGAGGACTTTGGAAAACAACGACTTGGAGAAGTTGAAGCAGAATTGAAGCAGAAATTG  2496

Qy  3394  ACCAAGCAGATAAATCAGTTATTAGTGTATTTCTTCTTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAAT  3453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2497  ACCAAGCAGATAAATCAGTTATTAGTGTATTTCTTCTTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAAT  2556

Qy  3454  CTTTTGATGAAAATGGAACAGAGCTTACTTATTCTTTCTTCTGAAACCAAGGCTTCTCTCCTAGTGA  3513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2557  CTTTTGATGAAAATGGAACAGAGCTTACTTATTCTTTCTTCTGAAACCAAGGCTTCTCTCCTAGTGA  2616

Qy  3514  GCACCATGAAAGTTGGAAACAAGACGTTATGTACAACACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCT  3573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2617  GCACCATGAAAGTTGGAAACAAGAGCCTTTGGAAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCT  2676

Qy  3574  TGAAACGTGAAAGTAAATCAGTTGAGAATCAGTGAGATCAGTGTGCTTGCTTCTCGCTTTCTCGCTTTCAATTTTTTTTCACAG  3633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2677  TGAAACGTGAAAGTAAATCAGTTGAGAATCAGTGAGATCAGTGTGCTTACTTCTCGCTTTCTCGCTTTCAATTTTTTTTCACAG  2736

Qy  3634  TTCAGATTTTTATGTTTTGGTTCATCATCGTTTCATCACTCTTTAAAAATGCTGTGGTTCCCATCAAAC  3693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2737  TTCAGATTTTTATGTTTTGGTTCATCATCGTTTCATCACTCTTTAAAAATGCTGTGGTTCCCATCAAAC  2796

Qy  3694  TTGTTCCAGACTTATATTTTCTCAGAAAACCTGGAGACAAACACCATTATAATACAAAAACAAGTC  3753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2797  TTGTTCCAGACTTATATTTTCTCAAAAACCTGGAGACAAACACCATTATAATACAAAAACAAGTC  2856

Qy  3754  TGCTTCTTCAAAATTCTGCT--------------GACTCAGATATCAGTGATCTTA  3795
          ||||||||||||||||||||              ||||||||||||||||||||||
Db  2857  TGCTTCTTCAAAATTCTGCTGGTGAGAGTGTNNGTGAGACTCAGATATCAGTGATCTTA  2916

Qy  3796  TTAGCTTTTCACAAGCCAGAACATAATGGTGACATGATTAATGACAGTGACTATGTAT  3855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2917  TTAGCTTTTCACAAGCCAGAACATAATGGTGACATGATTAATGACAGTGACTATGTAT  2976

Qy  3856  CCGTGGCTCCCATAGTGCGGCTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTG  3915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2977  CCGTGGCTCCCATAGTGCGGCTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTG  3036

Qy  3916  CAGCTGTTTCAACAGTACTATGGTTTATTCTTTACCTATATTAGTGAATATCATTAGTA  3975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3037  CAGCTGTTTCAACAGTACTATGGTTTATTCTTTACCTATATTAGTGAATATCATTAGTA  3096

Qy  3976  ACTACTATCTTTATCATTTAAAATGTGACTGAAACCATCCAGATCTCGGAGTACCCCATTCT  4035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3097  ACTACTATCTTTATCATTTAAAATGTGACTGAAACCATCCAGATCTCGGAGTACCCCATTCT  3156

Qy  4036  TTCAAGAAATTACTGATATAGTTTTTAAAATTGAGCTGTATTTCAAGCAGCTTTGCTTG  4095
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3157  TTCAAGAAATTACTGATATAGTTTTTAAAATTGAGCTGTATTTCAAGCAGCTTTGCTTG  3216

Qy  4096  G-AATCATTGTTACTGCAATGCCACCTTACTTGCCATGGAAAATGCAGAGAATCATAAG--  4154
          |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3217  GAAAATCATTGTAACTGCAATGCCACCTTACTTGCCATGGAAAA-TGCAGAGAATCATA-  3274

Qy  4155  ATCAAAGCTTATACTCAACTTAAACTTCAGGTCTTTTGCCATCTGCATATTGGATTGGA  4214
          ||||||||||||||||||||||||||||||||||||          ||||||||||||||
Db  3275  ----------------------------------AGGTCTTTTGCCATCTGCATATTGGA  3305

Qy  4215  CAAGCTGTTGTGATATCCCTTATTTTTATCATTCTTATTTTGATGCTAGGAAGCTTA  4274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3306  CAAGCTGTTGTGATATCCCTTATTTTTATCATTCTTATTTTGATGCTAGGAAGCTTA  3365

Qy  4275  CTGGCATTCATTATGGATTATATTTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTTGC  4334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3366  TTGGCATTCATTATGGATTATATTTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTTGC  3425

Qy  4335  CTTATTGGTTATGTTCCATCACGTATTCCGTCTCACTTCTCGTCTCTTTTTCCACCTTTAAG  4394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3426  CTTATTGGTTATGTTCCATCAGTTATTCCGTCTCACTTCTCGTCTCTTTTTCCACCTTTAAG  3485

Qy  4395  AAAATTTAAATACCAAAGAATTTTGGTCATTTATCTATTCTGTGGCAGCGTTGNCTTGT  4454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3486  AAAATTTAAATACCAAAGAATTTTGGTCATTTATCTATTCTGTGGCAGCGTTGGCTTGT  3545

Qy  4455  ATTGCAATCACTGAAATAACTTCTTCTTATGGGATACACAATTCTTCATTAT  4514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3546  ATTGCAATCACTGAAATAACTTCTTCTTATGGGATACACAATTCTTCATTAT  3605

Qy  4515  GCCTTTGTATCATCATTCCAATCATCACTTCAGTTGCCTGATTTCATTTCATAAAG  4574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3606  GCCTTTGTATCATCATTCCAATCATCACTTCAGTTGCCTGATTTCATTTCATAAAG  3665

Qy  4575  ATTTCTTGGAAGAATGTACGACAAAAATGTACGACCTATAATCCATGGATAGGCTTTCA  4634
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3666  ATTTCTTGGAAGAATGTACGACAAAAATGTACGACCTATAATCCATGGATAGGCTTTCA  3725

Qy  4635  GTAGCTGTTATATCGCCTTACCTGCCAGTGTACTTGTGGATTTCCTCTTACAATACTAT  4694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3726  GTAGCTGTTATATCCGCTTACCTGCCAGTGTACTTGTGGATTTCCTCTTACAATACTAT  3785

Qy  4695  GAGAAAAATATGAGGCAGATCAATAAGAAGATCCCTTTCAGAAACCTTTCAACG  4754
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  3786  GAGAAAAAATGAGGCAGATCAATAGAAGATCCCTTTTTCAGAACCTTTCAACG                3845
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4755  AAGTCTAAAAATAGGAAGCTTCCAGAACCACCACAGAACAATGAGGATGAAGATGAAGATGTC      4814
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3846  AAGTCTAAAAATAGAAGCTTCCAGAACCACCACAGAACAATGAGGATGAAGATGAAGATGTC       3905

Qy  4815  AAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCA         4874
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3906  AAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCA         3965

Qy  4875  TCCATTATGGTCAGCAATTGCATAAAGAATATGATGCAAGAAAGAGATTTTCTTCCTTTCA       4934
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3966  TCCATTATGGTCAGCAATTGCATAAAGAATATGATGCAAGAAAGAGATTTTCTTCCTTTCA       4025

Qy  4935  AGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTTTCTGTGTGAAAAAGGAGAGATC     4994
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4026  AGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTTTCTGTGTGAAAAAGGAGAGATC     4085

Qy  4995  TTAGGACTATTGGGTCCAAATGGTCTGGCAAAGCACAATTATTAATATTCTCGGTTGGT         5054
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4086  TTAGGACTATTGGGTCCAAATGGTCTGGCAAAGCACAATTATTAATATTCTCGGTTGGT         4145

Qy  5055  GATAATTGAACCAACTTCAGGCCCAGGTATTTTTAGGAGATTATTCTTCAGACAACAAGTGAA     5114
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4146  GATAATTGAACCAACTTCAGGCCCAGGTATTTTTAGGAGATTATTCTTCAGACAACAAGTGAA     4205

Qy  5115  GATGATGATTCACTGAAGTGTATGGGTTACTGTCCTCAGATAAACCCTTTGTGGCCAGAT       5174
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4206  GATGATGATTCACTGAAGTGTATGGGTTACTGTCCTCAGATAAACCCTTTGTGGCCAGAT       4265

Qy  5175  ACTACAATTGCAGGAACATTTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGAC       5234
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4266  ACTACAATTGCAGGAACATTTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGAC       4325

Qy  5235  ATGAAAGAAGTCATAAGTCGAATAACACCATGCACTTGATTTAAAGAACATCTTCAGAAG       5294
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4326  ATGAAAGAAGTCATAAGTCGAATAACACCATGCACTTGATTTAAAGAACATCTTCAGAAG       4385

Qy  5295  ACTGTAAGAAACTACCTGCAGGAATCAAACGAAAGTGTGTTTGCTCTAAGTATGCTA         5354
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4386  ACTGTAAGAAACTACCTGCAGGAATCAAACGAAAGTGTGTTTGCTCTAAGTATGCTA         4445

Qy  5355  GGGAATCCTCAGATTACTTGCTAGAGTGAACCATCACAGTGATCCCAAAGCCAAA             5414
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4446  GGGAATCCTCAGATTACTTGCTAGAGTGAACCATCTACAGGTATGGATCCCAAAGCCAAA       4505

Qy  5415  CAGCACATGTGGCGAGCAATTGCAACTGCAATTCCAAATGCATTTAAAAACAGAAAGCGGGCTGCTATTCTG   5474
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4506  CAGCACATGTGGCGAGCAATTGCAACTGCAATTCCAAATGCATTTAAAAACAGAAAGCGGGCTGCTATTCTG   4565

Qy  5475  ACCACTCACTATATGGAGGAGGCAGAGCTACAACATCTAAAGAGTAAATTGGAAAAGGCTAC     5534
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4566  ACCACTCACTATATGGAGGAGGCAGAGCTACAACATCTAAAGAGTAAATTGGAAAAGGCTAC     4625

Qy  5535  GGGCAGTTAAGATGTATCGGAACAGGTACACAATCTAAAGAGTAAATTTGGAAAAGGCTAC     5594
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4626  GGGCAGTTAAGATGTATCGGAACAGTCACACAATCTAAAGAGTAAATTTGGAAAAGGCTAC     4685

Qy  5595  TTTTTGGAAATTAAATTGAAGGACTAGAGAAACCTAGAAGTAGACCGCCTTCAAAGA         5654
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4686  TTTTTGGAAATTAAATTGAAGGACTAGAGAAACCTAGAAGTAGACCGCCTTCAAAGA         4745

Qy  5655  GAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCT       5714
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4746  GAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCT       4805

Qy  5715  TATAAAATTCCTAAGGAAGATGTTCAGTCCTTCCACATCTTTTTTTTAAGCTGGAGAA         5774
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4806  TATAAAATTCCTAAGGAAGAATGTTCAGTCCTTCCACATCTTTTTTTTAAGCTGGAGAA        4865

Qy  5775  GCTAAACATGCTTTTGCCATTGAAGAATAAGCTTTTCTCAAGCAACATTGGAACAGGTT       5834
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4866  GCTAAACATGCTTTTGCCATTGAAGAATAAGCTTTTCTCAAGCAACATTGGAACAGGTT       4925
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Qy  5835  TTTGTAGAACTCACTCAGAAGAACAAGAGGAAGAAGATATAGTTGTGGAACTTTAAACAGC    5894
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4926  TTTGTAGAACTCACTCAGAAGAACAAGAGGAAGAAGATAATAGTTGTGGAACTTTAAACAGC   4985

Qy  5895  ACACTTTGGTGGGAACGAACACAGAAGATAGAGTATTTGTATTGTTCGG               5954
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  4986  ACACTTTGGTGGGAACGAACACAGAAGATAGAGTAGTATTTGTATTGTTCGG            5045

Qy  5955  TCTGCTTACTGGGACTTCTTTCACTTAATTTAACTTGGTTTAAAAAGTTTT              6014
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5046  TCTGCTTACTGGGACTTCTTTCACTTAATTTAACTTGGTTTAAAAAGTTTT             5105

Qy  6015  TATTGGAATGGTAACTGGAGAACCAAGAACGCACTTGAAATTTTCTAAGCTCCTTAATT      6074
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5106  TATTGGAATGGTAACTGGAGAACCAAGAACGCACTTGAAATTTTCTAAGCTCCTTAATT     5165

Qy  6075  GAAATGCTGCTGGTGTGTTTGCTTTTGCTTTTGCTTTTGTATTGTATTAATTAAGTGA      6134
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5166  GAAATGCTGCTGGTGTGTTTGCTTTTGCTTTTGCTTTTGTATTGTATTAATTAAGTGA     5225

Qy  6135  AGCTGCATGTTGTATTGAAGTATATTGAACTATATAGTTGTATGTCATCTTTTTCACC      6194
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5226  AGCTGCATGTTGTATTGAAGTATATTGAACTATATAGTTGTATGTCATCTTTTTCACC     5285

Qy  6195  ATTCAGAAACACAGTGCTTCTGAATTGTGATTAAAGGATTGTAATAGTTTTATT          6254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5286  ATTCAGAAACACAGTGCTTCTGAATTGTGATTAAAGGATTGTAATAGTTTTATT         5345

Qy  6255  TTTAAGTTATCTTTAAGTTTATGGCCATCTTCTTAAATAAGTAACGTAATGTTCCAATCTAA   6314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5346  TTTAAGTTATCTTTAAGTTTATGGCCATCTTCTTAAATAAGTAACGTAATGTTCCAATCTAA  5405

Qy  6315  ATAAAAAACTAATACATAACTAATGCATAGAAAAGATACATAAAGCAATGCAATGTGAAAGTT   6372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5406  ATAAAAAACTAATTCATAACTAATGCATAGAAAAGATACATAAAGCAATGCAATGTGAAAGTT  5463
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RESULT 7
AAD37620
ID   AAD37620 standard; cDNA; 5262 BP.
XX
AC   AAD37620;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human transporter protein cDNA #3.
XX
KW   Human; novel human protein; NHP; transporter protein; mental disorder;
KW   cancer; gene therapy; drug screening; nutriceutical application;
KW   cosmetic application; polymorphism; ss.
XX
OS   Homo sapiens.
XX
PN   WO200231147-A2.
XX
PD   18-APR-2002.
XX
PF   04-OCT-2001; 2001WO-US031113.
XX
PR   10-OCT-2000; 2000US-0239629P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Hu Y, Nepomnichy B;
XX
DR   WPI; 2002-454552/48.
XX
PT   Novel nucleic acid molecule encoding novel human proteins, useful for
PT   therapeutic, diagnostic and pharmacogenomic applications.
XX
PS   Disclosure; Page 45-46; 46pp; English.
XX
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CC   The present sequence is a cDNA coding for novel human protein (NHP),
CC   human transporter protein. NHPs shares structural similarity with the
CC   mammalian ATP-binding cassette (ABC) transporters and multidrug
CC   resistance transporters. NHP polynucleotides are useful for the
CC   therapeutic, diagnostic and pharmacogenomic applications. They are used
CC   for detecting and treating mental disorders and cancers. They are also
CC   used in gene therapy. NHP polypeptides are useful for diagnosis, drug
CC   screening, clinical trial monitoring, treatment of diseases and
CC   disorders, and cosmetic or nutriceutical applications
XX
SQ   Sequence 5262 BP; 1615 A; 888 C; 1012 G; 1743 T; 0 U; 4 Other;

Query Match             80.4%;  Score 5247.4;  DB 6;  Length 5262;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 5248;  Conservative    4;  Mismatches    4;  Indels    6;  Gaps    0;

Qy    757 ACTGTTGATATGGTGGTATTTCAAATTCGGTCTCACCCTATTCCACATGCCTTGTTTACT 816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACTGTTGATATGGTGGTATTTCAAATTCGGTCTCACCCTATTCCACATGCCTTGTTTACT 60

Qy    817 TTTCAGAGCTGACAGATTGCTGCTCCATGCATTCGTCCAGTTCCTAAGAGAGACAGCT 876
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TTTCAGAGCTGACAGATTGCTGCTCCATGCATTCGTCCAGTTCCTAAGAGAGACAGCT 120

Qy    877 TGGGAGTATGCTAATCATCTTACCTGGGACTGAAACAGCTGCTTATTTGCCGTTAAAA 936
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGGGAGTATGCTAATCATCTTACCTGGGACTGAAACAGCTGCTTATTTGCCGTTAAAA 180

Qy    937 ATTACATGCAGTTACTGGTGGCTCCGGGTTGTTGTTTGTTTTCCTCTTTAATAGG 996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATTACATGCAGTTACTGGTGGCTCCGGGTTGTTGTTTGTTTTCCTCTTTAATAGG 240

Qy    997 TTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTTGGAGACAGACCAGAA 1056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTTGGAGACAGACCAGAA 300

Qy   1057 CACTTCTACTGAAGAATACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAA 1116
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CACTTCTACTGAAGAATACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAA 360

Qy   1117 TTCTTTTTCCACTATTTTTTTATTTCGTTAATATTAATTAGCATGATGCATCCAAATA 1176
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TTCTTTTTCCACTATTTTTTTATTTCGTTAATATTAATTAGCATGATGCATCCAAATA 420

Qy   1177 AGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTACTCTTTCTA 1236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTACTCTTTCTA 480

Qy   1237 ATCTAATTCTTGATATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGT 1296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ATCTAATTCTTGATATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGT 540

Qy   1297 CTACTGATCATCTCACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAGAAATGT 1356
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTACTGATCATCTCACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAGAAATGT 600

Qy   1357 TAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGTGGTTTCAAAGACTCCATGT 1416
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGTGGTTTCAAAGACTCCATGT 660

Qy   1417 CCTATGAACTTCGTTTTTTCCTGATATGATTCCAGTATCTTCTATTTATATGGATTCAA 1476
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CCTATGAACTTCGTTTTTTCCTGATATGATTCCAGTATCTTCTATTTATATGGATTCAA 720

Qy   1477 GAGCTGGCTGTTCAAAATCATGTGAGGCTGCTTACAGTTGAAGACCAAATGTTTCACAGTTT 1536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GAGCTGGCTGTTCAAAATCATGTGAGGCTGCTTACAGTTGAAGACCAAATGTTTCACAGTTT 780

Qy   1537 TACAAGCATCCATAGATGTCTGCCATTATACAGTTGAAGACCAAATGTTCTCTTTGGAAGG 1596
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TACAAGCATCCATAGATGTCTGCCATTATACAGTTGAAGACCAAATGTTCTCTTTGGAAGG 840

Qy   1597 AGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAAACTGCTGTGTTGTAGAAATAGATACCT 1656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 AGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAAACTGCTGTGTTGTAGAAATAGATACCT 900

Qy   1657 TTCCCGAGGAGTAATTTAATATACCTAGTTATAGCATTTCACCTTTGGATACTTTT 1716
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TTCCCGAGGAGTAATTTAATATACCTAGTTATAGCATTTCACCTTTGGATACTTTT 960

Qy   1717 TGGCAATTCATATCGTAGCAGAAAAGAAAATAAAAGAAATTTTAAGATAATGG 1776
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    961 TGGCAATTCATATCGTAGCAGAAAAGAAAAATAAAAGAAAATTTTAAGAATAATGG 1020

Qy   1777 GACTTCATGATACTGCCTTTGGCTTTCTCGGGTTCTTCGGGTTCTTCTTGTTATATACAAGTTTAATTTTTC 1836
          |||||||||||||||||||||||||||||||||||: ||||||||||||||||||||||||||||||||||||
Db   1021 GACTTCATGATACTGCCTTTGGCTTTCTCGGGTTCTTCGGGTTCTTCATAWACAAGTTTAATTTTTC 1080

Qy   1837 TTATGTCCCTTCTTATGGCAGTCATTGCGACAGCTCTTGTTGTTATTTCCTCAAAGTAGCA 1896
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TTATGTCCCTTCTTATGGCAGTCATTGCGACAGCTCTTGTTGTTATTTCCTCAAAGTAGCA 1140

Qy   1897 GCATTGTGATATTCTGCTTTTTTCCTTTATGGATTATCATCTGTATTTTTTGTTAA 1956
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCATTGTGATATTCTGCTTTTTTCCTTTATGGATTATCATCTGTATTTTTTGCTTTAA 1200

Qy   1957 TGCTGACACCTCCTTTTAAAAAATCAAAACATGTGGGATTAGTAGGAATTTTTGTTACTG 2016
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TGCTGACACCTCCTTTTAAAAAATCAAAACATGTGGAATAGTGGAATTTTTGTTACTG 1260

Qy   2017 TGGCTTTTGGATTTATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAG 2076
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGGCTTTTGGATTTATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAG 1320

Qy   2077 TGTGGCTTTTCAGTCCTTTCTGTCACTGTACTTTGTGATTGGTATTGCACAGGTCATGC 2136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TGTGGCTTTTCAGTCCTTTCTGTCACTGTACTTTGTGATTGGTATTGCACAGGTCATGC 1380

Qy   2137 ATTTAGAAGATTTAATGAAGGTGCTCATTTTCAAATTTCAAATTTCAAATTTCAAATCGTTAG 2196
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Db   1381 ATTTAGAAGATTTAATGAAGGTGCTTCATTTTCAAATTTCAAATTTCAAATCGTTAG 1440

Qy   2197 TAATTATTACAATTATCATGTCCACACTTAATAGAGTATATTCTATGTCCTCTTGGCTGTCT 2256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TAATTATTACAATTATCATGTCCACACTTAATAGAGTATATTCTATGTCCTCTTGGCTGTCT 1500

Qy   2257 ATCTTGATCAAGTCATTCCAGGGGAATTGGCTTACGGAGATCATCTTTATAATTTCTGA 2316
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Db   1501 ATCTTGATCAAGTCATTCCAGGGGAATTGGCTTACGGAGATCATCTTTATAATTTTCTGA 1560

Qy   2317 AGCCTTCATATTGGTCAAAGAGTAAAAGAAATATTGAGGGGCAATGTTA 2376
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Db   1561 AGCCTTCATATTGGTCAAAGAGTAAAAGAAATATTGAGGGGCAATGTTA 1620

Qy   2377 ATGGAAATATTAGTTTTAGTGAAATTATTGAGCCAGTTTCTTCAGAAATTGTAGGAAAAGT 2436
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Db   1621 ATGGAAATATTAGTTTTAGTGAAATTATTGAGCCAGTTTCTTCAGAAATTGTAGGAAAAGT 1680

Qy   2437 AAGCCATAGAATTAGTGTATTCAGAAGACATACAGAAGAAGAGGGTGAAAATGTGGAG 2496
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Db   1681 AAGCCATAGAATTAGTGGATTCAGAAGACATACAGAAGAAGAGGGTGAAAATGTGGAG 1740

Qy   2497 CTTTGAGAAATTTGTCATTTGACATTGGTTACTGCCTCTTGGCCGCCACA 2556
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTTTGAGAAATTTGTCATTTGACATTGGTTACTGCCTCTTGGCCGCCACA 1800

Qy   2557 GTGGAACAGGAAAGAGTACATTGATGAATATTCTTTGTGGGACTCTGCCCACCTTCTGATG 2616
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GTGGAACAGGAAAGAGTACATTGATGAATATTCTTTGTGGGACTCTGCCCACCTTCTGATG 1860

Qy   2617 GGTTTGCATCTATATGGACACAGAGTCTCAGAAATGATGAAAATGTTGAAGCAAGAA 2676
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 GGTTTGCATCTATATGGACACAGAGTCTCAGAAATAGATGAAAATGTTTGAAGCAAGAA 1920

Qy   2677 AAATGATTGCATTGTCCACAGTTAGATATACACTTTGATGTTTTGACAGTGAAGAAA 2736
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Db  1921  AAATGATTGGCATTTGTCCACAGTTAGATATACACTTTGATGTTTGACAGTGAGAGAAA   1980

Qy  2737  ATTTATCAATTTTGGCTTCAATCAAAGGGATACCAGCCAACAATATAATACAAGAAGTGC  2796
          |||||||||||||  |||||  |||||||||||||||||||||||||||||||||||||
Db  1981  ATTTATCAATTTTGCTTCAACAAAGGGATACCAGCCAACAATATAATACAAGAAGTGC    2040

Qy  2797  AGAAGGTTTTACTAGATTTAGACATGCAGACTATCAGAGATAACCAAGCTAAAAAATTAA  2856
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Db  2041  AGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAA  2100

Qy  2857  GTGGTGGTCAAAAAGAAAGCTGTGTCTTGGGAACCCAAAGATAC                  2916
          |||||||||||||||||||||||||||||||||||||||||||
Db  2101  GTGGTGGTCAAAAAGAAAGCTGTGTCTTGGGAACCCAAAGATAC                  2160

Qy  2917  TGCTGCTAGATGAATGACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGATGGAATC  2976
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Db  2161  TGCTGCTAGATGAATGACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGATGGAATC  2220

Qy  2977  TTTTAAAATACAGAAAAGCCAATGGGTGACAGTGTCAGTACTCATTTCATGGATGAAG    3036
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Db  2221  TTTTAAAATACAGAAAAGCCAATGGGTGACAGTGTCAGTACTCATTTCATGGATGAAG    2280

Qy  3037  CTGACATTCTTGCAGATAGGAAAGCTGTGTATCACCACAAGGAATGCTGAAAATGTGTTGGTT  3096
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Db  2281  CTGACATTCTGCGACATAGTGATATCACAAGGAATGCTGAAAATGTGTTGGTT          2340

Qy  3097  CTTCAATGTTCCTCAAAGTAAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACA  3156
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Db  2341  CTTCAATGTTCCTCAAAAGTAAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACA  2400

Qy  3157  AATATTGTGCCACAGAATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTT   3216
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Db  2401  AATATTGTGCCACAGAATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTT   2460

Qy  3217  TATTACAACAGAATGACCAACAACTTGTGTATAGCTTGTGCCTTTCAAGGACATGGACAAAT  3276
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Db  2461  TATTACAACAGAATGACCAACAACTTGTATAGCTTGTGCCTTTCAAGGACATGGACAAAT   2520

Qy  3277  TTTCAGGTTGTTTTCTCGCCCTAGACAGTCATTCAAATTGGGGTGTCATTTCTTATGGTG  3336
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Db  2521  TTTCAGGTTGTTTTCTCGCCCTAGACAGTCATTCAAATTGGGTGGCATTTCTTATGGGG   2580

Qy  3337  TTTCCATGACGACTTGGAAGACTGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTGACC   3396
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Db  2581  TTTCCATGACGACTTGGAAGACTATTTTTAAAGCTAGAAGTTGAAGCAGAAATTGACC    2640

Qy  3397  AAGCAGATTATAGTGTATTTACTCAGCAGCCACTGGAGGAGGAAATGGATTCAAAATCTT   3456
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Db  2641  AAGCAGATTATAGTGTATTTACTCAGCAGCCACTGGAGGAGGAAATGGATTCAAAATCTT   2700

Qy  3457  TTGATGAAATGGGAACAGCAGAGCTTACTTACTTCTTCTGAAAACCAAGGCTTCTCTAGTGAGCA  3516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  TTGATGAAATGGGAACAGCAGAGCTTACTTACTTCTTCTGAAAACCAAGGCTKCTCAGTGAGCA  2760

Qy  3517  CCATGAGCCTTGGAAACAACAGATGTATACAATAGCAAAGTTCATTTCTTTTACCTTGA   3576
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  CCATGAGCCTTGGAAACAACAGATGTATACAATAGCAAAGTTCATTTCTTTTACCTTGA   2820

Qy  3577  AACGTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTTGCTTTTTAATTTTTTTCACAGTTC  3636
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  AACGTGAAAGTAAATCAGTGAGATCAGTGTGCTTGCTTTTTAATTTTTTTCACAGTTC    2880

Qy  3637  AGATTTTATGTTTTTGGTTCATCACTCTTTAAAATGTCTGGTTCCCATCAAACTTG    3696
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  AGATTTTATGTTTTTGGTTCATCACTCTTTAAAATGTCTGGTTCCCATCAAACTTG    2940

Qy  3697  TTCCAGACTTATATTTTCTAAACCTGGAGACAAAACCACATAAATACAAAACAAGTCTGC  3756
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  TTCCAGACTTATATTTTCTAAAACCTGGAGACAAAACCACATAAATACAAAACAAGTCTGC  3000

Qy  3757  TTCTTTCAAAATTCTGCTGACTCAGATATCAGTTGATCTTATTAGCTTTTTTCACAAGCCAGA  3816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  TTCTTCAAAATTCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTTTCACAAGCCAGA  3060
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Qy  3817  ACATATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGCGG  3876
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  ACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGCGG   3120

Qy  3877  CTTTAAAATGTGATGCATTCAGAAAAGGACTATCGTGTTTTGCAGCTGTTTTCAACAGTACTA  3936
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Db  3121  CTTTAAATGTGRTGCATTCAGAAAAAGGACTGTGTTTTGCAGCTGTTTTCAACAGTACTA   3180

Qy  3937  TGGTTTATTCTTTACCTATATTAGTAGTGAATATCATTAGTAACTACTATCTTTATCATTTAA  3996
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Db  3181  TGGTTTATTCTTTACCTATATTAGTAGTGAATATCATTAGTAACTACTATCTTTATCATTTAA  3240

Qy  3997  ATGTGACTAGAACCATCCAGATCTGGAGTCGACTACCCATTCTTCTTGGAATTACTGATATAG  4056
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  ATGTGACTAGAACCATCCAGATCTGGAGTCGACCCCATTCTTCTTCAAGAAATTACTGATATAG  3300

Qy  4057  TTTTAAAATTGAGCTGTATTTCAAGCAGCTTGCTTGGAATCATTGTTACTGCAATGC    4116
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Db  3301  TTTTAAAATTGAGCTGTATTTCAAGCAGCTTGCTTGGAATCATTGTTACTGCAATGC    3360

Qy  4117  CACCTTACTTGCCATGGAAATGCAGAGAATCATAAGATCAAAGCTTATACTTCAACTTA   4176
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Db  3361  CACCTTACTTGCCATGGAAAATGCAGAGAATCATAAGATCAAAAGCTTAYACTTCAACTTA   3420

Qy  4177  AACTTTCAGGTCTTTGCCATCTGCATATTGGATTGGACAACAAGCTGTTGTTGATATCCCCT  4236
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Db  3421  AACTTTCAGGTCTTTTGCCATCTGCATATTGGATTGGACCAAGCTGTTGTTGATATCCCCT   3480

Qy  4237  TATTTTTATCATTCTTATTTGTGTGGCAGCGTTACTGGAGCTACTTCATTATGATGGATTAT  4296
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Db  3481  TATTTTTATCATTCTTATTTGTGTGGCAGCGTTATTGGAGCTTATTCATTATGGA-TAT    3540

Qy  4297  ATTTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTGCCTTATTGGTTATGTTCCATCAG    4356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  ATTTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTGCCTTATTGGTTATGTTCCATCAG    3600

Qy  4357  TTATTCTGTTCACTTATATTGCTTCTTCTTCACCTTAAGAAAATTTTAAATACCAAAGAAT  4416
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  TTATTCTGTTCACTTATATTGCTTCTTCTTCACCTTCAAGAAAATTTTAAATACCAAAGAAT  3660

Qy  4417  TTTGGTCATTTATCATTCGTGTGGCAGCGTTGNCTGTATTGCAATCACTGAAATAACTT   4476
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  3661  TTTGGTCATTTATCCATTCGTGTGGCAGCGTTGGCTGTATTGCAATCACTGAAATAACTT   3720

Qy  4477  TCTTTATGGGATACACAATTGCAACTATTCTTCATTATTGCCTTTTGTATCATCATTCCAA   4536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  TCTTTATGGGATACACAATTGCAACAATTCTTCATTATTGCCTTTGTATCATCATTCCAA   3780

Qy  4537  TCTATCCACTTCTAGGTTGCCTGATTTCTTCATAAAGATTTCTTGGAAGAATGTACGAA    4596
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Db  3781  TCTATCCACTTCTAGGTTGCCTGATTTCTTCATAAAAGATTTCTTGGAAGAATGTACGAA   3840

Qy  4597  AAAATGTGGACACCTTATAATCATGGGATAGGCTTTCAGTAGTCGTTTATATCGCCCTACC  4656
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Db  3841  AAAATGTGGACACCTTATAATCATGGGATAGGCTTTCAGTAGTCGTTTATATCGCCTTACC  3900

Qy  4657  TGCAGTGTGTACTGTGACTGTGATTTCCTCTACAACTACTGATGAGAAAAAATATGGAGGCAGAT  4716
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Db  3901  TGCAGTGTGTACTGTGACTGTGATTTCCTCTACAACTACTGATGAGAAAAAATATGGAGGCAGAT  3960

Qy  4717  CAATAAGAAAGATCCCTTTCAACGAAACCTTTCAACCAAGGCTCAAAAAATAGGAAGAGCTTC  4776
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961  CAATAAGAAAGATCCCTTTTCAACGAAACCTTTCAACCAAGGCTCAAAAAATAGGAAGAGCTTC  4020

Qy  4777  CAGAACCACCAGACAATGAGGATGAAGATGAAAGTGAAAGACTAAAAGTCA          4836
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Qy  4837  AAGAGCTGATGGGTTGCCCAGTGTTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGC  4896
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Qy   4897  ATAAAGAATATGATGACAAGAAAGATTTTCTTCCTTCAAGAAAAGTAAGAAAGTGGCAA  4956
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Db   4141  ATAAAGAATATGATGACAAGAAAGATTTTCTTCCTTCAAGAAAAGTAAGAAAGTGGCAA  4200

Qy   4957  CTAAATACATCTCTTCCTGTGTGAAAAAAGGAGATCTTAGGACTATTGGGTCCAAATG   5016
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Db   4201  CTAAATACATCTCTTTCTGTGTGAAAAAAGGAGATCTTAGGACTATTGGGTCCAAATG   4260

Qy   5017  GTGCTGGCAAAGCACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCC  5076
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Db   4261  GTGCTGGCAAAGCACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCC  4320

Qy   5077  AGGTATTTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATTCACTGAAGTGTA   5136
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Db   4321  AGGTATTTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATTCACTGAAGTGTA   4380

Qy   5137  TGGGTTACTGTCCTCAGATAAACCCTTTGTGGCCAGATACTACATTGCAGGAACATTTTG  5196
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Db   4381  TGGGTTACTGTCCTCAGATAAACCCTTTGTGGCCAGATACTACATTGCAGGAACATTTTG  4440

Qy   5197  AAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGCAAGTGACATGAAAGAAGTCATAAGTCGAA  5256
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Qy   5257  TAACACATGCACTTGATTTAAAAGAACATCTTCAGAGACTGTAAAGAAACTACTTGCAG  5316
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Db   4501  TAACACATGCACTTGATTTAAAAGAACATCTTCAGAGACTGTAAAGAAACTACTTGCAG  4560

Qy   5317  GAATCAAACGAAAGTTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGC  5376
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Db   4561  GAATCAAACGAAAGTTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGC  4620

Qy   5377  TAGATGAACCATCTACACGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTC  5436
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Db   4621  TAGATGAACCATCTACACGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTC  4680

Qy   5437  GAACTGCATTAAAAACAGAAAGCGGGCTGCTATTCTGCACCACTCACTATATGGAGGAGG  5496
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Qy   5497  CAGAGGCTGTCTCGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAA  5556
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Db   4741  CAGAGGCTGTCTCGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAA  4800

Qy   5557  CAGTACAACATCTAAAGAGTAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTGAAGG  5616
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Db   4801  CAGTACAACATCTAAAGAGTAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTGAAGG  4860

Qy   5617  ACTGGATAGAAAACCTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTCCCAA  5676
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Db   4861  ACTGGATAGAAAACCTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTCCCAA  4920

Qy   5677  ATGCAACCCGTCAGGAAGTTTTCTTCCTATTTGGCTTATAAAATTCCTAAGGAAGATG  5736
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Qy   5797  AAGAATATAGCTTTTCTCAAGCAACATTGGAACAGGTTTTTGTAGAACTCACTAAAGAAC  5856
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Qy   5857  AAGAGGAGGAAGAAGATAATAGTTGTGGAACTTAAACAGCACACTTTCGTGTGGAACGAACAC  5916
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Db   5101  AAGAGGAGGAAGAAGATAATAGTTGTGGAACTTAAACAGCACACTTTCGTGTGGAACGAACAC  5160

Qy   5917  AAGAAGATAGAGTAGTATTTTGAATTTGTATTGTTCGGTCTTACTCGGGACTTCTTTC  5976
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Db   5161  AAGAAGATAGAGTAGTATTTTGAATTTGTATTGTTCGGTCTGCTTACTCGGGACTTCTTTC  5220

Qy   5977  TTTTTCACTTAATTTTAACTTTGGTTTAAAAAGTTTTT  6014
           |||||||||||||||||||||||||||||||||||||
Db   5221  TTTTTCACTTAATTTTAACTTTGGTTTAAAAAGTTTTT  5258
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RESULT 8
AAD37618
ID   AAD37618 standard; cDNA; 4929 BP.
XX
AC   AAD37618;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human transporter protein cDNA #1.
XX
KW   Human; novel human protein; NHP; transporter protein; mental disorder;
KW   cancer; gene therapy; drug screening; nutriceutical application; gene;
KW   cosmetic application; polymorphism; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   site"
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FT                   site"
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FT                   site"
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XX
PD   18-APR-2002.
XX
PF   04-OCT-2001; 2001WO-US031113.
XX
PR   10-OCT-2000; 2000US-0239629P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Hu Y, Nepomnichy B;
XX
DR   WPI; 2002-454552/48.
DR   P-PSDB; AAE23656.
XX
PT   Novel nucleic acid molecule encoding novel human proteins, useful for
PT   therapeutic, diagnostic and pharmacogenomic applications.
XX
PS   Claim 1; Page 34-35; 46pp; English.
XX
CC   The present sequence is a cDNA coding for novel human protein (NHP),
CC   human transporter protein. NHPs shares structural similarity with the
CC   mammalian ATP-binding cassette (ABC) transporters and multidrug
CC   resistance transporters. NHP polynucleotides are useful for the
CC   therapeutic, diagnostic and pharmacogenomic applications. They are used
CC   for detecting and treating mental disorders and cancers. They are also
CC   used in gene therapy. NHP polypeptides are useful for diagnosis, drug
CC   screening, clinical trial monitoring, treatment of diseases and
CC   disorders, and cosmetic or nutriceutical applications
XX
SQ   Sequence 4929 BP; 1544 A; 827 C; 950 G; 1604 T; 0 U; 4 Other;
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Db   5221  TTTTTCACTTAATTTTAACTTTGGTTTAAAAAGTTTTT  5258
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Query Match   75.4%; Score 4918.4; DB 6; Length 4929;

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Best Local Similarity  99.8%;  Pred. No. 0;
Matches 4919;  Conservative  4;  Mismatches  6;  Indels  0;  Gaps  0;


Qy  1011 ATGTCCACTCGCAATTAGGGAGGTAGGAGTTGGAGACAGACCAGAACACTTCTACTGAAG 1070
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 AGTTCCACTCGCAATTAGGGAGGTAGGAGTTGGAGACAGACCAGAACACTTCTACTGAAG 60

Qy  1071 AATTACTTAATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATTCTTTTCCACTA 1130
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 AATTACTTAATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATTCTTTTCCACTA 120

Qy  1131 TTTTTTTTATTTTGGTTAATATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 1190
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTTTTTTTATTTTGGTTAATATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 180

Qy  1191 GTGCCTAATATAGAACTCAATCCATGGACAAGTTACTCTTCTAATCTAATTCTTGGA 1250
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTGCCTAATATAGAACTCAATCCATGGACAAGTTACTCTTCTAATCTAATTCTTGGA 240

Qy  1251 TATACTCCAGTGACTAATATTACAAGCAGCATCAGAAAGTGTCTACTGATCATCTA 1310
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TATACTCCAGTGACTAATATTACAAGCAGCATCAGAAAGTGTCTACTGATCATCTA 300

Qy  1311 CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAGAAGAGAATGTTAACATCCAGTCTC 1370
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAGAAGAGAATGTTAACATCCAGTCTC 360

Qy  1371 TCTAAGCCGAGCAACTTGTAGTGTGGTTTCTATTATTATATGGATTCAAGAGCTCGAGTCA 1430
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TCTAAGCCGAGCAACTTGTAGTGTGGTTTCTATTATTATATGGATTCAAGAGCTCGAGTCA 420

Qy  1431 TTTTTTCCTGATATGATTCCAGTATCTTCTATTATGGATTATATGAATTCACAGTTTCGT 1490
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TTTTTTCCTGATATGATTCCAGTATCTTCTATTATGGATTATATGAATTCACAGTTTCGT 480

Qy  1491 AAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGTTTCACAGTTTACAAGCATCCATA 1550
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGTTTCACAGTTTACAAGCATCCATA 540

Qy  1551 GATGCTGCCATTATACAGTTGAAGACCAAATGTTTCTCTTTGGAAGAGCTCGAGTCAACT 1610
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GATGCTGCCATTATACAGTTGAAGACCAAATGTTTCTCTTTGGAAGAGCTCGAGTCAACT 600

Qy  1611 AAAGTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCCGAGAGTA 1670
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AAAGTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCCGAGAGTA 660

Qy  1671 ATTTTAATAACCTAGTTATAGAGCATTTTCACCTTTTTGGATACTTTTGGCAATTCATATC 1730
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATTTTAATAACCTAGTTATAGAGCATTTTCACCTTTTTGGATACTTTTGGCAATTCATATC 720

Qy  1731 GTAGCAGAAAAAGAAAAAGAAAAAATAAAAGAATTTTAAAGATAAATGGGACTTCATGATACT 1790
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GTAGCAGAAAAAGAAAAAGAAAAAATAAAAGAATTTTAAAGATAAATGGGACTTCATGATACT 780

Qy  1791 GCCTTTTGGGTTTCCTGGGTTCTCTATATACAAGTTAATTTTCTTATGTCCCTTCTT 1850
         |||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db   781 GCCTTTTGGGTTTCCTGGGTTCTCTATAWACAAGTTTAATTTTCTTATGTCCCTTCTT 840

Qy  1851 ATGGCAGTCATTGCGACAGCTTCTTTGTTATTCCTCAAAGTAGCAGCATTGTGATATTT 1910
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ATGGCAGTCATTGCCACAGCTTCTTTGTATTTCCTCAAAGTAGCAGCATTGTGATATTT 900

Qy  1911 CTGCTTTTTTTCCTTTATGGATTATCATCGTATTTTGAATTTTTGTTACTGTGGCTTTTGGATTT 1970
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CTGCTTTTTTTCCTTTATGGATTATCATCGTATTTTGAATTTTTGTTACTGTGGCTTTTGGATTT 960

Qy  1971 TTTAAAAATCAAAACATGTGGAATAAGTTGAATTTTTTGTTACTGTTTTGGATTT 2030
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTTAAAAATCAAAACATGTGGAATAAGTTGAATTTTTTGTTACTGTTTTGGATTT 1020

Qy  2031 ATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCAGT 2090
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 AAAAGTAAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACA 2160


Qy  1021 ATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCAGT 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2091 CCTTTCGTCACTGTACTTTGTGATTGGTATTGCACAGGTCATGCATTTAGAAGATTTT 2150

Qy  1081 CCTTTCGTCACTGTACTTTGTGATTGGTATTGCACAGGTCATGCATTTAGAAGATTTT 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 AGTTCCACTCGCAATTAGGGAGGTAGGAGTTGGAGACAGACCAGAACACTTCTACTGAAG 1140

Qy  2151 AATGAAGGTGCTTCATTTCATTTTCAAATTGACTGCAGGCCATATCCTCTAATTATTACAATT 2210
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 AATGAAGGTGCTTCATTTCATTTTCAAATTGACTGCAGGCCATATCCTCTAATTATTACAATT 1200

Qy  2211 ATCATGCTCACACTTAATAGTATATTCTATGTCCTCTGGCTGTCTATCTGATCAAGTC 2270
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 ATCATGCTCACACTTAATAGTATATTCTATGTCCTCTGGCTGTCTATCTGATCAAGTC 1260

Qy  2271 ATTCCAGGGGAATTGGCTACCGAGATCATCTTTATATTTCTGAAGCCTTCATATTGG 2330
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 ATTCCAGGGGAATTGGCTTACCGGAGATCATCTTTATATTTCTGAAGCCTTCATATTGG 1320

Qy  2331 TCAAAGAGTAAAAGAAATATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT 2390
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 TCAAAGAGCAAAAGAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT 1380

Qy  2391 TTTAGTGAAATTATTGAGCCAGTTTCTTCAGAATTTGTAGGAAAAGAAGAGCCATAAGAATT 2450
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 TTTAGTGAAATTATTGAGCCAGTTTCTTCAGAATTTGTAGGAAAAGAAGAGCCATAAGAATT 1440

Qy  2451 AGTGGTATTCAGAGACATACAGAAAGAGAGGGTGAAAATGTGAGGGCTTTGAGAAATTTG 2510
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 AGTGGTATTCAGAGACATACAGAAAGAGAGGGTGAAAATGTGAGGGCTTTGAGAAATTTG 1500

Qy  2511 TCATTGACATATGAGGGTCAGAATTACTGCCTTACTCGGCCACAGTGGAACAGGAAAG 2570
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 TCATTTGACATATGAGGGTCAGATTACTACTGCCCTACTCGGCCACCAGTGGAACAGGAAAG 1560

Qy  2571 AGTACATTGATGAATATCTTGTGACTCTGCCCACCTTCGATGGGTTTCGATCTATA 2630
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 AGTACATTGATGAATATCTTGTGGACTCTGCCCACCTTCTGATGGGTTTCGATCTATA 1620

Qy  2631 TATGGACACAGAGTCTCAGAAATGATGAAAATGTTGAAGCAAGAAAATGATTGGCATT 2690
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TATGGACACAGAGTCTCAGAAATGATGAAAATGTTGAAGCAAGAAAATGATTGGCATT 1680

Qy  2691 TGTCCAGTTAGTATACACTTTGATGTTTTGCACAGTAGAAGAAAATTTATCAATTTTG 2750
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 TGTCCACAGTTAGTATACACTTTGATGTTTTGGACAGTAGAAGAAAATTATCAATTTTG 1740

Qy  2751 GCTTCAATCAAAGGGATACCAGCCAACATATCAAAGATAACCAAGCTAAAAAATTGGTCACTA 2810
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 GCTTCAATCAAAGGGATACCAGCCACCCAATATATCAAAGATAACCAAGCTAAAAAATTACTA 1800

Qy  2811 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGCTGGTGGTCAAAAA 2870
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGCTGGTGGTCAAAAA 1860

Qy  2871 AGAAAGCTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTCGTAGAATGAA 2930
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 AGAAAGCTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTCGTAGAATGAA 1920

Qy  2931 CCAACAGCTGGAATGGACCCCGTTCTCGACACATTGTATGGAATCTTTAAAATACAGA 2990
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CCAACAGCTGGAATGGACCCCGTTCTCGACACATTGTATGGAATCTTTAAAATACAGA 1980

Qy  2991 AAAGGCCAATCGGGTGACAGTGTTCAGTACTCATTCATTTGAAGCTGAACATTCTTGCA 3050
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTCATTGAAGCTGAACATTCTTGCA 2040

Qy  3051 GATAGGAAAGCTGTGATATCACAAGGAATGCTGAAAATGTGTTGTTCTTCAATGTTCCTC 3110
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 GATAGGAAAGCTGTGATATCGATATCACAAGGAATGCTGAAAATGTGTTGGTTCTTCAATGTTCCTC 2100

Qy  3111 AAAAGTAAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACA 3170
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 AAAAGTAAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACA 2160
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Right column:

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Qy  4251 CTTATTTTGATGCTAGGAAGCTTACTGGCATTCATTCATTTATGGATTATATTTTATACTGTA 4310
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 CTTATTTTGATGCTAGGAAGCTTATTGGCATTCATTCATTATGGATTATATTTTATACTGTA 3300

Qy  4311 AAGTTCCTTGCTGTGGTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACT 4370
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 AAGTTCCTTGCTGTGGTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACT 3360

Qy  4371 TATATTGCTTCTTAAGAAAATTTAAATACCAAAGAATTTGGTCATTTATC 4430
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TATATTGCTTCTTAAGAAAATTTAAATACCAAAGAATTTTGGTCATTTATC 3420

Qy  4431 TATTCTGTGGCAGCGTTGNCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGATAC 4490
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 TATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGATAC 3480

Qy  4491 ACAAATTGCAACTATTCTTCATTATGCCTTTGTATCATCATTCCAATCTATCATCCACTTCTA 4550
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 ACAAATTGCAACTATTCTTCATTATGCCTTTGTATCATCATTCCAATCTATCCACTTCTA 3540

Qy  4551 GGTTGCCTGATTTCTTCATAAAGATTTCTGGAAGAATGTACGAAAAAATGTGACACC 4610
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 GGTTGCCTGATTTCTTCATAAAGATTTCTTGGAAGAATGTACGAAAAAATGTGACACC 3600

Qy  4611 TATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGGCCTTACCTGCAGTGTGTACTG 4670
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 TATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGGCCTTACCTGCAGTGTGTACTG 3660

Qy  4671 TGGATTTTCCTCTACAATACTATAGAGAAAAAAAATGGGAGGCAGATCAATAAGAAAAGAT 4730
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 TGGATTTTCCTCTACAATACTATAGAGAAAAAAATGGGAGGCAGATCAATAAGAAAAGAT 3720

Qy  4731 CCCTTTTTCAGAAACTTTCAACGAAGTCTAAAATAGGAGCTCAAGAGCTTCCAGAACCACCAGAC 4790
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 CCCTTTTTCAGAAACTTTCAACGAAGTCTAAAATAGGAGCTCAAGAGCTTCCAGAACCACCAGAC 3780

Qy  4791 AATGAGGATGAAGATGTCAAAGCTGAAAGACTTAAGGTCAAAGAGTGTGGGT 4850
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 AATGAGGATGAAGATGTCAAAGCTGAAAGACTTAAGGTCAAAGAGTGTGGGT 3840

Qy  4851 TGCCAGTGTTGTGAGGAGAAACCATCCATTATGGTCATAAGAGAATATGAT 4910
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 TGCCAGTGTTGTGAGGAGAAACCATCCATTATGGTCATAAGAGAATATGAT 3900

Qy  4911 GACAAGAAAGATTTCTTCTTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCT 4970
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 GACAAGAAAGATTTCTTCTTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCT 3960

Qy  4971 TTCTGTGTGAAAAGGAGATCTTAGGACTATTGGGTCCAAAAGTGTGTGGCAAAAGC 5030
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961 TTCTGTGTGAAAAGGAGATCTTAGGACTATTGGGTCCAAATGTGTGGCAAAAGC 4020

Qy  5031 ACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGTATTTTTAGGA 5090
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021 ACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGTATTTTTAGGA 4080

Qy  5091 GATTATTCTTCAGAGACAAGTGAGCAAGTGATGATGATGATGTCAACTCACTCAGGTATGGTTACTGTCCT 5150
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081 GATTATTCTTCAGAGACAAGTGAGCAAGTGATGATGATGATGATGTCAACTCACTCAGGTATGGTTACTGTCCT 4140

Qy  5151 CAGATAAACCCTTTGTGGCCAGATCTACATTGCGGAACACATTTTGAAAATTTATGGAGCT 5210
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141 CAGATAAACCCTTTGTGGCCAGATCTACATTGCGGAACACATTTTGAAATTTATGGAGCT 4200

Qy  5211 GTCAAAGGAATGGAGTGCAAGTGACATGACATGAAAGAAGTCATAAGTCGAATAACACATGCACTT 5270
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201 GTCAAAGGAATGGAGTGCAAGTGACATGACATGAAAGAAGTCATAAGTCGAATAACACATGCACTT 4260

Qy  5271 GATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTCGCAGGAATCAAACGAAAG 5330
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4261 GATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTCGCAGGAATCAAACGAAAG 4320

Qy  5331 TTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTTACTTTGCTAGATGAACCATCT 5390
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Left column:

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Qy  3171 GAATCTCTTCTTCACTGGTTAAACAACATACCTGGAGCTACTTTATTACAACAGAAT 3230
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GAATCTCTTCTTCACTGGTTAAACAACATACCTGGAGCTACTTTATTACAACAGAAT 2220

Qy  3231 GACCAACAACTTGTATAGCTTGCCTTCAAGGACATGGACAAAATTTCAGGTTGTTT 3290
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GACCAACAACTTGTATAGCTTGCCTTCAAGGACATGGACAAAATTTCAGGTTGTTT 2280

Qy  3291 TCTGCCCTAGACAGTCATTCAAATTGGGTGTCATTTCTTATGGTGTTCCATGACCGACT 3350
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TCTGCCCTAGACAGTCATTCAAATTGGGTGCCATTTCTTATGGGTTTCCATGACGACT 2340

Qy  3351 TTGGAAGACGTATTTTAAAGCTAGAAGTTGAGCAGAAATTGACCAAGCAGATTATAGT 3410
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TTGGAAGACGTATTTTTAAAGCTAGAAGTTGAGCAGAAATTGACCAAGCAGATTATAGT 2400

Qy  3411 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTGATGAAATGGAA 3470
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GTATTTACTCAGCAGCCACGCCACTGGAGGAAGAAATGGATTCAAAAATCTTTGATGAAATGGAA 2460

Qy  3471 CAGAGCTTACTACTTCTTTCTGAAACCAAGGCTTCTCTCAGTGAGCAGCCATGAGCGCCTTTGG 3530
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGAGCTTACTACTTCTTTCTGAAACCAAGGCTKCTCCAGTGAGCAGCCATGAGCGCCTTTGG 2520

Qy  3531 AAACAACAGATGTATACAATAGCAAAGTTCATTTCTTTACCTTGAAACGTGAAAGTAAA 3590
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 AAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCTTGAAACGTGAAAGTAAA 2580

Qy  3591 TCAGTGAGATCAGTGTTGCTTCTGTCTTTTAATTTTTTCACAGTTCAGATTTTTATGTTT 3650
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 TCAGTGAGATCAGTGTTGCTTCTGTCTTTTAATTTTTTTCACAGTTTCAGATTTTTATGTTT 2640

Qy  3651 TTGGTTCATCACTCTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTATAT 3710
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 TTGGTTCATCACTCTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTATAT 2700

Qy  3711 TTTCTAAAAACCTGGAGACAAAACCACATAAATACAAAACAGTCTGCTTCTTCTCAAAATTCT 3770
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 TTTCTAAAAACCTGGAGACAAAACCACATAAATACAAAACAGTCTGCTTCTTCTCAAAATTCT 2760

Qy  3771 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTCACAAGCCAGAACATAATGGTGACG 3830
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTCACAAGCCAGAACATAATGGTGACG 2820

Qy  3831 ATGATTAATGACAGTGACTATGTACCGTGGCCTCCCCATAGTGCGGCTTTAAATGTGATG 3890
         |||||||||||||||||||||||||||||||||||||||||:||
Db  2821 ATGATTAATGACAGTGACTATGTACCGTGGCCTCCCCATAGTGCGGCTTTAAATGTGRTG 2880

Qy  3891 CATTCAGAAAAGGAGCTATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTATTCTTTA 3950
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 CATTCAGAAAAGGAGCTATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTATTCTTTA 2940

Qy  3951 CCTATATTAGTGAATATCATTCAATTACTACTATCTTTATCATTTAAAGTGACTGAAACC 4010
         |||||||||||||||||||||||||||||||||||||:||||
Db  2941 CCTATATTAGTGAATATCATTCAATTACTACTATCTTTATCATTTAAAGTGACTGAAACC 3000

Qy  4011 ATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGATATAGTTTTTAAAAATTGAG 4070
         |||||||||||||||||||||||||||||||||||||||||||||:|
Db  3001 ATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGATATAGTTTTTAAAAATTGAG 3060

Qy  4071 CTGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCC 4130
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 CTGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCC 3120

Qy  4131 ATGGAAAATGCAGAGAATCATAGATCAGAAGCTTATACTCAACTTAAACTTTCAGGTCTT 4190
         |||||||||||||||||||||||||||||||||||:|||
Db  3121 ATGGAAAATGCAGAGAATCATAGATCAGAAGCTTATACTCAACTTAAACTTTCAGGTCTT 3180

Qy  4191 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTTGATATCCCCTTATTTTTTATCATT 4250
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTTGATATCCCCTTATTTTTTATCATT 3240
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Qy

Db

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Db    4321  TTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 4380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    5391  ACAGGTATGATCCCAAAGCCACATGTGGCGAGCAATTCGAACTGCATTTAAA 5450
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4381  ACAGGTATGATCCCAAAGCCACACAGCACATGTGGCGAGCAATTCGAACTGCATTTAAA 4440
Qy    5451  AACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGGCTGTCTGT 5510
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4441  AACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGGCTGTCTGT 4500
Qy    5511  GATCCAGTAGCTATCATGGTGTCTGGGCAGTAAGATGTATCGGAACAGTAGTACAACATCTA 5570
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4501  GATCCAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTA 4560
Qy    5571  AAGAGTAAATTGGAAAAGGCTACTTTTTGGAAATAAATTGAAGGACTGGATAGAGAAAC 5630
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4561  AAGAGTAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTGAAGGACTGGATAGAGAAAC 4620
Qy    5631  CTAGAAGTAGACCGGCCTTCAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAG 5690
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4621  CTAGAAGTAGACCGGCCTTCAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAG 4680
Qy    5691  GAAAGTTTTCTCTATTTTGGCTATAAAATTCCTAAGGAGAGATGTTCAGTCCCTTTCA 5750
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4681  GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAGGAAGATGTTCAGTCCCTTTCA 4740
Qy    5751  CAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTT 5810
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4741  CAATCTTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTTGCCATTGAAGAATATAGCTTT 4800
Qy    5811  TCTCAAGCAACATTGGAACAGAGTTTTGTAGAACTCACTAAAGAACAAGAGGAGGAAGAT 5870
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4801  TCTCAAGCAACATTGGAACAGAGTTTTGTAGAACTCACTAAAGAACAAGAGGAGGAAGAT 4860
Qy    5871  AATAGTGTGGAACTTAAACAGCACACTTGGTGGGAACGAACACAAGAAGATAGAGTA 5930
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4861  AATAGTGTGGAACTTAAACAGCACACTTGGTGGGAACGAACACAAGAAGATAGAGTA 4920
Qy    5931  GTATTTTGA 5939
            |||||||||
Db    4921  GTATTTTGA 4929
```

```
RESULT 9
ABS57750
ID   ABS57750 standard; cDNA; 4917 BP.
XX
AC   ABS57750;
XX
DT   04-FEB-2003  (first entry)
XX
DE   Coding sequence of human ATP binding cassette ABCA5 transporter #1.
XX
KW   Human; ATP binding cassette; ABC; ABCA5; transporter;
KW   neurotoxin transport; beta-amyloid peptide; chromosome mapping;
KW   blood brain barrier transport; tissue typing; predictive medicine;
KW   ABCA5 mediated disorder; ABCA5 related disorder; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..4917
FT                  /tag= a
FT                  /product= "ABCA5"
FT                  /note= "ATP binding cassette (ABC) A5 transporter"
FT                  /transl_except= (pos:3160..3162, aa:Ser)
XX
PN   US200212307-A1.
XX
PD   05-SEP-2002.
XX
PF   01-MAR-2002; 2002US-00090458.
```

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XX
PR   02-MAR-2001; 2001US-0272885P.
XX
PA   (ACTI-) ACTIVE PASS PHARM INC.
XX
PI   Chen H, Kilinski L, Le Bihan S;
XX
DR   WPI; 2003-066798/06.
DR   P-PSDB; ABG72423.
XX
PT   Novel isolated ATP binding cassette transporter family polypeptide,
PT   ABCA5, useful for treating disorders associated with aberrant or unwanted
PT   ABCA5 transporter expression or activity.
XX
PS   Claim 2; Fig 1; 52pp; English.
XX
CC   The invention describes an isolated ATP binding cassette (ABC)
CC   transporter family polypeptide (I), designated ABCA5. (I) or the
CC   polynucleotide encoding it (II) are useful as targets for developing
CC   modulating agents to regulate a variety of cellular processes,
CC   particularly the transport of neurotoxic molecules, e.g., beta-amyloid
CC   peptide (Abeta), across cell membranes or, e.g., the blood brain barrier
CC   (BBB), as targets for developing modulating agents of multi-drug
CC   resistance, as diagnostic and therapeutic tools, or to treat disorders
CC   associated with aberrant or unwanted ABCA5 transporter expression or
CC   activity. (I), (II) or a host cell (III) expressing (II) are useful in
CC   screening assays, detection assays (e.g., chromosomal mapping, tissue
CC   typing, forensic biology), predictive medicine (e.g., diagnostic assays,
CC   prognostic assays, monitoring clinical trials and pharmacogenomics), and
CC   in methods of treatment (e.g., therapeutic and prophylactic). (I) or
CC   (III) are useful as reagents or targets in assays applicable to treatment
CC   and diagnosis of ABCA5-mediated or related disorders. (II) is useful to
CC   screen for naturally occurring ABCA5 substrates; to screen for drugs or
CC   compounds which modulate ABCA5 activity; as a bait protein in a yeast two
CC   -hybrid or three-hybrid assay; and to identify other proteins which bind
CC   to or interact with ABCA5. (II) is useful in: gene therapy; to detect
CC   ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5
CC   activity; to locate gene regions associated with genetic disease or to
CC   associate ABCA5 with the disease, to identify an individual from a minute
CC   biological sample (tissue typing), and to aid in forensic identification
CC   of the biological sample. This sequence encodes a novel human ATP binding
CC   cassette (ABC) A5 transporter
XX
SQ   Sequence 4917 BP; 1540 A; 821 C; 955 G; 1599 T; 0 U; 2 Other;

Query Match             73.7%;  Score 4807.4;  DB 10;  Length 4917;
Best Local Similarity   98.8%;  Pred. No. 0;
Matches 4891;  Conservative    0;  Mismatches    7;  Indels  50;  Gaps    3;
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Qy    1011  ATGTCCACTGCAATTAGGGAGGTTGGAGACAGAGACCAGAACACTTCTACTGAAG 1070
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1  ATGTCCACTGCAATTAGGGAGGTGGAGACAGAGACCAGAACACTTCTACTGAAG 60
Qy    1071  AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCTTTTTCCACTA 1130
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCTTTTTCCACTA 120
Qy    1131  TTTTTTTTTATTTTGGTTAATATAATTAATTAGCATGATGCATCCAAATAGAAAATATGAAGAA 1190
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  TTTTTTTTTATTTTGGTTAATATAATTAATTAGCATGATGCATCCAAATAGAAAATATGAAGAA 180
Qy    1191  GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATTCTTGGA 1250
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATTCTTGGA 240
Qy    1251  TATACTCCAGTGACTAATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 1310
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  TATACTCCAGTGACTAATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 300
Qy    1311  CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAAATGTTAACATCCAGTCTC 1370
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAAATGTTAACATCCAGTCTC 360
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us-10-005-338b-1.rng

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Qy  1441 AGTGGTATTCAGAAGACATACAGAAGAAAGAAGAGGTGAAAATGTGGAGCTTGAGAAATTG 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2511 TCATTTGACATATGAGGGTCAGATTACTGCCTTACTTGGCCCACAGTGAACAGGAAAG 2570

Qy  1501 TCATTTGACATATGAGGGTCAGATTACTGCCTTACTTGGCCCACAGTGAACAGGAAAG 1560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2571 AGTACATTGATGAATATTCTTGTGGACTCTGCCACCTTCGTGATGGGTTTGCATCTATA 2630

Qy  1561 AGTACATTGATGAATATTCTTGTGGACTCTGCCACCTTCGTGATGGGTTTGCATCTATA 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2631 TATGGACACAGAGTCTCAGAAATAGATGAAAGTTGAAGCAAGAAAATGATTGGCATT 2690

Qy  1621 TATGGACACAGAGTCTCAGAAATAGATGAAAGTTGAAGCAAGAAAATGATTGGCATT 1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2691 TGTCCACAGTTAGTATACACTTTGATGTTTGACAGTAGAAGAAATTTATCAATTTTG 2750

Qy  1681 TGTCCACAGTTAGTATACACTTTGATGTTTGACAGTAGAAGAAATTTATCAATTTTG 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2751 GCTTCAATCAAAGGATCCAACAATATAATACAAGAAGTGCAGAAGGTTTTACTA 2810

Qy  1741 GCTTCAATCAAAGGATCCAACAATATAATACAAGAAGTGCAGAAGGTTTTACTA 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2811 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 2870

Qy  1801 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2871 AGAAAGCTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA 2930

Qy  1861 AGAAAGCTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2931 CCAACAGCTGAATGGGTGACAGTGTTCAGTACTCATTCATGGATGAAGCTGACATTCTTGCA 2990

Qy  1921 CCAACAGCTGAATGGGTGACAGTGTTCAGTACTCATTCATGGATGAAGCTGACATTCTTGCA 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2991 AAAGCCAATCGGTGACAGTGTTCAGTGTTCATGGATGAAGCTGACATTCTTGCA 3050

Qy  1981 AAAGCCAATCGGTGACAGTGTTCAGTGTTCATGGATGAAGCTGACATTCTTGCA 2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3051 GATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTGGTCTTCAAATGTTCCTC 3110

Qy  2041 GATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTGGTCTTCAAATGTTCCTC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3111 AAAAGTAAATGGGGATCGGCTACCGCCTGGAACAACATACCTGGACTACTTATTACACAGAAT 3170

Qy  2101 AAAAGTAAATGGGGATCGGCTACCGCCTGGAACAACATACCTGGACTACTTATTACACAGAAT 3160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3171 GAATCTCTTTCTTCACTGGTTAAACAACATACCTGGACTACTTATTACACAGAAT 3230

Qy  3171 GAATCTCTTTCTTCACTGGTTAAACAACATACCTGGACTACTTATTACACAGAAT 3230
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GAATCTCTTTCTTCACTGGTTAAACAACATACCTGGACTACTTATTACACAGAAT 2220

Qy  3231 GACCAACAACTGTGTATAGCTTGCCTTTCAAGGACATGACAAATTTTCAGGTTGTTT 3290
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GACCAACAACTGTGTATAGCTTGCCTTTCAAGGACATGACAAATTTTCAGGTTGTTT 2280

Qy  3291 TCTGCCCTAGACAGTCATTCAAATTGGGTGTCATTTCTTATGGTGTTCCATGACGACT 3350
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TCTGCCCTAGACAGTCATTCAAATTGGGTGTCATTTCTTATGGTGTTCCATGACGACT 2340

Qy  3351 TTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATGACCAAGCAGATTATAGT 3410
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATGACCAAGCAGATTATAGT 2400

Qy  3411 GTATTACTCAGCACTCTTCTCTGAGCACCAACCAAGTCTTTGATGAAATGGAA 3470
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GTATTACTCAGCACTCTTCTCTGAGCACCAACCAAGTCTTTGATGAAATGGAA 2460

Qy  3471 CAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCTCTCAGTGAGCACCATGAGCCTTTGG 3530
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCTCTCAGTGAGCACCATGAGCCTTTGG 2520

Qy  3531 AAACAACAGATGTATACAATAGACAAGTTTCATTTCTTAACCTTGAAACGTGAAAGTAAA 3590
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1371 TCTAAGCCCAGCAACTTTGTAGGTGTGGTTTTCAAAGACTCCATGTCCTATGAACTTCGT 1430
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TCTAAGCCCAGCAACTTTGTAGGTGTGGTTTTCAAAGACTCCATGTCCTATGAACTTCGT 420

Qy  1431 TTTTTCCTGATATGATCCAGTATCTTCTATTTATATGGATTCAAGAGCTGGCTGTTCA 1490
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TTTTTCCTGATATGATCCAGTATCTTCTATTTATATGGATTCAAGAGCTGGCTGTTCA 480

Qy  1491 AAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTCACAGTTTTACAAGCATCCATA 1550
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTCACAGTTTTACAAGCATCCATA 540

Qy  1551 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGAGCTGGAGTCAACT 1610
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGAGCTGGAGTCAACT 600

Qy  1611 AAAGCTGTTATTATGGGAGAAACTGCTGTGTGTGTAGAAATAGATACCTTTCCCGAGGAGTA 1670
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AAAGCTGTTATTATGGGAGAAACTGCTGTGTGTGTAGAAATAGATACCTTTCCCGAGGAGTA 660

Qy  1671 ATTTAATATACCTAGTTATAGACATTTCACCTTTGGATACTTTTGGCAATTCATATC 1730
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATTTAATATACCTAGTTATAGACATTTCACCTTTGGATACTTTTGGCAATTCATATC 720

Qy  1731 GTAGCAGAAAAAAGAAAAATAAAGAATTTTAAAGATATAATGGGACTTCATGATACT 1790
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GTAGCAGAAAAAAGAAAAATAAAGAATTTTAAAGATATAATGGGACTTCATGATACT 780

Qy  1791 GCCTTTGGCTTCCTGGGTTCTTCTATATACAAGTTTAATTTTCTTATGTCCCTTCTT 1850
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GCCTTTGGCTTCCTGGGTTCTTCTATATACAAGTTTAATTTTCTTATGTCCCTTCTT 840

Qy  1851 ATGGCAGTCATTGCGACAGCTTCTTGTATTTCCTCAAAGTAGCAGCATTGTGATATTT 1910
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ATGGCAGTCATTGCGACAGCTTCTTGTATTTCCTCAAAGTAGCAGCATTGTGATATTT 900

Qy  1911 CTGCTTTTTTCCTTATGGATTATCATCGTATTTTTGCTTAATGCTGACACCTCTT 1970
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CTGCTTTTTTCCTTATGGATTATCATCGTATTTTTGCTTAATGCTGACACCTCTT 960

Qy  1971 TTTAAAAAATCAAAACATGTGGAATAGTTGAATTTTTGTTACTGTGGCTTTTGGATTT 2030
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTTAAAAAATCAAAACATGTGGAATAGTTGAATTTTTGTTACTGTGGCTTTTGGATTT 1020

Qy  2031 ATTGGCCTTATGATAATCCTATGAGAAGTTTCCCAAATCGTAGTGTGGCTTTCAGT 2090
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 ATTGGCCTTATGATAATCCTATGAGAAGTTTCCCAAATCGTAGTGTGGCTTTCAGT 1080

Qy  2091 CCTTTCTGCACTGTGTACTTTGTGATTGGTGTATGCACAGGTCACGCATTTAGAAGATTTT 2150
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CCTTTCTGCACTGTGTACTTTGTGATTGGTGTATGCACAGGTCACGCATTTAGAAGATTTT 1140

Qy  2151 AATGAAGGTGCTTCATTTCAAATTTGACTGCAGGCCCATATCCTTAAATTATTACAATT 2210
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 AATGAAGGTGCTTCATTTCAAATTTGACTGCAGGCCCATATCCTTAAATTATTACAATT 1200

Qy  2211 ATCATGCTCCACACTTAATACTTAATGTCCTCTTGGCTGTCATCTTGATCAAGTC 2270
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 ATCATGCTCCACACTTAATACTTAATGTCCTCTTGGCTGTCATCTTGATCAAGTC 1260

Qy  2271 ATTCCAGGGAATTGGCTTACGGAGATCATCTTATATTTCTGAAGCCTTCATATTGG 2330
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 ATTCCAGGGAATTGGCTTACGGAGATCATCTTATATTTCTGAAGCCTTCATATTGG 1320

Qy  2331 TCAAAGAGCAAAAGAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGAAATATTAGT 2390
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 TCAAAGAGCAAAAGAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGAAATATTAGT 1380

Qy  2391 TTTAGTGAAATTATTGAGCCAGTTCTTCAGAATTTGTAGGAAAAAGAAGCCATAAGAATT 2450
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 TTTAGTGAAATTATTGAGCCAGTTCTTCAGAATTTGTAGGAAAAAGAAGCCATAAGAATT 1440

Qy  2451 AGTGGTATTCAGAAGACATACAGAAAGAAGAGGGTGAAAATGTGGAGGCTTTGAGAAATTTG 2510
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CC   The present sequence is a cDNA coding for novel human protein (NHP),
CC   human transporter protein. NHPs shares structural similarity with the
CC   mammalian ATP-binding cassette (ABC) transporters and multidrug
CC   resistance transporters. NHP polynucleotides are useful for the
CC   therapeutic, diagnostic and pharmacogenomic applications. They are used
CC   for detecting and treating mental disorders and cancers. They are also
CC   used in gene therapy. NHP polypeptides are useful for diagnosis, drug
CC   screening, clinical trial monitoring, treatment of diseases and
CC   disorders, and cosmetic or nutriceutical applications
XX
SQ   Sequence 4785 BP; 1489 A; 807 C; 917 G; 1568 T; 0 U; 4 Other;

Query Match   72.9%; Score 4754.8; DB 6; Length 4785;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 4756; Conservative 4; Mismatches 4; Indels 7; Gaps 0;

Qy   1011 ATGTCCACTGCAATTAGGGAGGTAGGAGTTGGACAGACCAGAACACTTCTACTGAAG 1070
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGTCCACTGCAATTAGGGAGGTAGGAGTTGGACAGACCAGAACACTTCTACTGAAG 60

Qy   1071 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCTTTTTCCACTA 1130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCTTTTTCCACTA 120

Qy   1131 TTTTTTTTATTTGGTTAATATTAATTAATTAGCATGATGATGCATCCAAATAAGAAATATGAAGAA 1190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTTTTTTTATTTGGTTAATATTAATTAATTAGCATGATGATGCATCCAAATAAGAAATATGAAGAA 180

Qy   1191 GTGCCTAATATAGAACTCAATCCTATGGACAAGTTACTCTTCTAATCTAATTCTTGGA 1250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTGCCTAATATAGAACTCAATCCTATGGACAAGTTACTCTTCTAATCTAATTCTTGGA 240

Qy   1251 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 1310
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 300

Qy   1311 CCTGATGTCATAATTACTGAAGAATATACAAATGAAAATGAAAAAGAAATGTTAACATCCAGTCTC 1370
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCTGATGTCATAATTACTGAAGAATATACAAATGAAAATGAAAAAGAAATGTTAACATCCAGTCTC 360

Qy   1371 TCTAAGCCGAGCAACTTGTAGGTGTTTGGTTTCAAAGACTCCATGTCCATGAACTTCGT 1430
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TCTAAGCCGAGCAACTTGTAGGTGTTTGGTTTCAAAGACTCCATGTCCATGAACTTCGT 420

Qy   1431 TTTTTCCTGATATGATTCCAGTATCTTCTATTATATGGATTCAAGAGCTGGCTGTTCA 1490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TTTTTCCTGATATGATTCCAGTATCTTCTATTATATGGATTCAAGAGCTGGCTGTTCA 480

Qy   1491 AAATCATGTGAGCCTGCTCAGTACTAGGTCCTCAGTTTCACAGTTTACAAGCATCCATA 1550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAATCATGTGAGCCTGCTCAGTACTAGGTCCTCAGTTTCACAGTTTACAAGCATCCATA 540

Qy   1551 GATGGTGCCATTATACAGTGAAGACCAATGTTTCTTCTTGGAAGGAGCTGGAGTCAACT 1610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GATGGTGCCATTATACAGTGAAGACCAATGTTTCTTCTTGGAAGGAGCTGGAGTCAACT 600

Qy   1611 AAAGCTGTTATTATGGGAGAAACTGCTGTGTGTAGAAATAGATACTTTCCCGAGGAGTA 1670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AAAGCTGTTATTATGGGAGAAACTGCTGTGTGTAGAAATAGATACTTTCCCGAGGAGTA 660

Qy   1671 ATTTAATATACCTAGTATAGCATTTGGATACTTTTGGCAATTCATATC 1730
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATTTAATATACCTAGTATAGCATTTGGATACTTTTGGCAATTCATATC 720

Qy   1731 GTAGCAGAAAAAGAAAAAAATAAAGAATTTTAAAGATAATGGGACTTCATGATACT 1790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GTAGCAGAAAAAGAAAAAAATAAAGAAAAAAATAAAGAATTTTAAAGATAATGGGACTTCATGATACT 780

Qy   1791 GCCTTTTGGCTTCCTGGGTTCTTCATACAGTTTAATTTTCTTATGTCCCTTCTT 1850
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   781 GCCTTTTGGCTTCCTGGGTTCTTCATAWACAGTTTAATTTTCTTATGTCCCTTCTT 840

Qy   1851 ATGGCAGTCATTGCGACAGCTTCTTGTTATTCCTCAAAGTAGCAGATTGTGATATTT 1910

RESULT 10
AAD37619
ID   AAD37619 standard; cDNA; 4785 BP.
XX
AC   AAD37619;
XX
DT   10-SEP-2002 (first entry)
XX
DE   Human transporter protein cDNA #2.
XX
KW   Human; novel human protein; NHP; transporter protein; mental disorder;
KW   cancer; gene therapy; drug screening; nutriceutical application; gene;
KW   cosmetic application; polymorphism; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..4785
FT   /tag= a
FT   /product= "Human transporter protein #2"
FT   /transl_except= (pos:808..810, aa:Tyr)
FT   /transl_except= (pos:2494..2496, aa:Ser)
FT   /transl_except= (pos:2878..2880, aa:Val)
FT   misc_feature   810
FT   /tag= b
FT   /note= "This degenerate base represents a polymorphic
FT   site"
FT   misc_feature   2494
FT   /tag= c
FT   /note= "This degenerate base represents a polymorphic
FT   site"
FT   misc_feature   2878
FT   /tag= d
FT   /note= "This degenerate base represents a polymorphic
FT   site"
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PN   WO200231147-A2.
XX
PD   18-APR-2002.
XX
PF   04-OCT-2001; 2001WO-US031113.
XX
PR   10-OCT-2000; 2000US-0239629P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Hu Y, Nepomnichy B;
XX
DR   WPI; 2002-454552/48.
DR   P-PSDB; AAE23657.
XX
PT   Novel nucleic acid molecule encoding novel human proteins, useful for
PT   therapeutic, diagnostic and pharmacogenomic applications.
XX
PS   Claim 1; Page 39-41; 46pp; English.
XX

Qy   5732 AGATGTTCAGTCCCTTCCACAATCTTTTTTTAAGCTGAAGAAGCTAAACATGCTTTTGC 5791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4710 AGATGTTCAGTCCCTTTCACAATCTTTTTTTTAAGCTGAAGAAGCTAAACATGCTTTTGC 4769

Qy   5792 CATTGAAGAATATAGCTTTTCTCAAGCAACATTGGAACAGGTTTTGTAGAACTCACTAA 5851
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Db   4770 CATTGAAGAATATAGCTTTTCTCAAGCAACATTGGAACAGGTTTTGTAGAACTCACTAA 4829

Qy   5852 AGAACAAGAGGAGGAAGAAGATAATAGTTGTGGAACTTAAACAGCACACTTGGTGGGAACG 5911
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Qy   5912 AACACAAGAAGATAGAGTAGTATTTTGA 5939
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Db  1921 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGATGGAATCTTTAAAATACAGA 1980
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Qy  2991 AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTCATGGATGAAGCTGACATTCTTGCA   3050
         
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Db  2041 GATAGGAAAGCTGTGATATCACAAGGAAGTCTGAAATGTGTTGGTTCTTCAAATGTTCCTC 2100
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Qy  3111 AAAAGTAAATGGGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACA 3170
         
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Qy  3171 GAATCTCTTTCTTCACTGGTTAAACAACATATTTATTACACAACAGAT             3230
         
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Qy  3231 GACCAACAACTTGTGTATAGCTTGCCTTTCAGGACATGGACAAAATTTCAGGTTTGTTT   3290
         
Db  2221 GACCAACAACTTGTGTATAGCTTGCCTTTCAGGACATGGACAAAATTTCAGGTTTGTTT   2280
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Qy  3291 TCTGCCCTAGACAGTCATTCAAATTTGGGTGTTCATTTCTTATGTGTTTCCATGACGACT 3350
         
Db  2281 TCTGCCCTAGACAGTCATTCAAATTTGGGTGTTCATTTCTTATGTGTTTCCATGACGACT 2340
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Db  2461 CAGAGCTTACTTATTCTTTCTGAAACCAAGGCTKCTCAGTGAGCACCAAGCCTTTGG     2520
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Qy  3591 TCAGTGAGATCAGTGTTGCTTCTGCTTTAATTTTTTCACAGTCAGATTTTTATGTTT     3650
         
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Db  2641 TTGGTTCATCACTCTTTAAAAATGCTGTGGTTCCCATCAAACTGTTCCAGACTTATAT   2700
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Qy  3711 TTTCTAAAACCTGGAGACAAACCACATAAATACAAAGTCTGCTCTTCTTCAAAATTCT   3770
         
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Qy  3771 GCTGACTCAGATATCAGTGATCTTATTAGCTTCACAGCCAGAACATAATGGTGACG     3830
         
Db  2761 GCTGACTCAGATATCAGTGATCTTATTAGCTTCACAGCCAGAACATAATGGTGACG     2820
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Db  2821 ATGATTAATGACAGTGACTATGTTTTGCAGCTGTCTCCGTGGCGCGCTTTAAATGTGRTG 2880
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Qy  3891 CATTCAGGAAAAGGACTATGTTTTTCAACAGTGTCGTCAACAGGTTTATTCTTTA     3950
         
Db  2881 CATTCAGGAAAAGGACTATGTTTTTCAACAGTGTCGTCAACAGGTTTATTCTTTA     2940
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Qy  3951 CCTATATTAGTGAATATCATTAGTAACTACTTTATCATTTAAATGTGACTGAAACC     4010
         
Db  2941 CCTATATTAGTGAATATCATTAGTAACTACTTTATCATTTAAATGTGACTGAAACC     3000
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Qy  4011 ATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGATATAGTTTTTAAAATTGAG 4070
         
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Db   841 ATGGCAGTCATTGCGACAGCTTGTTATTCCTCAAAGTAGCAGCATTGTGATATT     900
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Qy  1911 CTGCTTTTTTTCCTTTATGGATTATCATCTGTATTTTTGCTTAAATGCTGACACCTCTT 1970
         
Db   901 CTGCTTTTTTTCCTTTATGGATTATCATCTGTATTTTTGCTTAAATGCTGACACCTCTT  960
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Qy  1971 TTTAAAAATCAAAACATGTGGAATTGAATTTTGTTACTGTGGCTTTTGGATTT     2030
         
Db   961 TTTAAAAATCAAAACATGTGGAATTGAATTTTGTTACTGTGGCTTTTGGATTT      1020
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Qy  2031 ATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTTTTTCAGT   2090
         
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Qy  2151 AATGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAATT 2210
         
Db  1141 AATGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAATT 1200
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Db  1201 ATCATGCTCACACTTAATAGTATATTCCCTCTGGCTGTCTATCTTGATCAAGTC     1260
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Qy  2271 ATTCCAGGGGAATTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCCTTCATATTGG 2330
         
Db  1261 ATTCCAGGGGAATTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCCTTCATATTGG 1320
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Qy  2331 TCAAAGTAAAAGAATTATGAGGAGTTATCAGAGGGCAATGTTAATGAAATATTAGT     2390
         
Db  1321 TCAAAGTAAAAGAATTATGAGGAGTTATCAGAGGGCAATGTTAATGAAATATTAGT     2450
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Db  1381 TTTAGTGAAATTATTGAGACCAGTTCTTCTTGGGACTTCGCCCACCTCGCCCACCTCATA 1440
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Qy  2451 AGTGGTATTCAGAAGACATACAGAAGAAGAAGAAGGTGAAAATGTGGAGGCTTTGAGAAATTTG 2510
         
Db  1441 AGTGGTATTCAGAAGACATACAGAAGAAGAAGAAGGTGAAAATGTGGAGGCTTTGAGAAATTTG 1500
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Db  1621 TATGGCAACACAGAGTCTCAGAAATAGATGAAAATGTTTGAAGCAAGAAAAAATGATTGGCATT 1680
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Qy  2931 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTAAAATACAGA 2990
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Qy   5151 CAGATAAACCCTTTGTGGCCAGATACTACATTGAGGAACATTTGAAATTTATGGAGCT 5210
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Qy   5211 GTCAAAGGAATGAGTGCAAGTGACATGAAAGAAGTCATAAGTCGAATAACACATGCACTT 5270
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Db   4201 GTCAAAGGAATGAGTGCAAGTGACATGAAAGAAGTCATAAGTCGAATAACACATGCACTT 4260

Qy   5271 GATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAG 5330
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Db   4261 GATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAG 4320

Qy   5331 TTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 5390
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Db   4321 TTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 4380

Qy   5391 ACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTTAAA 5450
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Db   4381 ACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTTAAA 4440

Qy   5451 AACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGGCGTGTCTGT 5510
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Db   4441 AACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGGCGTGTCTGT 4500

Qy   5511 GATCGAGTAGCTATCATGGTGTCTGGCAGTTAAGATGTATCGGAACAGTACACACATCTA 5570
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Db   4561 AAGAGTAAATTGGAAAAGCTACTTTTGGAAATTAAATTCAGTATATTTCCCAAATGCAAGCCGTCAG 4620

Qy   5631 CTAGAAGTAGACCGGCCTTCAAAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAG 5690
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Qy   5691 GAAAGTTTTCTTCTTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTTCA 5750
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Db   4681 GAAAGTTTTCTTCTTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTTCA 4740

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Db   4741 CAATCTTTTTTAAGCTGGAAGAAGT 4767
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RESULT 11
ADM01475
ID   ADM01475 standard; cDNA; 3347 BP.
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AC   ADM01475;
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DT   20-MAY-2004   (first entry)
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DE   Human cDNA of the invention SEQ ID NO:160.
XX
KW   ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS   Homo sapiens.
XX
PN   EP1347046-A1.
XX
PD   24-SEP-2003.
XX
PF   12-APR-2002; 2002EP-00008400.
XX
PR   22-MAR-2002; 2002JP-00137785.
XX
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI   Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI   Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
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Qy   4071 CTGTATTTCAAGCAGCTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCC 4130
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Qy   4131 ATGGAAAATGCAGAGAATCAGAGATCAAAGCTTATACTCAACTTCAACTTTCAGTGTCTT 4190
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Qy   4191 TTGGCCATCTGCATATTGGATTGGACAAGCTGTTGTGATATCCCCTTATTTTTATCATT 4250
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Qy   4251 CTTATTTGATGTCTAGGAAGCTTACTGGCATTTCATTATGGAATTATATTTTTATACTGTA 4310
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Qy   4491 ACAATTGCAACTATTCTTCATTATGCCTTTGTATCATCATTCCAATCTATCTCCACTTCTA 4550
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Qy   4551 GGTTGCCTGATTCTTCATAAAGATTTCTTGGAAGATGTACGAAAAAATGTGGACACC 4610
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Db   3601 TATAATCCATGGGATAGGCTTTCAGTGAGCTGTGTTATATCGCCTTACCTGCAGTGTGTACTG 3660

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Db   3661 TGGATTTTCCTTCTTACAATACTATGAGGAAATATGGAGGCAGATCAATAAGAAAAGAT 3720

Qy   4731 CCCTTTTTCAGAAAACCTTTCAACGAAGCTTCAGAGACCACCAGAC 4790
          |||||||||||||||||||||||||||||||||||||||||||||
Db   3721 CCCTTTTTCAGAAAACCTTTCAACGAAGCTTCAGAGACCACCAGAC 3780

Qy   4791 AATGAGGATGAAGAAGATGAAGATGAAGATGCAAAGCTAAAGGTCAAAGAGCTGATGGGT 4850
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Db   3781 AATGAGGATGAAGAAGATGAAGATGAAGATGCAAAGCTAAAGGTCAAAGAGCTGATGGGT 3840

Qy   4851 TGCCAGTGGTGTGAGGAGGAAACCATCCATTAGTGTCGCAATTTGCATAAAGAATATGAT 4910
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Db   3841 TGCCAGTGGTGTGAGGAGGAAACCATCCATTAGTGTCGCAATTTGCATAAAGAATATGAT 3900

Qy   4911 GACAAGAAAGATTTCTTCTTCCAAGAAAAGTAAGAAAGTGCAACTAAATACATCTCT 4970
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Db   3901 GACAAGAAAGATTTCTTCTTCCAAGAAAAGTAAGAAAGTGGCAACTAAATACATCTCT 3960

Qy   4971 TTCTGTGTGAAAAAAGGAGGAGAGATCTTAGGACTATTGGGTCCAAATGTGCTGGCAAAGC 5030
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Db   3961 TTCTGTGTGAAAAAAGGAGGAGAGATCTTAGGACTATTGGGTCCAAATGTGCTGGCAAAGC 4020

Qy   5031 ACAATTATTAATATTCTGGTTGATATTGAACCACTTCAGGCCCAGGTATTTTTAGGA 5090
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Db   4021 ACAATTATTAATATTCTGGTTGATATTGAACCACTTCAGGCCCAGGTATTTTTAGGA 4080

Qy   5091 GATTATTCTTCAGAGACAAGTGAAGATGATTCACTGAAGTGTATGGGTTACTGTCCT 5150
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Db   4081 GATTATTCTTCAGAGACAAGTGAAGATGATTCACTGAAGTGTATGGGTTACTGTCCT 4140
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DR   WPI; 2003-723558/69.
DR   P-PSDB; ADM03918.
XX
PT   New polynucleotides and polypeptides are useful in gene therapy, for
PT   developing a diagnostic marker or medicines for regulating their
PT   expression and activity, or as a target of gene therapy.
XX
PS   Claim 1; SEQ ID NO 160; 305pp; English.
XX
CC   The invention relates to a novel human polynucleotide and the encoded
CC   polypeptide. A polynucleotide of the invention may have a use in gene
CC   therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC   as a primer for synthesizing the polynucleotide or as a probe for
CC   detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC   useful in gene therapy, for developing a diagnostic marker or medicines
CC   for regulating their expression and activity, or as a target of gene
CC   therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC   are useful as pharmaceutical agents. The present sequence represents a
CC   cDNA sequence of the invention.
XX
SQ   Sequence 3347 BP; 1049 A; 551 C; 643 G; 1104 T; 0 U; 0 Other;

Query Match   49.9%;   Score 3258.2;   DB 11;   Length 3347;
Best Local Similarity 98.5%;   Pred. No. 0;
Matches 3327;   Conservative   0;   Mismatches   4;   Indels   47;   Gaps   2;

Qy   2999 TCGGGTGACAGTGTTCAGTACTCATTCATTGCAGAGCTGCACATTCTTGCAGATAGGAA 3058
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCGGGTGACAGTGTTCAGTACTCATTCATTGCAGAGCTGCACATTCTTGCAGATAGGAA   60

Qy   3059 AGCTGTGATATCACAAGGAATGCTGAAAATGTGTTGGTTCTTCCTCAAAAGTAA 3118
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGCTGTGATATCACAAGGAATGCTGAAAATGTGTTGGTTCTTCCTCAAAAGTAA   120

Qy   3119 ATGGGGGATCGGCTACCGCCTGAGCTACACATAGACAAATATTGTGCCCAGAATCTCT 3178
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ATGGGGGATCGGCTACCGCCTGAGCTACACATAGACAAATATTGTGCCCAGAATCTCT   180

Qy   3179 TTCTTCACTGGTTAAACAACATACCTGGAGCTACTTATTACAACAGAATGACCAACA 3238
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TTCTTCACTGGTTAAACAACATACCTGGAGCTACTTATTACAACAGAATGACCAACA   240

Qy   3239 ACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAATGGGATTCAAAATCTTTCAAATCTTTGTTTTCTGCCCT 3298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAATGGGATTCAAAATCTTTCAAATCTTTGTTTTCTGCCCT   300

Qy   3299 AGACAGTCATTCAAATTGGGTGTCATTTCTTATGGTGTTCCATGCGGACTTTGGAAGA 3358
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGACAGTCATTCAAATTGGGTGTCATTTCTTATGGTGTTCCATGCGGACTTTGGAAGA   360

Qy   3359 CGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGTGTATTTAC 3418
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGTGTATTTAC   420

Qy   3419 TCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTGATGAAATGGAACAGAGCTT 3478
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTGATGAAATGGAACAGAGCTT   480

Qy   3479 ACTTATTCTTCTGAAACCAAGGCTTCCATTCTTCTCCAGTGAGCACCATGAGCCTTTGGAAACAACA 3538
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ACTTATTCTTCTGAAACCAAGGCTTCCATTCTTCTCCAGTGAGCACCATGAGCCTTTGGAAACAACA   540

Qy   3539 GATGTATACAATAGACAAAGTTCATTCTTCATTTCATTCTTTACCTTGAAACGTGAAAGTAAATCAGTGAG 3598
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GATGTATACAATAGACAAAGTTCATTCTTCATTTCATTCTTTACCTTGAAACGTGAAAGTAAATCAGTGAG   600

Qy   3599 ATCAGTGTTGCTTCGCTTCGTCTTTTATTTTTTTCACAGTTTATGTTTTTGGTTCA 3658
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 ATCAGTGTTGCTTCGCTTCGTCTTTTATTTTTTTCACAGTTTATGTTTTTGGTTCA   660

Qy   3659 TCACTCTTTAAAAATGCTGTGGTTCCATCAAACTTGTTCCAGACTTATATTTTCTAAA 3718
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TCACTCTTTAAAAATGCTGTGGTTCCATCAAACTTGTTCCAGACTTATATTTTCTAAA   720

Qy   3719 ACCTGGAGACAAACCACATAAAATACAAAACAAGTCTGCTTCTTCAAAATTCTGCT----- 3773
            ||||||||||||||||||||||||||||| |||||||||||
Db   721 ACCTGGAGACAAACCACATAAATAACAAAACAAGTCTGCTTCTTCAAAATTCTGCTGGTGA   780

Qy   3774 -----------GACTCAGATACTCAGTGATCTTATTAGCTTTTCACAAGCCAGAACATAA   3822
                       ||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GAGTGTGTGAAGACTCAGATATCTGTGATCTTATTAGCTTTTCACAAGCCAGAACATAA   840

Qy   3823 TGGTGACGATGATTAATGACAGTGACTATGTATCCGTGCCTCCCCATAGTGCGGCTTTAA 3882
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   841 TGGTGACGATGATTAATGACAGTGACTATGTATCCGTGCCTCCCCATAGTGCGGCTTTAA   900

Qy   3883 ATGTGATGCATTCAGAAAGGACTATGTTTTGCAGCTGTTTTGCAGCTGTTTTGCAAGTAGTGGTTT   3942
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATGTGATGCATTCAGAAAGGACTATGTTTTTGCAGCTGTTTTGCAGCTGTTTTTGCAACAGTAATGGTTT   960

Qy   3943 ATTCTTACCTATATTAGTGAATATCATTAGTAACTACTACATCTTTATCATTTAAAATGTGA 4002
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ATTCTTACCTATATTAGTGAATATCATTAGTAACTACTACATCTTTATCATTTAAAATGTGA 1020

Qy   4003 CTGAAACCATCCAGATCTGAGTACCCCATTCTTCAAGAAATTACTGATATAGTTTTA 4062
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CTGAAACCATCCAGATCTGAGTACCCCATTCTTCAAGAAATTACTGATATAGTTTTA 1080

Qy   4063 AAATTGAGCTGTATTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGCCACCTT 4122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AAATTGAGCTGTATTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGCCACCTT 1140

Qy   4123 ACTTTTGCCATCGAAAATGCAGAGAATCATAAGATCAAAGCTTATACTCAACTTAAACTT 4182
            |||||||||||||||||||||||||||||||||||
Db   1141 ACTTTTGCCATCGAAAATGCAGAGAATCATA------------------------------ 1170

Qy   4183 CAGGTCTTTTGCCATCTGACATATTGGATTGGACAAGCTGTTGTGTGATATCCCCTATTTT 4242
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 -AGGTCTTTTGCCATCTGATATTGGATTGGACAAGCTGTTGTGTGATATCCCCTATTTT   1229

Qy   4243 TTATCATTCTTATTTGATGCTGAGGAAGCTTACTCGCATTCATTCATGGTGATATATTTT 4302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1230 TTATCATTCTTATTTGATGCTGAGGAAGCTTACTCGCATTCATTCATGGTGATATATTTT 1289

Qy   4303 ATACTGTAAAGTTCCTTGCGTGTGGTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTC 4362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1290 ATACTGTAAAGTTCCTTGCGTGTGGTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTC 1349

Qy   4363 TGTTCACTTATATTGCTTCTTCATGTGTTCCATGCGGACTTTGGAAGA 4422
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1350 TGTTCACTTATATTGCTTCTTCATGTGTTCCATGCGGACTTTGGAAGA 1409

Qy   4423 CATTTATCTATTCTGTGGCAGCGTTGNCTTGATTGCAATCACTGAAATAACTTTCTTTA 4482
            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   1410 CATTTATCTATTCTGTGGCAGCGTTGGCTTGATTGCAATCACTGAAATAACTTTCTTTA 1469

Qy   4483 TGGGATACACAATTGCAACATTCTTCATTGGTGTCTTTGTATCATCATCCAATCTATC 4542
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1470 TGGGATACACAATTGCAACATTCTTCATTGGTGTCTTTGTATCATCATCCAATCTATC 1529

Qy   4543 CACTTCCTAGGTTGCCTGATTTCTTCATAAAGATTCTTGGAAGATGTACGAAAAAATG 4602
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1530 CACTTCCTAGGTTGCCTGATTTCTTCATAAAGATTCTTGGAAGATGTACGAAAAAATG 1589

Qy   4603 TGGACACCTATAATCCATGGGATAGGCTTCAGTAGCGTTATATCGCCTTACCTGCGAGT 4662
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1590 TGGACACCTATAATCCATGGGATAGGCTTCAGTAGCGTTATATCGCCTTACCTGCGAGT 1649

Qy   4663 GTGTACTTGTGGATTTTCCTCTTACACATGAGAAAAAATATGGAGGGCAGATCAATAA 4722
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1650 GTGTACTTGTGGATTTTCCTCTTACACATGAGAAAAAATATGGAGGGCAGATCAATAA 1709

Qy   4723 GAAAAGATCCCTTTTCAGAAACCTTTGTTCCATCAAACTTGTTCCAGAACTTAA 4782
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1710 GAAAAGATCCCTTTTCAGAAACCTTTGTTCCATCAAACTTGTTCCAGAACTTCCAGAAC 1769

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Qy   4783  CACCAGACAATGAGGATGAAGATGTCAAAGTCGAAAGTGAAAGACTAAAGGTCAAAGAGC  4842
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1770  CACCAGACAATGAGGATGAAGATGTCAAAGTCGAAAGTGAAAGACTAAAGGTCAAAGAGC  1829

Qy   4843  TGATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGTGTCAGCAATTTGCATAAAG  4902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1830  TGATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGTGTCAGCAATTTGCATAAAG  1889

Qy   4903  AATATGATGACAAGAGAAGATTTCTCTTCAAGAAAAGTAAAGAAAGTGGCAACTAAAT    4962
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1890  AATATGATGACAAGAGAAGATTTCTCTTCAAGAAAAGTAAAGAAAGTGGCAACTAAAT    1949

Qy   4963  ACATCTCTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTTCCAAATGGTGCTG   5022
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1950  ACATCTCTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTTCCAAATGGTGCTG   2009

Qy   5023  GCAAAAGCACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGTAT   5082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2010  GCAAAAGCACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGTAT   2069

Qy   5083  TTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATTCACTGAAGTGTATGGGTT    5142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2070  TTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATTCACTGAAGTGTATGGGTT    2129

Qy   5143  ACTGTCCCTCAGATAAACCCTTGTGGCCAGATAACTACACATTGCAGGAACATTTTGAAATT   5202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2130  ACTGTCCCTCAGATAAACCCTTGTGGCCAGATAACTACACATTGCAGGAACATTTTGAAATT   2189

Qy   5203  ATGAGCTGTCAAAGGAATGAGTGCAAGTGCAAGTGACATGAAAGAGTCATAAGTCGAATAACAC  5262
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2190  ATGAGCTGTCAAAGGAATGAGTGCAAGTGCAAGTGACATGAAAGAGTCATAAGTCGAATAACAC  2249

Qy   5263  ATGCACTTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAAACTACCTGCAGGAATCA  5322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2250  ATGCACTTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAAACTACCTGCAGGAATCA  2309

Qy   5323  AACGAAAGTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATG  5382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2310  AACGAAAGTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATG  2369

Qy   5383  AACCATCTACAGGTGATGGATCCCAAAGCCAAAGCACAGTGGCGAGCAATTCGAACTG   5442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2370  AACCATCTACAGGTGATGGATCCCAAAGCCAAAGCACAGTGGCGAGCAATTCGAACTG   2429

Qy   5443  CATTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGAGGCAGAGG  5502
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2430  CATTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGAGGCAGAGG  2489

Qy   5503  CTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTAC  5562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2490  CTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTAC  2549

Qy   5563  AACATCTAAAGAGTAAATTGGAAAAGGCTACTCTTTTTGGAAATTAAATTGAAGGACTGGA  5622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2550  AACATCTAAAGAGTAAATTGGAAAAGGCTACTCTTTTTGGAAATTAAATTGAAGGACTGGA  2609

Qy   5623  TAGAAAACCTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAA  5682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2610  TAGAAAACCTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAA  2669

Qy   5683  GCCGTCAGGAAAGTTTTCTCTATTTGGCTCTATAAAATTCCTAAGGAAGATGTTCAGT   5742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2670  GCCGTCAGGAAAGTTTTTCTCTATTTGGCTCTATAAAATTCCTAAGGAAGATGTTCAGT   2729

Qy   5743  CCCTTTCACAATCTTTTTTAAGCTGGAAGAAGTCTAAACATGCTTTTGCCATTGAAGAAT  5802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2730  CCCTTTCACAATCTTTTTTAAGCTGGAAGAAGTCTAAACATGCTTTTGCCATTGAAGAAT  2789

Qy   5803  ATAGCTTTTCTCAAGCAACATTGGAACACAGGTTTTTGTAGAACTCACTCAAAGAACAGAGAGG  5862
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2790  ATAGCTTTTCTCAAGCAACATTGGAACACAGGTTTTTGTAGAACTCACTCAAAGAACAAGAGG  2849

Qy   5863  AGGAAGATAATAGTGTGCGAACTTAAACAGCACACTTTGGTGGGAACGAACGAACAAGAAG  5922
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Db   2850  AGGAAGATAATAGTGTGCGAACTTAAACAGCACACTTTGGTGGGAACGAACGAACAAGAAG  2909

Qy   5923  ATAGAGTAGTAGTATTTGTATTGTTCGGTCTGCTTACTGGGACTTCTTTCTTTTTTC  5982
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2910  ATAGAGTAGTAGTATTTGTATTGTTCGGTCTGCTTACTGGGACTTCTTTCTTTTTC  2969

Qy   5983  ACTTAATTTAACTTGGTTTAAAAAGTTTTTATTGGAATGGTAACTGAGGAATGGTAACTGAGAACCAAGA  6042
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2970  ACTTAATTTAACTTGGTTTAAAAAGTTTTTATTGGAATGGTAACTGAGGAATGGTAACTGAGAACCAAGA  3029

Qy   6043  ACGCACTTGAAATTTTCAAGCTCCTTAATTGAAATGTCTGGTTGTGTGTTTGTTTGCTTT  6102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3030  ACGCACTTGAAATTTTCAAGCTCCTTAATTGAAATGTCTGGTTGTGTGTTTGTTTGCTTT  3089

Qy   6103  TCTTTAAATAAAACGTATGTATAATTAAGTGAAGCTGCATGTTTGTATTGAAGTATATTG  6162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3090  TCTTTAAATAAAACGTATGTATAATTAAGTGAAGCTGCATGTTTGTATTGAAGTATATTG  3149

Qy   6163  AACTATATAGTTGTATGTCATCTTTTCACCATTCAGAACACAGTGCTTCTGAATTTGTG  6222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3150  AACTATATAGTTGTATGTCATCTTTTCACCATTCAGAAACAGTGCTTCTGAATTTGTG  3209

Qy   6223  ATTTAAAGGAATTGTAATAGAATAGTTTTATTTTTAAGTTTATCTTTAAGTTTATGCCATC  6282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3210  ATTTAAAGGAATTGTAATAGAATAGTTTTATTTTTAAGTTTATCTTTAAGTTTATGCCATC  3269

Qy   6283  TTCTTAAATAAGTAAGTACGTAATGTTCCAATCTAAATAAAAAAAACTAATAACTAATAATGCAT  6342
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3270  TTCTTAAATAAGTAAGTACGTAATGTTCCAATCTAAATAAAAAAAACTAATAACTAATAATGCAT  3329

Qy   6343  AGAAAAGATACATAAAGC  6360
           ||||||||||||||||||
Db   3330  AGAAAAGATACATAAAGC  3347
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PT   which the gene is involved, or as target molecules for gene therapy.
XX
PS   Claim 1; SEQ ID NO 984; 205pp; English.
XX
CC   The present invention relates to novel human secretory or membrane
CC   proteins (ADA54072-ADA55710) and their coding sequences (ADA2433-
CC   ADA54071). The coding sequences are useful in the gene therapy of
CC   diseases caused by abnormalities of the proteins, e.g. cancer,
CC   inflammatory diseases, osteoporosis or neurological disease.
XX
SQ   Sequence 3268 BP; 1022 A; 540 C; 622 G; 1084 T; 0 U; 0 Other;

Query Match   48.7%; Score 3178; DB 10; Length 3268;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 3224; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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Qy   3102 ATGTTCCTCAAAAGTAAATGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATAT 3161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6 ATGTTCCTCAAAAGTAAATGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATAT 65

Qy   3162 TGTGCCACAGAATCTCTTTCTTCCACTGGTAAACAACATATACCTGGAGCTACTTTATTA 3221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 TGTGCCACAGAATCTCTTTCTTCCACTGGTAAACAACATATACCTGGAGCTACTTTATTA 125

Qy   3222 CAACAGAATGACCACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAATTTTCA 3281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 CAACAGAATGACCACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAATTTTCA 185

Qy   3282 G----------------------GTTGTTTCTGCCCTAGACAGTCAT 3308
              |                      |||||||||||||||||||||||||
Db    186 GGAATTGCTTGATGATGACAAAAGGATGGTATTGAGTGTTTGTTTTCTGCCCTTAGACAGTCAT 245

Qy   3309 TCAAAATTGGGTGTCATTCTTATGGTGTTTCATGACGACTTGGAAGACGTATTTTTA 3368
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 TCAAAATTGGGTGTCATTCTTATGGTGTTTCATGACGACTTGGAAGACGTATTTTTA 305

Qy   3369 AGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATATAGTGTATTTACTCAGCAGCCA 3428
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 AGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATATAGTGTATTTACTCAGCAGCCA 365

Qy   3429 CTGGAGGAGAAATGGATTCAAAATCTTTGATGAAATGGAACAGAGCTTACTTATTCTT 3488
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 CTGGAGGAGAAATGGATTCAAAATCTTTGATGAAATGGAACAGAGCTTACTTATTCTT 425

Qy   3489 TCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTGAAAACAACAGATGTATACA 3548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 TCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTGAAAACAACAGATGTATACA 485

Qy   3549 ATAGCAAAGTTCATTCTTTCACCTTAACTTGTTCCAATCTGAAACGTGAAAATCAGTGATGAATCAGTGGTG 3608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 ATAGCAAAGTTCATTCTTTCACCTTAACTTGTTCCAATCTGAAACGTGAAAATCAGTGATGAATCAGTGGTG 545

Qy   3609 CTTCTGCTTTAATTTTTTCACAGTTGTTGGTTCATCACTCCTTT 3668
              |||||||||||||||||||||||||||||||||||||||||||||
Db    546 CTTCTGCTTTAATTTTTTCACAGTTGTTGGTTCATCACTCCTTT 605

Qy   3669 AAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTATATTTTCAAACCTGGAGAC 3728
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 AAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTATATTTTCAAACCTGGAGAC 665

Qy   3729 AAACCACATAAATACAAAACAAGCTCGCTTCTTCAAAATTCGCTACTAGATATCAGT 3788
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 AAACCACATAAATACAAAACAAGCTCGCTTCTTCAAAATTCGCTACTAGATATCAGT 725

Qy   3789 GATCTTATTAGCTTTTTCACAAGCCAGAACATAATGTGACGATGATTAATGACAGTGAC 3848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 GATCTTATTAGCTTTTTCACAAGCCAGAACATAATGTGACGATGATTAATGACAGTGAC 785

Qy   3849 TATGTATCCGTGGCTCCCATAGTGCGGCTTTAAATGGTGATGCATTCAGAAAAGGACTAT 3908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 TATGTATCCGTGGCTCCCATAGTGCGGCTTTAAATGGTGATGCATTCAGAAAAGGACTAT 845

Qy   3909 GTTTTTGCAGCTGTTTCAACAGTACTACTATGGTTTATTCTTTACCTATTATTAGTGAATATC 3968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 GTTTTTGCAGCTGTTTCAACAGTACTACTATGGTTTATTCTTTACCTATTATTAGTGAATATC 905

Qy   3969 ATTAGTAACTACTATCTTTATCATTTAAATGTGACTGAAACCATCCGAGTCTCGAGTACC 4028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 ATTAGTAACTACTATCTTTATCATTTAAATGTGACTGAAACCATCCGAGTCTCGAGTACC 965

Qy   4029 CCAATCTCTTCAAGAAATTACTGACATAGTTTTAAAAATGAGCTGTATTTTCAAGCAGCT 4088
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 CCAATCTCTTCAAGAAATTACTGACATAGTTTTAAAATTGAGCTGTATTTTCAAGCAGCT 1025

Qy   4089 TTGCTTGGAATCATTGTTACTGACATGCCACCTTACTTGCCATGGAAAATGCAGAGAAT 4148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 TTGCTTGGAATCATTGTTACTGCCATGCCACCTTACTTGCCATGGAAAATGCAGAGAAT 1085

Qy   4149 CATAAGATCAAAGCTTATACTCAACTTCAACTAAACTTCAGGTCTTTGCCATCTGCATATTGG 4208
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1086 CATAAGATCAAAGCTTATACTCAACTTCAACTAAACTTCAGGTCTTTGCCATCTGCATATTGG 1145

Qy   4209 ATTGGACAAGCTGTTGTTGATATCCCCTATTTTATCATTCTTATTTTGATGCTAGGA 4268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1146 ATTGGACAAGCTGTTGTTGATATCCCCTATTTTTATCATTCTTATTTTGATGCTAGGA 1205

Qy   4269 AGCTTACTGGCATTTCATTATGGATTATATTTTATACTGTAAAGTTCCTTGCTGTGTT 4328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1206 AGCTTACTGGCATTTCATTATGGATTATATTTTTATACTGTAAAGTTCCTTGCTGTGTT 1265

Qy   4329 TTTTGCCTTATTGGTATGTTCCATCAGTTATCCTGTTTCACTTATATTGCTTCTTTCACC 4388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1266 TTTTGCCTTATTGGTTATGTTCCATCAGTTATCCTGTTTCACTTATATTGCTTCTTTCACC 1325

Qy   4389 TTTTAAGAAAAATTTTAAAATACCAAAGAATTTGGTCATTTAATCTATTCGTGTGGCAGCGTTG 4448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1326 TTTTAAGAAAATTTTAAATACCAAAGAATTTGGTCATTTAATCTATTCGTGTGGCAGCGTTG 1385

Qy   4449 NCTTGTATTGCAATCACTCACTGAAAATAACTTTCTTTATGGGGATAACAAATGCAACTATTCTT 4508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1386 GCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGGATAACAACTAACAATTCTT 1445

Qy   4509 CATTATGCCTTTGTATCATCATTCCAATCTATCCACTTCAGGTTGCCTTACTTATTCTTC 4568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1446 CATTATGCCTTTGTATCATCATTCCAATCTATCCACTTCAGGTTGCCTTACTTATTCTTC 1505

Qy   4569 ATAAAGATTTCTTGGAAGAATGTACGAAAAAAATGTGGACACTTATAATCCATGGGATAGG 4628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1506 ATAAAGATTTCTTGGAAGAATGTACGAAAAAATGTGGACACTTATAATCCATGGGATAGG 1565

Qy   4629 CTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGACTGTGGGATTTTCCTCTTACAA 4688
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1566 CTTTCAGTAGCTGTTATATCGCCTTCACCTGCAGTGTGACTGTGGGATTTTCCTCTTACAA 1625

Qy   4689 TACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAGATCCCTTTTCAGAAACCTT 4748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1626 TACTATGAGAAAAATATGGAGGCAGATCAATAAGAAAGATCCCTTTTCAGAAACCTT 1685

Qy   4749 TCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCTTCAAAGTCAAGGACATGAAGAAGATGAA 4808
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1686 TCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCTTCAAAGTCAAGGACATGAAGAAGATGAA 1745

Qy   4809 GATGTCAAAGTCGAAAGACTAAAGGTCAAGGCGATTTGGTTGCCAGTGGTTGTGAGGAG 4868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1746 GATGTCAAAGTCGAAAGACTAAAGGTCAAGGCGATTTGGTTGCCAGTGGTTGTGAGGAG 1805

Qy   4869 AAACCATCCATTATGGTCAGCAATTGCATAAGAGAAGATTTCTT 4928
              |||||||||||||||||||||||||||||||||||||||||||||
Db   1806 AAACCATCCATTATGGTCAGCAATTGCATAAGAGAAGATTTCTT 1865

Qy   4929 CTTTCAAGAAAAGTAAAGAAAGTGGCAACTAAAACATCTCTTTCTGTGTGAAAAAAGGA 4988
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1866 CTTTCAAGAAAAGTAAAGAAAGTGGCAACTAAAACATCTCTTTCTGTGTGAAAAAAGGA 1925

Qy   4989 GAGATCTTAGGACTATTGGGTCCAAAATCGTGCTGGCAAAAGCACAATTATTAATATTCTG 5048
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 1926 GAGATCTTAGGACTATTGGGTCCAAATGGTGCTGGCAAAAGCACAATTATTAATATTCTG 1985

Qy 5049 GTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTTAGGAGATTATTCTTCAGAGACA 5108
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1986 GTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTTAGGAGATTATTCTTCAGAGACA 2045

Qy 5109 AGTGAAGATGATGATTCACTGAAGTGTATGGGTTACTGTCCTCAGATAAACCCTTTGTGG 5168
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2046 AGTGAAGATGATGATTCACTGAAGTGTATGGGTTACTGTCCTCAGATAAACCCTTTGTGG 2105

Qy 5169 CCAGATACTACATTGCAGGAACATTTGAAATTTATGAGCGTGTCAAAGGATGAGTGCGCA 5228
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2106 CCAGATACTACATTGCAGGAACATTTGAAATTTATGAGCGTGTCAAAGGATGAGTGCGCA 2165

Qy 5229 AGTGACATGAAAGAAGTCATAAGTCGAATAACACATGCCACTTGATTTAAAAGAACATCTT 5288
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2166 AGTGACATGAAAGAAGTCATAAGTCGAATAACACATGCCACTTGATTTAAAAGAACATCTT 2225

Qy 5289 CAGAAGACTGTAAAGAAACTACCTGCAGGAATCAACAAACGAAAGTGTGTTTTGCTCTAAGT 5348
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2226 CAGAAGACTGTAAAGAAACTACCTGCAGGAATCAACAAACGAAAGTGTGTTTTGCTCTAAGT 2285

Qy 5349 ATGCTAGGGAATCCTCAGATTACTTGCTAGATGAACCATCTACAGGTATGGATCCCAAA 5408
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2286 ATGCTAGGGAATCCTCAGATTACTTGCTAGATGAACCATCTACAGGTATGGATCCCAAA 2345

Qy 5409 GCCAAACAGCACATGTGCGAGCAATTCGAACTGCATTTAAAAACAGAAAGCGGGCTGCT 5468
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2346 GCCAAACAGCACCATGTGCGAGCAATTCGAACTGCATTTAAAAACAGAAAGCGGGCTGCT 2405

Qy 5469 ATTCTGACCACTACTATATGGAGGAGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATG 5528
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2406 ATTCTGACCACTACTATATGGAGGAGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATG 2465

Qy 5529 GTGTCTCGGGCAGTTAAGATGTATCGGAACAGTACAACATCTAAAGAGTAAATTTGGAAAA 5588
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2466 GTGTCTCGGGCAGTTAAGATGTATCGGAACAGTACAACATCTAAAGAGTAGATTTGGAAAA 2525

Qy 5589 GGCTACTTTTTGGAAATTAAATTGAAGGACTGGATAGAAAACCTAGAAGTAGACCGCCTT 5648
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2526 GGCTACTTTTTGGAAATTAAATTGAAGGACTGGATAGAAAACCTAGAAGTAGACCGCCTT 2585

Qy 5649 CAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATT 5708
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2586 CAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATT 2645

Qy 5709 TTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTTCACAATCTTTTTTTAAGCTG 5768
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2646 TTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTTCACAATCTTTTTTTAAGCTG 2705

Qy 5769 GAAGAAGCTAAACATGCTTTGCCATTGAAGAATATAGCTTTTCTCAAGCAACATTGGAA 5828
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2706 GAAGAAGCTAAACATGCTTTGCCATTGAAGAATATAGCTTTTCTCAAGCAACATTGGAA 2765

Qy 5829 CAGGTTTTGTAGAACTCACTAAAGAACAAGAGGAAGATAATAGTTGTGGAACTTTA 5888
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2766 CAGGTTTTGTAGAACTCACTAAAGAACAAGAGGAAGATAATAGTTGTGGAACTTTA 2825

Qy 5889 AACAGCACACTTGGTGGGAACGAACAACAAGAGTAGTAGTGTATTTGAATTGTATT 5948
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2826 AACAGCACACTTGGTGGGAACGAACAACAAGAGTAGTAGTGTATTTGAATTGTATT 2885

Qy 5949 GTTCGGTCGCTACTGGGACTTGCTTACTTCACTTAATTTAACTTTGGTTTAAAAA 6008
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2886 GTTCGGTCGCTACTGGGACTTGCTTACTTCACTTAATTTAACTTTGGTTTAAAAA 2945

Qy 6009 GTTTTTATTGGAATGGTAACTGGAGAACCAAGAACGCACTTGAAATTTTTCTAAGCTCC 6068
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2946 GTTTTTATTGGAATGGTAACTGGAGAACCAAGAACGCACTTGAAATTTTTCTAAGCTCC 3005

Qy 6069 TTAATTGAAATGCTTGGTGGTTTGTGTTTGCTTTGTTTTGCTTTCTTAAATAAAACGTATGTATAATT 6128
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3006 TTAATTGAAATGCTTGGTGGTTTGTGTTTGCTTTGTTTTGCTTTCTTAAATAAAACGTATGTATAATT 3065
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Qy 6129 AAGTGAAGCTGCATGTTGTATTGAAGTAGTATATAGTTGTGATGTCATCTT 6188
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db 3066 AAGTGAAGCTGCATGTTGTATTGAAGTAGTATATAGTTGTGATGTCATCTT 3125

Qy 6189 TTCACCATTCAGAAACAGTGCTTCTGAATTGTGATTAAAGGAATTGTAATAGAATAGT 6248
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3126 TTCACCATTCAGAAACAGTGCTTCTGAATTGTGATTAAAGGAATTGTAATAGAATAGT 3185

Qy 6249 TTTATTTTAAGTTATCTTAAGTTATGCCATCTTCTAAATAAGTACGTAATGTTCCA 6308
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3186 TTTATTTTAAGTTATCTTAAGTTATGCCATCTTCTAAATAAGTACGTAATGTTCCA 3245

Qy 6309 ATCTAAATAAAAAACTAATACAT 6331
        ||||||||||||||||||||||
Db 3246 ATCTAAATAAAAAAACTAATACAT 3268
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RESULT 13
ADF74739
ID   ADF74739 standard; cDNA; 3950 BP.
XX
AC   ADF74739;
XX
DT   26-FEB-2004 (first entry)
XX
DE   Murine dnaform 43395 cDNA encoding an ATP binding cassette (SeqID 18).
XX
KW   gene; ss; murine; mouse; receptor; TGF beta family protein;
KW   modified low-density lipoprotein; ATP-binding transporter activity;
KW   immunoglobulin-like activity; retinal fibrosis; nephritis;
KW   heart related ischaemia; hyperlipidaemia; familial hypercholesterolaemia;
KW   myocardial infarction; diabetes mellitus; cystic fibrosis;
KW   Dubin-Johnson syndrome; Byler's disease; lupus erythromatode;
KW   rheumatoid arthritis; hepatitis; nephrotropic; vasotropic; hepatotropic;
KW   antilipaemic; antiinflammatory; immunosuppressive; LDL.
XX
OS   Mus musculus.
XX
PN   WO200309135-A1.
XX
PD   06-NOV-2003.
XX
PF   23-APR-2003; 2003WO-JP005174.
XX
PR   23-APR-2002; 2002JP-00120853.
PR   26-APR-2002; 2002JP-00125934.
PR   30-APR-2002; 2002JP-00128505.
PR   02-MAY-2002; 2002JP-00130914.
PR   04-DEC-2002; 2002JP-00352270.
PR   04-DEC-2002; 2002JP-00352619.
PR   04-DEC-2002; 2002JP-00352730.
XX
PA   (RIKE) RIKEN KK.
PA   (DNAF-) DNAFORM KK.
PA   (MITU) MITSUBISHI CHEM CORP.
XX
PI   Hayashizaki Y, Kamiya M, Kubodera H;
XX
DR   WPI; 2003-854404/79.
DR   P-PSDB; ADF74752.
XX
PT   Mouse TGF-beta binding, modified LDL binding, ATP-binding transporter and
PT   immunoglobulin-like proteins for screening potential drug substances
PT   modifying their activity or expression.
XX
PS   Claim 12; SEQ ID NO 18; 226pp; Japanese.
XX
CC   This invention relates to novel nucleic acids and encoded polypeptides
CC   identified in a full-length cDNA library. Specifically, it refers to
CC   novel murine proteins (or mutants derived thereof) that either bind to
CC   TGF beta family proteins, bind to modified low-density lipoprotein (LDL),
CC   exhibit ATP-binding transporter activity or immunoglobulin-like activity.

CC   The present invention describes appropriate expression vectors, specific
CC   antibodies as well as sense and antisense oligonucleotides, which can be
CC   used to modulate protein activity. These proteins have various and
CC   distinct uses, for example the TGF beta binding proteins are useful for
CC   the treatment and prevention of retinal fibrosis, nephritis and heart
CC   related ischaemia; proteins that bind modified LDL can treat
CC   hyperlipidaemia, familial hypercholesterolaemia and myocardial infarction
CC   ; proteins with ATP-binding transporter activity are useful for treating
CC   diabetes mellitus, cystic fibrosis, Dubin-Johnson syndrome and Byler's
CC   disease; while those with immunoglobulin-like activity can be used to
CC   treat or prevent lupus erythromatodes, rheumatoid arthritis and
CC   hepatitis. Accordingly, these proteins are described with various
CC   activities such as nephrotropic, vasotropic, hepatotropic, antilipaemic,
CC   antiinflammatory and immunosuppressive. This polynucleotide is a full
XX   length murine cDNA sequence encoding a polypeptide of the invention.
SQ   Sequence 3950 BP; 1055 A; 802 C; 863 G; 1230 T; 0 U; 0 Other;

Query Match   45.0%;   Score 2934.4;   DB 10;   Length 3950;
Best Local Similarity   86.2%;   Pred. No.0;
Matches 3247; Conservative   0; Mismatches 522; Indels   0; Gaps   0;

Qy   991 AATAGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTGGAGACAGA 1050
              ||| |||| |||| | ||||||||||||||||||||||||||||||||||||||||||
Db   181 AGTAAACTGACCTAGAAACATGGCTACTGCAATTAGGGATGTGGGAGTTTGGAGACAGA 240

Qy   1051 CCAGAACACTTCACTGAAGAATTACTTAATTAAATGCAGAACCAAAAAGAGTAGTGTTC 1110
             |||||||||||||||||||||| ||| ||| || |||||||||||||||||||||||||
Db   241 CCAGAACACTTCACTGAAAAATTACCTAATTAAATGCAGGATCAAAAAAAGTAGTGTTC 300

Qy   1111 AGGAAATTCTTTTTCCACTATTTTTTTATTTTGGTAATATTAATTAGCATGATGCATC 1170
             |||||||| ||||||||||||| ||||| ||||||||||||||||||||||||||||||
Db   301 AGGAAATTCTTTTTCCCTCCATTTTTATTTTGGCTGTATATTAGTTAGCATGATGCATC 360

Qy   1171 CAAATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATTCCTATGGACAAGTTTACTC 1230
             ||||||||||||||||| ||| |||| ||||||||||||||||||||||||||||||||
Db   361 CAAATAAGAAATATGAAGAGGTATCTGATATATGAGCTCAGCCCTATGGACAAATTCAGCC 420

Qy   1231 TTTCTAATCTAATTCTTGGATATACTCCAGTGACTATATTACAAGGCAGCATCATGCAGA 1290
             ||||||||||||||| ||||||| |||| | |||||||||||||||||||||||||||||
Db   421 TTTCCAACGTTATTCTTGGATCACTCCCGTGACTAACATTACAAGCAGCATTATGCAGA 480

Qy   1291 AAGTGTCTCACTGATCATCCACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAG 1350
             |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   481 GGGTTGTACCGATCATCTTCCCAAGGTATAGTTACTTACTGAAGAATACGCAAATGAAAG 540

Qy   1351 AAATGTTAACATCCAGTCTCTCAAGGCCGAGCAACTTGTAGGTGTGGTTTCAAAGACT 1410
             || ||||||||||||||| |||||| |||||||||||||||||||||||||||||||||
Db   541 AACTGGTAGCCGCAAGTCTTTCTCAAGTTCCAGCAACTTCGTAGGTGTGGTTTTCGAAGACA 600

Qy   1411 CCATGTCCTATGAACTTCGTTTTTTTCCTGATAATCATGTGAGGCTGCTCAGTATCTTCATTTATATGG 1470
             |||||||||||||||||| ||| ||||||||||||||||| |||| |||| |||||||||
Db   601 CCATGTCCTATGAACTCGTTTTTTTCCTGAAAATCATGTGAAAATCCAGTCCTCATTTATATGA 660

Qy   1471 ATTCAAGAGCTGGCTGTGTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTCA 1530
             ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   661 ATTCAAGAGAAGGCTGTTTCAAAGACATGTGATGCTGCTCAGTACTGGTCTTTGGGGTTTA 720

Qy   1531 CAGTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTT 1590
             |||||||||| |||||||| ||||||||||||| |||||||||||||||||||||||||
Db   721 CAGTTCTGCAGGCATCGATAGATGCTGCCATTATACAGCTGAAGACCAATGTTCTGTGT 780

Qy   1591 GGAGGGAGCTGGAGTCAACTAAAGCTGTTATTATATGGGAGAAACTGCTGTTGTAGAAATAG 1650
             ||||||||||||||||||||||| |||| |||||| |||||||||| |||||||||||||||
Db   781 GGAGCGAGCTGGAGTCGACCAAAGCTGTGATCATGGGAGAGCCGGTCGTGTTGTGGGAGATTG 840

Qy   1651 ATACCTTCCCCGGAGGAGTAATTTAATATACCTAGTTATAGCATTTTCACCTTTTGGAT 1710
             || |||||| |||||||||| |||| ||||| ||| || |||||||| |||||||||||
Db   841 ACACCTTCCCGGAGGGGTCATCCTACATCACCTGTTAGCCTTTCCGGCCCTTCGGGCT 900

Qy   1711 ACTTTTGGCAATTCATATGCTAGCAGGAAAAAAGAAAATAAAGGATTTTAAAGA 1770
             || |||||| ||||| |||| ||| ||||||||||||||||||| |||||||||
Db   901 ACTTCCTGCAATCCACATCGTGGCAATGCCATTGGGACAATCCGGACAAAGGAATTTTAAAGA 960

Qy   1771 TAATGGGACTTCATGATGACTGCCTTTGGCTTTCCTGGGTTCTTCTATATACAAGTTTAA 1830
             |||||||||||||||||| ||||||||||||||||||||||||||||||||| ||||||||
Db   961 TAATGGGACTTCATGACACTGCTTTTTGGCTTTTCCTGGGTTCTTCTGTACCGCAAGCTTGA 1020

Qy   1831 TTTTCTTATGTCCCTTCTTATGGCAGTCAGTCATTGCGACAGCTTCTTTGTTATTCCTCAAA 1890
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTTTCCTTATGTCCCTGCTTATGGCGTGCATCGCAACAGCTTCTTCGTTATTCCCTCAGA 1080

Qy   1891 GTAGCAGCATTGTGATATTCTGCTTTTTTCCTTATGGATTATCATCGTATTTTTG 1950
             ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   1081 GTAGCAGCATTGTGATCTTTCCACTGTTCTTCCTTATATGGATTGTCATCGTGTTTTTTG 1140

Qy   1951 CTTAATGCTGCACACCTCTTTTAAAAAATCAAAACATGTGGAAATAGTTGAATTTTTTG 2010
             |||||||||||||||||||| |||||||||| |||||||||||||||||||||||||||
Db   1141 CTTTAATGTCGACGCCTCTTTTTTTAAAAATCAAACACGTGGGAGTCGTTGAGTTTTTTG 1200

Qy   2011 TTACTGTGGCTTTTGGATTTATTGGCCTATGATAATCCTCATAGAAAGTTTCCAAAT 2070
             ||| ||||||| |||| |||| |||||| ||||||||||| |||||||||| |||||||
Db   1201 TCACCGTGGTGTTTGGATTTGTTGGCCTGCTGATTGTCCTCATAGAAAGTTTCCCCAGGT 1260

Qy   2071 CGTAGTGGTGGCCTTTCAGTCCTTTCTGTCACTGTACTTTTGTGATTGGTATTGCACAGG 2130
             | |||| |||| |||| |||| ||| ||||| ||| ||||||||||||||||||||||||
Db   1261 CGCTGGTGTGGCCTTCAGTTTCCTTTGTGTCAGTGTGCCTTTCTGATTGGGATTGCACAGG 1320

Qy   2131 TCATGCATTAGAAGATTTAATGAAGGTGCTTCATTTCAAATTTGACTGCAGGCCCAT 2190
             |||||||| |||||||| ||| |||||||| ||||||||||||| |||||||||| |||
Db   1321 TCATGCATTAGAAGATTTAATGAGGGTGCCCTTTATTTTCTTATTTGACTGAAGGGTCCCT 1380

Qy   2191 ATCCTCTAATTATTACAATTATCATGCTCACACTTAATAGTATATTCTATGTCCTCCTGG 2250
             |||||||||||||| ||||||||||||| || |||| |||| ||||||||||||||||||
Db   1381 ATCCTCTAATTATTACTATTATCATCGTCTTGACAGTGTGTTCTATGTCCTCCTGG 1440

Qy   2251 CTGTCTATCTTGATCAAGTCATTCCAGGGGAATTGGCTTACGGAGATCATCTTTATATT 2310
             ||||| ||| ||||| |||||||||||||| |||||||||||||||| |||||||| |||
Db   1441 CTGTGTATCTCGACCAAGTCATTCCAGGGAATTTGGCTTGAGGAGTCATCTTTGTATT 1500

Qy   2311 TTCTGAAGCCTTCATATTGGTCAAAGAGTCAAAGGAATTATGAGGAGTTATCAGAGGGCA 2370
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   1501 TTTTGAAGCCATCGTATTGGTCATCAAAAAACAAAGAAACTATAAGGAGCTATCGGAGGGCA 1560

Qy   2371 ATGTTAATGGAAATATTAGTTTTAGTGAAATATTGAGCGCCAGTTTCTTCAGAATTTGTAG 2430
             |||| |||||||| ||| ||| |||||| |||| |||| ||| |||||||||||||| |||
Db   1561 ACATTAATGGCAATATAGTCTCAATGAAATTGTTGAGCGCCCGTTTCTTCAGAATTTATAG 1620

Qy   2431 GAAAAGAAGCCATAAGAATTAGTGGTATTCAGAAGACATACAGAAAGAAGGGTGAAAATG 2490
             ||||||||||||||||| ||||| || |||||||| ||| ||| ||||||||||||||||
Db   1621 GGAAAGAAGCTATAAGAATAAGTGGTATTCAGAAATCCTATAGAAACTGAGAACG 1680

Qy   2491 TGGAGGCTTTGAGAAATTTGTCATTGACATATGAGGGTCAGATTACTGCCTTACTTG 2550
             ||||||| ||||||||||| |||||||||||| ||||||||||||| |||||||||||
Db   1681 TGGAGGGCTTTGAGAAATTTGTCACTTGACAATATATGAAGGTCAGATTACTGCACTGCTGG 1740

Qy   2551 GCCACAGTGGAACAGGAAAGAGTACATTGATGAATATTCTTGTGGACTCTGCCCACCTT 2610
             ||||||||||||||||||||||||| |||||||||||||||| |||||||||||||||||
Db   1741 GCCCACAGTGGAACAGGAAAAAGCACACTGATGAATATTCTTCTGTGGACTGTGTCCACCCT 1800

Qy   2611 CTGATGGGTTTGCATCTATATATGGACACACAGAGTCTCAGAAATAGATGAAATGTTGAAG 2670
             ||||||||| ||| ||| ||||||||||||||||| |||||||||| ||||| ||||||||
Db   1801 CTGATGGGTTTGCTTCTTCATATATATGGACACACAGAGTCTCTGAAATAGATGAAATGTTGAAG 1860

Qy   2671 CAAGAAAATGATTGGCATTTGTCCACAGTTAGATATACACTTTGATGTTTTGACAGTAG 2730
             |||||||||| ||||||| |||| |||||||||||||||||| |||||||||||||||||
Db   1861 CAAGAAAAATGATTGGCATATGTCCGGTCGATATACTCAGCAGTATTAAACTTTGATGTTCTGACAGTAG 1920

Qy   2731 AAGAAAATTTATCAATTTGGCTTCAATCAAAGGGATACCAGCCAACAATATAATACAAG 2790
             || ||||| |||| |||||||| |||||||||||||||||||||||||||||| ||||||
Db   1921 AAGAAAATTTATCAAATTTTGGCTTCAATCAAAGGAATACCAGCCCAACAATATAATTCAAG 1980

Qy   2791 AAGTGCAGAGGGTTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAA 2850
             ||||||||||||| |||| ||| ||||||| |||||| ||| |||||||| |||||||||
Db   1981 AAGTGCAGAAAGTGTTGCTGGATCTGGATCTGGACACTGCAGCCATCCAAAGATAATCAAGCGCAAAA 2040

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Qy  2851 AATTAAGTGGTGGTCAAAAAGAGAAGAGAAGTGTCATTAGGAATTGTCTGTTCTTGGGAACCCAA 2910
              |||||||||| |||   |||| || ||  |||||| |||| ||||||| ||| || |||||| |||
Db  2041 AGTTAAGCGGTGGTCAGAGAAAGAGAGCTGTCTGTAGGAATTGTCAGTTCTCGGGAATCCAA 2100

Qy  2911 AGATACTGCTGCTAGATGAACCAACAGCTGGAATGGACCCCGTTCTCCGACATATTGTAT 2970
              |||| |||||| ||||| |||||| |||| ||||||||| |||||| |||| || ||| ||
Db  2101 AGATACTCCTGCTAGACGAGACGAGCCTACAGCAGGAATGGACCCCTGCTCTCGCCATATTGTTT 2160

Qy  2971 GGAATCTTTAAAATACAGAAAGCCAATCGGGTGACAGTGTTCAGTGACTCATTCATGG 3030
              |||||||| |||| ||| ||||| ||||| ||| ||||| ||| ||| ||||||||||
Db  2161 GGAATCTTCTAAAGTATAGAAAGGCTAACAGAGTGACCGTGTTAGTACTCACTTCATGG 2220

Qy  3031 ATGAAGCTGACATTCTTGCAGATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTG 3090
              ||||| |||||||||||| |||| ||||| |||| ||||||||| ||||| ||||| |||
Db  2221 ATGAGGCTGACATTCTTGCCCAGATAGGAAAGCTGTCATATCACAAGGAATGCTGAAGTGTG 2280

Qy  3091 TTGGTTCTTCAAATGTCCTCAAAAGTAAATGGGGATCGGCTACCGCCTGAGCATGTACA 3150
              |||||||||||||| |||||||||||||| ||||| ||| ||||| |||||||||||||
Db  2281 TTGGTTCTTCAATTTCCTCAAAAGTAAAGAGTAAACGGGATCGGCTACCGCCTGAGCATGTATA 2340

Qy  3151 TAGACAAATATTGTGCCACAGAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAG 3210
              |||||| | |||||||||| ||||||| |||| |||| ||||| ||||||| ||||||||
Db  2341 TAGACAGATACTGTGCCACAGAATCACTGTCGCGCTGGTTAGGCAGCACATACCCGCAG 2400

Qy  3211 CTACTTTATTACACACAGATGACCAACAACTGTGTATAGCTTGCCTTTCAAGGACATGG 3270
              ||| |||| ||| ||||| ||||||| ||||| ||| |||| ||||| ||||| ||||||
Db  2401 CCGCGCTACTGCAGCAGAATGACCAGCAGCTCGTGTACAGCCTGTTTCAAAGACATGG 2460

Qy  3271 ACAAAATTTCAGGTTGTTTCGCCCTAGACAGTCATTCAAATTGGGTGTCATTTCTT 3330
              || |||||||||||| ||||| |||||||||||||| |||| |||||||| ||||||
Db  2461 ACAAAATTTCAGGCTTGTTTCGCTCTAGACAGTCATTCAAACCTGGGTGTTATTTCTT 2520

Qy  3331 ATGGTGTTCCATGACGACTTGGAAGACGTATTTTAAAGCTAGAAGTGAAGCAGAAA 3390
              |||||||||||||| ||||||||||| |||||||||| |||||||||||||||||||
Db  2521 ATGGTGTTCCATGACCAGACTTGGAAGATGTATTTTTAAAGCTAGAAGTGAAGCAGAAA 2580

Qy  3391 TTGACCAAGCAGATTATAGTGTATTTACTCAGCAGCCACTGGAGGAAAATGGATTCAA 3450
              ||||||||||||| ||||||| ||||| ||||||||||| || |||||||| ||||||
Db  2581 TTGACCAAGCAGACTATAGTGTATTTACCAGCAGCCAGCCGGGGAGGAAGAAGAAACAGATTCAA 2640

Qy  3451 AATCTTTGATGAAATGGAAACAGAGCTTACTTATTCCTTCTGAAACCAAGGCTTCTCTAG 3510
              || |||||||||||| |||| ||||||||||| |||| ||||||| ||||||| |||||
Db  2641 AATCCTTTGATGAAATGGAACAGAGCTTACTTATTCCTTCTGAAACGAAGCTTCTTCAG 2700

Qy  3511 TGAGCACCATGAGCCTTGGAAACAACAGATGTATACAACAGATTTCATTTCTTTA 3570
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Db  2701 TGAGCACCATGAGCCTCGGAAGCAACGTGTCTACGATGTCAAAGTTTCATTTCCTCT 2760

Qy  3571 CCTTGAAACGTGAAAGTAAATCAGTGAGACACAGTGTTGCTTCGCTTTAATTTTTTTCA 3630
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Db  2761 CATTGAAACGAGAAAGCAAATCAGTGCGGCGCTGTGTGCTTCTGCTTTAATTTTTTTTG 2820

Qy  3631 CAGTTCAGATTTTTATGTTTTTGGTCATCACTCTTTAAAAATGCTGTGTTCCCATCA 3690
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Db  2821 CAGTTCAGATTTTTATGTTTTTCTCCATCACTCTTTAAAAATGCTGTGTTCCCATCA 2880

Qy  3691 AACTTGTTCCGACTTATATTTCTAAAACCTGGAGACAAACCACCATAATACAAAACAA 3750
              |||||||||| |||| |||||| |||| |||||||| |||| |||| ||||||||||||
Db  2881 AACTCGTTCCAGACTTGTATTTCCTAAAGCCTGGGATAAACCTCATAAATACAAAACA 2940

Qy  3751 GTCTGCTTCTTCAAAATTCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTCACAA 3810
              |||||||||||||||||||| |||||||||| |||||||||| ||||||| |||||||
Db  2941 GCCTGCTCTTCAAAATTCTACTGACTCAGATATCAATGGTCTTATTGAGTTTTTTGCAC 3000

Qy  3811 GCCAGAACATAATGCGTGACGATGATTAATGACAGTGATCCTGGCTCCCCCATA 3870
              ||||||||| ||||| ||||| |||||| ||||||| | ||| ||||| ||||||
Db  3001 ACCAGAACATAATGTGGCAATGTTAATGACAGTGATCGCTGCTCCCTCCACA 3060

Qy  3871 GTGCGGCTTAAATGTGATGCATTCAGAAAGGACTATGTTTTGCAGCTGTTTTCAACA 3930
              ||||||| ||||||||||| |||| |||||||| |||||||| |||| ||| ||||||
Db  3061 GTGCGGCTCCAATGTGGTGCGTTCTGAAAAGGACTATGTTTTTCTGCTGTTTTCAACA 3120

Qy  3931 GTACTATGGTTTATTCTTTACCTATTAGTGAATATCAGTAACTAACTATCTTTATC 3990
              ||| |||||||| |||||||| ||| |||||| || || |||| |||||| |||||
Db  3121 GTACTATGGTTTATTGTTTGCCAGTCATGATGATGACGATCCATCCATTCTTCAAGAAATTACTG 3180
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Qy  3991 ATTTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTCAAGAAATTACTG 4050
              ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  3181 ATTTAAATGTGACTGAAGCCATCCAGACCTGGAGTACCCCGTTCATTCAAGAAATTACTG 3240

Qy  4051 ATATAGTTTTAAAATTGAGCTATATTTCAAGCAGCTTGCTGGAATCATTGTTACTG 4110
              ||| ||||||||| ||||||||| ||||| ||||||||||||||| |||||| ||||
Db  3241 ACATTGTTTTAAAATTGAGCTATATTTTCAAGCAGCTTGCTTGGAATCATTGTTACTG 3300

Qy  4111 CAATGCCACCTTACTTGCCATGGAAAATGCAGAGAAATGCAGAGAATCATAAGCTTATACTC 4170
              |||||||||||||| |||||||||| ||||||| ||||| ||||||| |||||||||||||
Db  3301 CAATGCCACCTTACCTGCCATGGAAAATGCAGAGAAATGCAGAGAATCATAAGCTTATACTC 3360

Qy  4171 AACTAAAACTTCAGGTCTTTGATGCCATCGCATTGGATTGGACAAGCAGTTGTTGATA 4230
              |||||||||||| ||||| ||||||||||| |||||||||||||||| |||||||||
Db  3361 AACTAAAACTTCCGGGTCTTTTGCCATCAGCCATTGGGTTGGACAAGCTGTGTGGATA 3420

Qy  4231 TCCCCTATTTTTATCATTCTTATTTTGATGCTAGGAAGCTACTGGCATTCATTATG 4290
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Db  3421 TTCCCCTGTTTTTTGTTTCTGATTTTGATGCTGGGGGAAGTTTATTGCATTCATCATG 3480

Qy  4291 GATTATATTTTTACTGTAAAGTTCCTGCTGTGGTTTTTTGCCTTATTGGTTATGTTC 4350
              |||||| ||||| ||||||||||| |||| ||||||||||| |||| |||||||||
Db  3481 GACTGTATTTTTATCCTGCAAAATTTCTTGTGTGGTGTTTGGCCTCATTGCTTATGTGC 3540

Qy  4351 CATCAGTTATTCTGTCACTTATATTGCTTCTTCACCTTAAGAAATTTAAATACCA 4410
              ||||| |||| ||||||| |||||| ||| || ||||| ||||||| |||||||||
Db  3541 CCTCCGTCATTCTGTTCAGTACAGCCTCGTTCACTTCAGCTTCAAGAAAATTTTAAATACCA 3600

Qy  4411 AAGAATTTGGTCATTTATCTATCTGTGCAGCGTTGCNCTTGTTATTGCAATCACTGAAA 4470
              ||||||||||||||| |||| |||| ||||||||| |||||||||||||||||||||||
Db  3601 AGGAATTTGGTCATTTATCTAT CTGTGCACCGGCTTGTGGCAATCACGCGGAAA 3660

Qy  4471 TTAACTTCTTATGGGATACACAATTGCAACTATTCTTCATTATGCCTTTGTATCATCA 4530
              || || ||||| |||||||||||||| ||| ||||||||||| ||||||||| |||||
Db  3661 CAACTTCTTCTTCTGCAATATGCAGTTCAGTAGTTACCGCTGTCTTCATTCATTACACCTTCTGCATAGCCA 3720

Qy  4531 TTCCAATCTATCCACTTCAGGTTGCCTGATTTCTTGGAAGAATG 4590
              |||||||||||||||||||||||| ||||| ||||||||||||||
Db  3721 TTCCAATCTACCCCTCCTGGGTGTCATTTGTCTGATTTTCTCATAAAAGGGGTTCTTGGAAGAATA 3780

Qy  4591 TACGAAAAAATGTGGACACCTATAATCCATGGAGCTTTCAGTAGCTGTTATATCGC 4650
              |||| |||||||||||| |||||| ||||||||| |||||| |||| ||| ||||
Db  3781 TGCCAAAAATGAGAATCTACACACCCGGGATAGACTTTTAGTTGTGTGTGTRAATCATC 3840

Qy  4651 CTTACCTGCGAGTGCGTGTACTGGTGGATTTTCCTCTTACAATACTATGAGAAAAAATATGGAG 4710
              |||||||||||| |||||| ||| ||||| ||||| ||||| |||||||||||||| ||||||
Db  3841 CGTACCTGCAGTGTACTGCGGATTTTCCTGGATTTTCCTTCTTACAACACTATGAGAAAATACATGGAG 3900

Qy  4711 GCAGATCAATAAGAAAGATCCCTTTTTCAGAAAACCTTTCAACGAAGTC 4759
              |||||| |||| ||||||||||||||||||| |||   |||||| |||
Db  3901 GCAGATCATTAAGAAGGATCCCTTTTTCAGGGGCCCTTTCACAAAAGGC 3949
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RESULT 14

ADF74738

KW   antilipaemic; antiinflammatory; immunosuppressive; LDL.
XX
OS   Mus musculus.
XX
PN   WO200309I435-A1.
XX
PD   06-NOV-2003.
XX
PF   23-APR-2003; 2003WO-JP005174.
XX
PR   23-APR-2002; 2002JP-00120853.
PR   26-APR-2002; 2002JP-00125934.
PR   30-APR-2002; 2002JP-00128505.
PR   02-MAY-2002; 2002JP-00130914.
PR   04-DEC-2002; 2002JP-00352270.
PR   04-DEC-2002; 2002JP-00352619.
PR   04-DEC-2002; 2002JP-00352730.
XX
PA   (RIKE) RIKEN KK.
PA   (DNAF-) DNAFORM KK.
PA   (MITU) MITSUBISHI CHEM CORP.
XX
PI   Hayashizaki Y, Kamiya M, Kubodera H;
XX
DR   WPI; 2003-654404/79.
DR   P-PSDB; ADF74751.
XX
PT   Mouse TGF-beta binding, modified LDL binding, ATP-binding transporter and
PT   immunoglobulin-like proteins for screening potential drug substances
PT   modifying their activity or expression.
XX
PS   Claim 12; SEQ ID NO 17; 226pp; Japanese.
XX
CC   This invention relates to novel nucleic acids and encoded polypeptides
CC   identified in a full-length cDNA library. Specifically, it refers to
CC   novel murine proteins (or mutants derived thereof) that either bind to
CC   TGF beta family proteins, bind to modified low-density lipoprotein (LDL),
CC   exhibit ATP-binding transporter activity or immunoglobulin-like activity.
CC   The present invention describes appropriate expression vectors, specific
CC   antibodies as well as sense and antisense oligonucleotides, which can be
CC   used to modulate protein activity. These proteins have various and
CC   distinct uses, for example the TGF beta binding proteins are useful for
CC   the treatment and prevention of retinal fibrosis, nephritis and heart
CC   related ischaemia, proteins that bind modified LDL can treat
CC   hyperlipidaemia, familial hypercholesterolaemia and myocardial infarction
CC   ; proteins with ATP-binding transporter activity are useful for treating
CC   diabetes mellitus, cystic fibrosis, Dubin-Johnson syndrome and Byler's
CC   disease; while those with immunoglobulin-like activity can be used to
CC   treat or prevent lupus erythromatodes, rheumatoid arthritis and
CC   hepatitis. Accordingly, these proteins are described with various
CC   activities such as nephrotropic, vasotropic, hepatotropic, antilipaemic,
CC   antiinflammatory and immunsuppressive. This polynucleotide is a full
CC   length murine cDNA sequence encoding a polypeptide of the invention.
XX
SQ   Sequence 3831 BP; 1021 A; 767 C; 838 G; 1205 T; 0 U; 0 Other;

Query Match   43.0%; Score 2807; DB 10; Length 3831;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 3112; Conservative 0; Mismatches 491; Indels 1; Gaps 1;

Qy   991 AATAGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTGGAGACAGA 1050
          ||||||||||||||||| |||||||| |||||||||||||||||||||||||||||
Db   227 ATTAAACTGACCTAGAAAAACATGGCTACTGCAATTAGGGATGTGGGAGTTGGAGACAGA 286

Qy   1051 CCAGAACACTTCTACTGAAGAATTACTTAATTAAAATGCAGAACCAAAAAGAGTAGTGTTC 1110
          |||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db   287 CCAGAACACTTCTACTGAAAAATTACCTAAT'TAAATGCAGGACTAAAAAAAGTAGTGTTC 346

Qy   1111 AGGAAATTCTTTTCCACTATTTTTTTTATTTTGGTTAATATTAATTAACATGATGCATC 1170
          ||||||||| || ||| |||||| |||||| | || |||||| ||||||||||||||
Db   347 AGGAAATTCTTTTTCCTCCATTTTCTTTATTTTGGCTGATATTAGTTAGCATGATGCATC 406

Qy   1171 CAAATAAGAAATATGAAGAAGTGCCTAATATAGAACTCCATCCTATGGACAAGTTTACTC 1230
          |||| |||||| || ||| |||||| |||||||||||| |||||||||||||||||

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Qy  3390 ATTGACCAAGCAGATATAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCA 3449
         ||||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||
Db  2627 ATTGACCAAGCAGACGACTATAGTGTATTTACACAGCAGCAGCCCGGGGAGGAGAACAGATTCA 2686

Qy  3450 AAATCTTTGATGAAATGGAACAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCTCTA 3509
         ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2687 AAATCCTTTGATGAAATGGAACAGAGTTACTATTCTCCTGAAACGAAAGCTTCTTCA 2746

Qy  3510 GTGAGCACCATGAGCCTTGGAAACACAGATGTATACAATAGCAAAGTTTCATTTCTTT 3569
         ||||||||||||||||||||||||||||||||||||||||  |||||||||||||||
Db  2747 GTGAGCACCATGAGCCTCTGGAAGCAGCAGCAAGTGTCTACGATTGCAAAGTTTCATTTCCTC 2806

Qy  3570 ACCTTGAAAGTGAAAGTAAATCAGTGAGATCAGTGTTGCTTCTGCTTCTGCTTTTTTTC 3629
         ||||||||||||||| |||||||||||||||||||||||||||||||||| ||||||||
Db  2807 TCATTGAAACGAGAAAGCAAATCAGTGCGCGTGTTGGTTGTTGTTCTGCTTTTAATTTTTTT 2866

Qy  3630 ACAGTTCAGATTTTTATGTTTGGTTCATCATCTTTTAAAAAATGCTGGTTCCCATC 3689
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Db  2867 GCAGTTCAGATTTTTATGTTTTTCTCCATCATTCTTTTAAAAAATGCTGGTTCCCATC 2926

Qy  3690 AAACTTGTTCCAGACTTATATTTTCTAAAACCTGGAGACAAACCACATAAAATACAAAACA 3749
         ||||| |||||||||||||||||||||||||||||||||||| ||||||||||| ||||||
Db  2927 AAACTCGTTCCAGACTTGTATTTCTAAAATCCTGGAGATAAACCTCATAAATATACAAAACA 2986

Qy  3750 AGTTCTGCTTCTTCAAAATTCTGCTACTCAGATATCAGTGATCTTATTAGCTTTTTTCACA 3809
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Db  2987 AGCCTCTGCTTCAAAATTCTCAAAATTCTACTGACTCAGATATCAATGGTCTTATTGAGTTTTTTGCA 3046

Qy  3810 AGCCAGAACATAATGGTGACGATGATTAATGACAGTGACTATGTCCGGCTGTCCCCAT 3869
         ||||||||||||||||||||| ||||||||||||||||||||||| |||||||||||
Db  3047 CACCAGAACATAATGGTGGCAATGTTTAATGACAGTGACTATGTGTCTGCTCCTCAC 3106

Qy  3870 AGTGCGGCTTTAAATGTGATGCATTCAGAAAAGACTATGTTTTTGCAGCTGTTTTCAAC 3929
         ||||||||||||| ||||||||||||||||||||||||||||||||||||| |||||||
Db  3107 AGTGCGGCTCTCAATGTGGTGCGTTCGAAAAGGACTATGTTTTTTGCTGCTGTTTTTCAAC 3166

Qy  3930 AGTACTATGGTTTATTCTTTACCTATATTAGTGAATATCATTAGTAACTACTATCTTTAT 3989
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3167 AGTACTATGGTTTATTTCTTTGTTGCCAGTCATGATGAACATCATTAGTAACTACTATCTTTAT 3226

Qy  3990 CATTTAAATGGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTCAGAAAATTACT 4049
         |||||||| ||||||||||||||||||||||||| |||||||||||||||||||||||
Db  3227 CATTTAAATGGACTGAAGCTGAAGCCATCCAGACCTGGAGTACCCGTTCATTCAAGAAAATTACT 3286

Qy  4050 GATATAGTTTTTAAAATTGAGCTGTATTTTCAAGCAGCTGTATTGTTACTCATTGTTACT 4109
         |||||||||||| |||||| |||||||||||||||||||||||||||||||||||||||
Db  3287 GACATTGTTTTTAAAATTAAAATTGAGCTATATTTTCGATTTTGATGCTGGGAAGTTTATTTGCATTTCATCAT 3346

Qy  4110 GCAATGCCACCTTACTTTGCCATGCGAAATGAATTCAGAGAATCATAAGATCAAAGCTTATATC 4169
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3347 GCAATGCCACCTTACTTTGCCATGCGAAATGAATTCAGAGAATCATAAGATCAAAGCTTATATCT 3406

Qy  4170 CAACTTAAACTTTCAGGTCTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGAT 4229
         ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3407 CAACTAAACTTTCGGGTCTTTGCCATCTCATCAGCCTTATTGGGTTGGGTTGGACAAGCTGTTGGTGGAT 3466

Qy  4230 ATCCCCTTATTTTTTATCATTCTTATTTTGATGCTGGAATCATTGTTACT 4289
         ||| |||||||||||||||| |||||||||||||||||||||||||||||
Db  3467 ATTCCCTTGTTTTTTGTGTTTTTCTGATTTTGATGCTGCGGAAGTTTATTTGCATTTCATCAT 3526

Qy  4290 GGATTATATTTTTATACTGTAAAGTTCCTTGCCTTTCAAGGACATG 4349
         |||||||||||||||||| |||||||||||||||||||||||||||
Db  3527 GGACTGTATTTTTATCCTGCTCAAAATTCTTGCGTGCTTTGCCTGTGTTTTGCCTGTGTGTG 3586

Qy  4350 CCATTCAGTTATTCTGTTCACTTATTGCTTCTTCACCTTTAAGAAAATTTAAAATACC 4409
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Qy  4410 AAAGAATTTTGGTCATTTATCATTTTTAAAGCTAGAAGTTGAAGCAGAA 4469
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Db  3647 AAGGAAATTTTGGTCATTTATCATTTATCATTCTTGTGGCCAATTGGCCGTTGTGGCCATTCACGGCAATCACGGAA 3706
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Db  1487 CTGTGTATCTGACCAAGTCATTCCAGGGGGAATTGGCTTGAGGAGGTCATCTTTGTATT 1546

Qy  2311 TTCTGAAGCCTTCATATTGGTC-AAAGAGTAAAGAATAATTATGAGGTTATCAGAGGGC 2369
         |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  1547 TTTTGAAGCCATCGTATTGGTCAAAGAAACAAAGAAACTATAAGGAGCTATCGGAGGGC 1606

Qy  2370 AATGTTAATGGAAATATTAGTTTTTAGTGAAATTATTGAGCCAGTTCTTCTTCAGAATTGTA 2429
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1607 AACATTAATGGCAATATAGTTCTTCAATGAAATTGTTGAGCCCGTTCTTCTTCAGAATTTATA 1666

Qy  2430 GGGAAAGAAGGCCATAAGAATTAGTGGTATTCAGAAGACATACAGAAGAAGGGTGAAAAT 2489
         |||||||| |||||||||||||||||||||||||||||||||||||||||||| |||||
Db  1667 GGGAAGAAGAGCTATAAGGATAAGGTGGTATTCAGAAATCCTATAGAAAGAAAACTGACAAC 1726

Qy  2490 GTTGGAGGCCTTGAGAAATTGTCATTTGACATATATGAGGGTTCAGATTACTTGCCTTACTT 2549
         ||||||| ||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  1727 GTTGGAGGCGTTTGAGAAATTTGTCATTTGACATATATGAGAAGTTCAGATTACTTGCACTGCTG 1786

Qy  2550 GGCCACAGTTGGAACAGGAAAGAGTACATTGATGAAATATTCTTTTGTGGACTCTGCCCACCT 2609
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Db  1787 GGCCACAGTGGGAACAGGAAAAAGCCACACTGATGAATATATTCTCGTGTGGACTGTGTCCACCC 1846

Qy  2610 TCTGATGGGTTTGCATCTATAATGGACACAGAGTCTTCAGAAATAGAAATGTTTGAA 2669
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Db  1847 TCTGATGGGTTTGCTTCTTTATAATGGACACAGAGTCTCTGAAATAGAAATGTTTGAA 1906

Qy  2670 GCAAGAAAATGATTGGCATTTGTCCACAGTTAGATATACACTTGATGTTTTGACAGTA 2729
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Db  1907 GCAAGAAAAATGATTGGCATATGTCCGAGTCAGTATGCAGATATAAACTTTTGATGTTTTTGA CAGTA 1966

Qy  2730 GAAGAAAATTTATCAATTTGGCTTCAATCAAAGGGATACCAGCCAACAATATAATACAA 2789
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1967 GAAGAAAATTTATCAATTTGGCTTCAATCAAAGGGATACCAGCCAACAATATAATTCAA 2026

Qy  2790 GAAGTGCAGAGAAGGTTTTACTAGAGTTTAGACATGCAGACTAGAGAGACTACAAGCTAAA 2849
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Db  2027 GAAGTGCAGAAGTGTTGCTCGATCTGGACATGCAAGCCATCCAAAGATAATCAAGCGAA 2086

Qy  2850 AAATTAAGTGGTGGTCAAAAAGAAAGAAAGTGTCATTGGAAGTGCTGTCTTGGGACCCA 2909
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Db  2087 AAGTTAAGCGGTGGTCAGAGAAAGGAAGCTGTCTCTGTAGGAATTGCAGTTGAGCAGTGCAGTA 2146

Qy  2910 AAGATACTGCTGCTAGATGAACCAACAGCTGAATGGACCCCGTGTTCTCGACATATTGTA 2969
         |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2147 AAGATACTTCCTGCTAGACGAGCCTACACGCAGGAATGGACCCCCGTGCTCTCCGCATATTGTT 2206

Qy  2970 TCGGAATCTTTTAAAATACAGAAAAGCCAATCGGGTGACAGTGTTCAGTACTTCATTTCATG 3029
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Db  2207 TCGGAATCTTTTAAAATACAGAAAAGGCTAACAGTCGTGTTTAGTACTCACTTTCATG 2266

Qy  3030 GATGAAGCTGACATTCTTGCCAGATAGGAAAGCTGTGATATCACAAGGAATGCTGAAAATGT 3089
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2267 GATGAGGCTGACATTCTTGCCGACACCAGCTTGTCACACCAGGAAAGCTGTCATATCACACAAGGAATGCTGAAGTGT 2326

Qy  3090 GTTGGTTCTTCAATGTTCCTCAAAAGTAAAAATGGGGATCGGCTACCGCCTGAGCATGTAC 3149
         ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  2327 GTTGGTTCTTCAATTTTCCTAAAAGAGTAAAATCGGGAATCGGCTACCGCCTGAGCATGTAT 2386

Qy  3150 ATAGACAAATATTGTGCCACAGATTCTCTTCTTCACTGGTTAAACAACATATACCTGGA 3209
         ||||||||| |||||||||||||||||||| |||||||||||||||| ||||||||||
Db  2387 ATAGACAGATACTGTGCCGCCACAGAGTTCTTCGTCGTTGGTTAGGCAGCACACCACCGCA 2446

Qy  3210 GCTACTTATTACAACAGATGACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATG 3269
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2447 GCCGCGCTACTGCAGCAGAATGACCACCAGCTGTGTCAGTACACCGCGTTCAAAGACATG 2506

Qy  3270 GACAAAATTTTCAGGTTTTGTTTTCTGCCCTAGACAGTCATTCAAATTTGGCTGTCATTTCT 3329
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Db  2507 GACAAATTTTTCAGGCTTTGTTTTCTGCTCAGACAGTTCATTCATTCAACCTGGGTGTTATTTCT 2566

Qy  3330 TATGGTGTTTCCATGACGACTTGGAAGACGTATTTTTAAAGCTAGAAGTTGAAGCAGAA 3389
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Db  2567 TATGGTGTTTCCATGACAACATTGGAAGATGTATTCTTTAAAGCTAGAAGTTGAGCAGAGA 2626
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Db  121                                                              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3634  TTCAGATTTTTATGTTTTGGTTCATCATCTCTTTAAAAAATGTGTGGTTCCATCAAAC  3693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181   TTCAGATTTTTATGTTTTGGTTCATCATCTCTTTAAAAAATGTGTGGTTCCATCAAAC  240

Qy  3694  TTGTTCCAGACTATATTTTCTAAAACCTGGAGACAAACCACATAAATACAAAACAAGTC  3753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241   TTGTTCCAGACTATATTTTCTAAAACCTGGAGACAAACCACATAAATACAAAACAAGTC  300

Qy  3754  TGCTTCTTCAAAATCTCGCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGCC  3813
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Db  301   TGCTTCTTCAAAATCTCGCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGCC  360

Qy  3814  AGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGCTCCCCATAGTG  3873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361   AGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTG  420

Qy  3874  CGGCTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTA  3933
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421   CGGCTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTA  480

Qy  3934  CTATGGTTTATTCTTACCTATATTAGTGAATATCATTAGTGAATATCATTAGCTTTATCATT  3993
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Db  481   CTATGGTTTATTCTTACCTATATTAGTGAATATCATTAGTGAATATCATTAGCTTTATCATT  540

Qy  3994  TAAATGTGACTGAAACCATCCAGATCGGAGTACCCCATTCTTCAAGAAATTACTGATA  4053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541   TAAATGTGACTGAAACCATCCAGATCGGAGTACCCCATTCTTCAAGAAATTACTGATA  600

Qy  4054  TAGTTTTAAAATTGAGCTGTATTTCAAGCAGCTTGCTTGGAATCATTGTTACTGCAA  4113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601   TAGTTTTAAAATTGAGCTGTATTTCAAGCAGCTTGCTTGGAATCATTGTTACTGCAA  660

Qy  4114  TGCCACCTTACTTGCCATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATACTCAAC  4173
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Db  661   TGCCACCTTACTTGCCATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATACTCAAC  720

Qy  4174  TTAAACTTCAGGTCTTTTGCCATCTGCATATTGGACAAGCTGTTGTTGGATATCC  4233
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Db  721   TTAAACTTCAGGTCTTTTGCCATCTGCATATTGGACAAGCTGTTGTTGGATATCC  780

Qy  4234  CCTTATTTTTTATCATTCTTATTTGATGCTAGGAAGCTACTGGCATTCATTATGGAT  4293
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Db  781   CCTTATTTTTTATCATTCTTATTTGATGCTAGGAAGCTACTGGCATTCATTATGGAT  840

Qy  4294  TATATTTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTGCCTATTGGTTATGTTCCAT  4353
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Db  841   TATATTTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTGCCTATTGGTTATGTTCCAT  900

Qy  4354  CAGTTATTCTGTTCACTTATATTGCTTCTTCTTCACCCTTAAGAAAAAATTTAAATACCAAAG  4413
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Db  901   CAGTTATTCTGTTCACTTATATTGCTTCTTCTTCACCCTTAAGAAAAAATTTAAATACCAAAG  960

Qy  4414  AATTTGGTCATTATCTATTCTGGCAGCGGTTGCAATCACTGAAATAA  4473
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Db  961   AATTTGGTCATTATCTATTCTGGCAGCGGTTGCAATCACTGAAATAA  1020

Qy  4474  CTTTCTTTATGGGATACACAATGCAACTATTCTTCATTATGCCTTTTGTATCATTC  4533
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Db  1021  CTTTCTTTATGGGATACACAACAATGCAACTATTCTTCATTATGCCTTTTGTATCATTC  1080

Qy  4534  CAATCTATCCACTTCTAGGTTGCCTGATTTCTTCATAAAGATTTCTTGGAAGAATGTAC  4593
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Db  1081  CAATCTATCCACTTCTAGGTTGCCTGATTTCTTCATAAAGATTTCTTGGAAGAATGTAC  1140

Qy  4594  GAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTT  4653
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Db  1141  GAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTT  1200

Qy  4654  ACCTGCAGTGTACTGTGTGGATTTTCCCTTACAATACTATGAGAAAAAATGAGGAGCA  4713
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Qy  4470  ATAACTTCTTATGGGATACACAATTGCAACTATTCTTCATTATGCCTTTTGTATCATC  4529
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Db  3707  ACAACTTCTTTCTGCAATATGCAGTTACGGCTGTCTTTCATTACACCTTCTGCATAGCC  3766

Qy  4530  ATTCCAATCATCCACTTCTAGGTTGCCTGAATTCTTTCATAAAGATTTCTTGGAAGAAT  4589
          |||||||||||| ||||||  || |||||| ||||||||  |||||||||||||||||
Db  3767  ATTCCAATCACCCTCCTCCTGGGGTTGTCTGATTTCTTTCATAAAGGGGTTCTTGGAAGAAT  3826

Qy  4590  GTAC  4593
          ||||
Db  3827  ATGC  3830
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RESULT 15
ADC51606

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ID   ADC51606 standard; DNA; 2723 BP.
XX
AC   ADC51606;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human macroprotein-94.64 coding sequence, SEQ ID 1.
XX
KW   Human; macroprotein-94.64; dementia; arrhythmia; asthma; diabetes; gene;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            12..2486
FT                  /*tag= a
FT                  /product= "Human macroprotein-94.64"
XX
PN   CN138726-A.
XX
PD   04-DEC-2002.
XX
PF   26-APR-2001; 2001CN-00112765.
XX
PR   26-APR-2001; 2001CN-00112765.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y, Xie Y;
XX
DR   WPI; 2003-269487/27.
DR   P-PSDB; ADC51607.
XX
PT   New human macroprotein-94.64, encoding polynucleotide, antagonist and
PT   recombinant production, useful for treating dementia, arrhythmia, asthma
PT   and diabetes.
XX
PS   Claim 6; SEQ ID NO 1; 35pp; Chinese.
XX
CC   The present invention relates to human macroprotein-94.64 (ADC51607) and
CC   its coding sequence (ADC51606). The protein is useful for treating
CC   dementia, arrhythmia, asthma and diabetes.
XX
SQ   Sequence 2723 BP; 855 A; 460 C; 518 G; 890 T; 0 U; 0 Other;
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Query Match          41.1%;   Score 2683.8;   DB 10;   Length 2723;
Best Local Similarity 99.9%;   Pred. No. 0;
Matches 2685;   Conservative   0;   Mismatches   3;   Indels   3;   Gaps   0;
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Qy  3454  CTTTTGATGAAATGGAACAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCTCTAGTGA  3513
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Db  1     CTTTTGATGAAATGGAACAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCTCTAGTGA  60

Qy  3514  GCACCATGAGCCTTTGGAAACAACAGCTGTATACAATAGCAAAGTTCATTTCTTTACCT  3573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61    GCACCATGAGCCTTTGGAAACAACAGCTGTATACAATAGCAAAGTTCATTTCTTTACCT  120

Qy  3574  TGAAACGTGAAAGTAAATCAGTGAGATCAGTGTTGCTTCTGCTTTAATTTTTTCACAG  3633
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Qy   5794 TTGAAGAATATAGCTTTTCTCAAGCAACATTGGAACAGAGTTTTTGTAGAACTCACTAAAG 5853
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TTGAAGAATATAGCTTTTCTCAAGCAACATTGGAACAGAGTTTTTGTAGAACTCACTAAAG 2400

Qy   5854 AACAAGAGGAGGAAGATAATAGTTGTGGAACTTAAACAGCACACTTGGTGGGAACGAA 5913
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 AACAAGAGGAGGAAGATAATAGTTGTGGAACTTAAACAGCACACTTGGTGGGAACGAA 2460

Qy   5914 CACAAGAAAGATAGAGTAGTATTTTGAATTTGTATTGTTCGGTCTGCTTACTGGGACTTCT 5973
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CACAAGAAAGATAGAGTAGTATTTTGAATTTGTATTGTTCGGTCTGCTTACTGGGACTTCT 2520

Qy   5974 TTCTTTTTCACTTAATTTAACTTTGGTTTAAAAGTTTTTTATTGGAATGGTAACTGGA 6033
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Db   2521 TTCTTTTTCACTTAATTTAACTTTGGTTTAAAAAGTTTTTTATTGGAATGGTAACTGGA 2580

Qy   6034 GAACCAAGAACGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGTGTG 6093
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Db   2581 GAACCAAGAACGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGTGTG 2640

Qy   6094 TTTTGCTTTCTTTAAATAAAACGTATGTATAAAACGTATGTAAGTGAAGCTGCA 6141
          |||||||||||||||||||||||||||||||||||||||
Db   2641 TTTTGCTTTTCTTTAAATAAAACGTATGTAATAATTAAGTGAAGCCCGAA 2688
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Search completed: December 4, 2004, 07:17:06
Job time : 2772 secs

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Db   1201 ACCTGCAGTGTGTACTGTGGATTTCCTCCTTACAATACTATGAGAAAAATGGAGGCA 1260

Qy   4714 GATCAATAAGAAAAGATCCCTTTTCAGAAACCTTCAACGAAGTCTAAAAATAGGAAGC 4773
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Db   1261 GATCAATAAGAAAAGATCCCTTTTCAGAAACCTTCAACGAAGTCTAAAAATAGGAAGC 1320

Qy   4774 TTCCAGAACCACCAGACAATGAGGATGAAGATGTCAAAGTGAAAGACTAAAGG 4833
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Db   1321 TTCCAGAACCACCAGACAATGAGGATGAAGATGTCAAAGTGAAAGACTAAAGG 1380

Qy   4834 TCAAAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCATCCATTATGGTCAGCAATT 4893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TCAAAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCATCCATTATGGTCAGCAATT 1440

Qy   4894 TGCATAAAGAATATGATGACAAGAAAGATTTTCTTCTTTCAAGAAAAGTAAAGAAAGTGG 4953
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Db   1441 TGCATAAAGAATATGATGACAAGAAAGATTTTCTTCTTTCAAGAAAAGTAAAGAAAGTGG 1500

Qy   4954 CAACTAAATACATCTCTTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCCAA 5013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CAACTAAATACATCTCTTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCCAA 1560

Qy   5014 ATGTGCTGCAAAAGCACAATTATTATATTCTGGTTGGTGATATTGAACCAACTTCAG 5073
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ATGTGCTGCAAAAGCACAATTATTATATTCTGGTTGGTGATATTGAACCAACTTCAG 1620

Qy   5074 GCCAGGTATTTTTAGGAGTATTCTTCAGAGACAAGTGAAGATGATGATTCACTGAAGT 5133
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Db   1621 GCCAGGTATTTTTAGGAGATTATTCTTCAGAGACAACATGAAGATGATGATTCACTGAAGT 1680

Qy   5134 GTATGGGTTACTGTCCTCAGATAAAACCCTTGTGGCCAAGATACTACATTGCGAGGAACATT 5193
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Db   1681 GTATGGGTTACTGTCCTCAGATAAAACCCTTGTGGCCAAGATACTACATTGCGAGGAACATT 1740

Qy   5194 TTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGAAAAGAAGTCATAAGTC 5253
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Db   1741 TTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAGAAGTCATAAGTC 1800

Qy   5254 GAATAACACATGCACTTGATTTAAAAGAACATCTTCAGAAAGACTGTAAAGAAACTACCTG 5313
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Db   1801 GAATAACACATGCACTTGATTTAAAAGAACATCTTCAGAAAGACTGTAAAGAAACTACCTG 1860

Qy   5314 CAGGAATCAAACAAACGAAAGTTGTGTTTGCTCTAAGTAATGCTAGGGAATCCTCAGATTACTT 5373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CAGGAATCAAACAAACGAAAGTTGTGTTTGCTCTAAGTAATGCTAGGGAATCCTCAGATTACTT 1920

Qy   5374 TGCTAGATGAACCATCTACAGGTATGATGAATCCCAAAGCCAAACAGCACATGTGGCGAGCAA 5433
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Db   1921 TGCTAGATGAACCATCTACAGGTATGATGAATCCCAAAGCCAAACAGCACATGTGGCGAGCAA 1980

Qy   5434 TTCGAACTGTCATTTAAAACAGAAAGGCGGCTGCTATTCTGACCACTCACTCACTGTATCG 5493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TTCGAACTGTCATTTAAAACAGAAAGGCGGCTGCTATTCTGACCACTCACTCACTGTATCG 2040

Qy   5494 AGGCAGAGCGTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCG 5553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AGGCAGAGCGTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCG 2100

Qy   5554 GAACAGTACAAACATCTAAAGACTAAAGAAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTGA 5613
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Db   2101 GAACAGTACAAACATCTAAAGACTAAAGAAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTGA 2160

Qy   5614 AGGACTCGATAGAAAACTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCC 5673
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGGACTCGATAGAAAACTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCC 2220

Qy   5674 CAAATGCAAGCCGTCAGGAAAGTTTTCTTCATTTGGCTTATAAAATTCCTAAGGAAG 5733
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CAAATGCAAGCCGTCAGGAAAGTTTTCTTCATTTGGCTTATAAAAATTCCTAAGGAAG 2280

Qy   5734 ATGTTCAGTCCCTTCACAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCA 5793
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ATGTTCAGTCCCTTCACAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCA 2340
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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2004 Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:   December  4, 2004, 06:17:02 ; Search time 18029 Seconds
                                           (without alignments)
                              13188.155 Million cell updates/sec

Title:         US-10-005-338B-1
Perfect score: 6525
Sequence:    1 aaaatgttgatatttctct..........ttgatcataataagtgaaat 6525

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters:      65645750


Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    EST:*
              1: gb_est1:*
              2: gb_est2:*
              3: gb_htc:*
              4: gb_est3:*
              5: gb_est4:*
              6: gb_est5:*
              7: gb_est6:*
              8: gb_gss1:*
              9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.		Score	% Match	Query Length	DB	ID	Description
1		2934.4	45.0	3950	3	AK047188	AK047188 Mus muscu
2		2807	43.0	3831	3	AK046203	AK046203 Mus muscu
3		1209.6	18.5	1529	3	AK034961	AK034961 Mus muscu
4		.1182	18.1	1346	3	U66672	U66672 Homo sapien
5		978.2	15.0	6017	3	CR627382	CR627382 Homo sapi
6		837	12.8	850	6	CD250953	CD250953 AGENCOURT
7	c	789.2	12.1	838	6	CD629433	CD629433 560461653
8		761.4	11.7	872	6	BQ722933	BQ722933 AGENCOURT
9		760.6	11.7	809	3	BC029426	BC029426 Homo sapi
10		751	11.5	4620	9	AY414282	AY414282 Homo sapi
11		741.4	11.4	773	5	BQ441353	BQ441353 AGENCOURT
12		740.2	11.3	874	6	CD629439	CD629439 560462273J
13	c	736.8	11.3	912	6	CD629443	CD629443 560464011J
14	c	731	11.2	747	5	BU686259	BU686259 UI-CF-DU1
15		729	11.2	730	6	CF272622	CF272622 TPU00182
16		722.4	11.1	771	4	BG564439	BG564439 602584385
17	c	722.2	11.1	826	6	CD629435	CD629435 560462577J
18		721	11.0	909	6	CD629437	CD629437 560462653
19		719.4	11.0	793	6	CB241963	CB241963 UI-CF-FN0
20		706.6	10.8	744	6	CD629440	CD629440 560462811H
21		681.6	10.4	756	4	BG435656	BG435656 602506942
22		680.4	10.4	744	3	AL700140	AL700140 DKFZp686H
23	c	676.4	10.4	697	5	BQ774317	BQ774317 UI-H-EZ1-
24	c	673.6	10.3	752	6	CD629427	CD629427 551464711J
25	c	668	10.2	926	5	BU146839	BU146839 AGENCOURT 55058933J
26	c	663.4	10.2	699	6	CD629421	CD629421 55058933J
27	c	661.6	10.1	728	5	BU623566	BU623566 UI-H-FG1-
28		658.4	10.1	672	6	CD629436	CD629436 56046265H
29		657.2	10.1	712	7	CN404315	CN404315 170006001
30		655.4	10.0	792	4	BG564921	BG564921 60258984_H
31		652.4	10.0	800	5	BU750944	BU750944 CH3H036_H
32	c	648.8	9.9	729	6	CD629441	CD629441 56046281J
33		646	9.9	735	6	BG926885	BG926885 HNC24-1-E
34		643	9.9	663	6	CD629438	CD629438 56046273H
35		641	9.8	664	6	CB044826	CB044826 NISC_gc06
36		634.4	9.7	670	6	BG570726	BG570726 602591840
37		633.4	9.7	4594	9	AY414284	AY414284 Mus muscu
38		633	9.7	633	3	CA773136	CA773136 im60b03.y
39		631.8	9.7	3890	3	BC053340	BC053340 Mus muscu
40		630.4	9.7	768	5	BU853701	BU853701 AGENCOURT
41		628.6	9.6	724	6	CB962917	CB962917 AGENCOURT
42		625.2	9.6	694	2	BF969534	BF969534 60227186_J
43		623.8	9.6	4620	9	AY414283	AY414283 Pan trog1
44		623	9.5	623	9	CA773849	CA773849 im58a04.y
45		619.4	9.5	672	6	CD629426	CD629426 55146471H

ALIGNMENTS

```
RESULT 1
AK047188
LOCUS       AK047188              3950 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length
            enriched library, clone:B930033A02 product:ATP-BINDING CASSETTE
            PROTEIN homolog [Homo sapiens], full insert sequence.
ACCESSION   AK047188
VERSION     AK047188.1  GI:26338625
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Carninci,P. and Hayashizaki,Y.
TITLE       High-efficiency full-length cDNA cloning
JOURNAL     Meth. Enzymol. 303, 19-44 (1999)
MEDLINE     99279253
PUBMED      10349636
REFERENCE   2
AUTHORS     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE     20499374
PUBMED      11042159
REFERENCE   3
AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ozawa,K., Tanaka,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS     The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE       Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
```

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TITLE       Group Phase I & II Team.
            Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 3950)
AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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            Takeda,Y., Tanaka,A., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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Qy  3031  ATGAAGCTGACATTCTTGCAGATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTG  3090
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Qy  3151  TAGACAAATATTGTGCCACAGAGAATCTCTTCTCACTGGTTAAACAACATACCTGGAG  3210
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Db  2581  TTGACCAAGCAGACTATAGTGTATTTCACAGCCGCCCGGGGAGGAAGAAGACAGAATTCAA  2640

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Qy  4051  ATATAGTTTTAAAAATACAGAAAATGCGAAAATGCAGAAATCAAAGCTTATTACTC  4110
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Qy    4471  TAACTTTCTTTATGGGATACACAATTCCAACTATTCTTCATTATGCCCTTTGTATCATCA  4530
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Db    3721  TTCCAATCATCACCCTCTCCTCCGGGTTGTCTGATTTCTTTCATTCATAAGGGTTCTTTGGAAGAATA  3780

Qy    4591  TACGAAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTTATATCGC  4650
            |||||||||| ||||||||||||||  |||||  ||||||||||| |||||||  |||||
Db    3781  TGCCAAAAATGAGAAATCCTACCACATCCCTGGATAGACTTTTTAGTTGCTGTAATCATGC  3840

Qy    4651  CTTACCTGCAGTGTGTACTGTGGATTTCCTCTTACAATACCATGAGAAAAAATATGGAG  4710
            | |||||||||||||| |||| ||||||||||||||||||||||||||||| |||||||
Db    3841  CGTACCTGCAGTGTATACTGTGGATTTCCTCTTACAACACCATGAGAAATACATCGGAG  3900

Qy    4711  GCAGATCAATAAGAAAGATCCCCTTTTCAGAAACCTTTCAACGAAGTC  4759
            ||||||||| ||||||| ||||||||||||||||  ||
Db    3901  GCAGATCATCATAAGAAAGGATCCATTTTTGTCAGGGCCCCTTTCACAAAAGGC  3949
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RESULT 2
AK046203
LOCUS       AK046203              3831 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male corpora quadrigemina cDNA, RIKEN
            full-length enriched library, clone:B230352G14 product:ATP-BINDING
            CASSETTE PROTEIN homolog [Homo sapiens], full insert sequence.
ACCESSION   AK046203
VERSION     AK046203.1  GI:26091381
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   MEDLINE   99279253
    PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   MEDLINE   20499374
    PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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                    Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
                    Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,K., Matsuura,S., Kawai,J.,
                    Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
          TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
                    sequencing pipeline with 384 multicapillary sequencer
          JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
           MEDLINE   20530913
            PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3831)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/,
            URL:http://fantom.gsc.riken.jp/,
            Fax:81-45-503-9222,
            Tel:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1..3831
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:B230352G14"
                     /db_xref="taxon:10090"
                     /clone="B230352G14"
                     /sex="male"
                     /tissue_type="corpora quadrigemina"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     misc_feature    1..3831
                     /note="ATP-BINDING CASSETTE PROTEIN homolog [Homo sapiens]
                     (SPTR|CAB93535, evidence: FASTY, 89.4%ID, 76.5%length,
                     match=3750)"
ORIGIN
Query Match             43.0%;  Score 2807;  DB 3;  Length 3831;
Best Local Similarity   86.3%;  Pred. No. 0;
Matches 3112; Conservative    0; Mismatches 491; Indels    1; Gaps    1;

Qy    991  AATAGGTTTATTCAGAAAACATGTCCACTGCAATTAGGAGGTAGGAGTTTGGAGAGACAGA  1050
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    227  ATTAAACTGACCTAGAAAACATGTCCACTGCTACTGCAATTAGGAGGTAGGAGTTTGGAGAGACAGA  286
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Qy 2131 TCATGCATTTAGAGAGATTTAATGAAGGTGCTTCATTTCAAATTGACTGCAGGCCAT 2190
          |||||||||||||||||||||||||| ||| |||| |||| |||||||||| |||
Db 1367 TCATGCATTTAGAGAGATTTAATGAGGTGCCTTATTTTCTAATTGACTGAAGGTCCCT 1426

Qy 2191 ATCCTCTAATTATTACAATTATCATGCTCACACTTAATAGTATATTCTATGTCCTCTTGG 2250
          |||||||| || ||||||| ||||||| ||| |||||||||||| |||| ||||||||||
Db 1427 ATCCCTCTAATTATTACTATTATCATGCTCGAGTGTGTTCTATGTCCTATGTCCTCCTGG 1486

Qy 2251 CTGTCTATCTTGATCAAGTCATTCCAGGGGAATTGGCTTACCGGAGATCATCTTTATATT 2310
          | |||||||||||| |||||| ||||||| |||||||| ||||||||| |||||| ||||
Db 1487 CTGTGTATCTGACCAAGTCATTGGCTTGAGGAGGGGAATTGGCTTGAGAGGTCATCTTGTATT 1546

Qy 2311 TTCTGAAGCCTTCATTATTGGTC-AAAGAGTAAAAGAATTATGAGGAGTTATCAGAGGGC 2369
          ||| |||||| ||||||| ||| |||| ||||||||||||||||| ||||||||||||
Db 1547 TTTTGAAGCCATCGTATTGGTCAAAAAACAATATAGGAGCTATCGGAGGGC 1606

Qy 2370 AATGTTAATGCAAATATTAGTTTTAGTGAAATTATTGAGCCAGTTGCTTCTTCAGAATTGTA 2429
          || |||||||||||||||||||| |||||||||||||||| |||| || ||||||| ||
Db 1607 AACATTAATGGCAATATTGTTCTCAATGAAATTGTTGAGCCCCGTTTCTTCAGAATTTATA 1666

Qy 2430 GGAAAAGAGCCATAAGAATTAGTGTATTCAGAAGACATACAGAAGAGGGTGAAAAT 2489
          ||||||||||| |||||||||||||||||||| ||| |||||||| ||| |||||||
Db 1667 GGGAAGAGAGCTATAGAATTAAGTGGTATTCAGAAATCCTATAGAAAAACTGAGAAC 1726

Qy 2490 GTGGAGGCTTTGAGAAATTTGTCATTGACATATGAGGGTCAGATTACTGCCTTACTT 2549
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Db 1727 GTGGAGGCTTTGAGAAATTTGTCATTGACATATGACATATGAAGGTCAGATTACTGCACTGCTG 1786

Qy 2550 GGCCCAGTGCAAGCAGAGAAGAGTACATTGATGAGATATTCTTTGTGGACTCTCGCCCACCT 2609
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Db 1787 GGCCCACAGTGGAACTGGAAAAAGCACACTGATGAATATTCTGTGTGGACTGTGTCCACCC 1846

Qy 2610 TCTGATGGGTTTGCATCTATATTGGACACAGAGTCTCAGAAATAGATAGTGTTGAA 2669
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Db 1847 TCTGATGGGTTTTGGCTTCCTATATATGGACACAGAGTCTCGAAATAGATGAAATGTTTGAA 1906

Qy 2670 GCAAGAAAAATGATTGGCATTTGGCTTCAATCAAAGGATACCAGCCAACAATAATACAA 2729
          |||||||||| ||||| ||| ||||||||| ||||||||||||||| ||||||| ||||
Db 1907 GCAAGAAAAATGATTGGCATTTGGCTTCAATCAAAGGATACCAGCCAACAATAATATCAA 1966

Qy 2730 GAAGAAAATTTATCAATTTGGCTTCAATGTTAGACATGCAAAGATAACCAAGCTAAA 2789
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Db 1967 GAAGAAAAT TATCATTTTGGCTTCAATCAAAGGAATACCAGCCAACAATATAATTCAA 2026

Qy 2790 GAAGTGCAGAAGTTTACTAGATTTAGACATGCAGAGATATCAAAGATAACCAAGCTAAA 2849
          ||||||||||||||| ||| ||| || || || |||||||||||||| ||||| ||||
Db 2027 GAAGTGCAGAAAGTGTTGCTGGATCTGGACATGCAAGCCATCAAAGATAATCAAGCGAAA 2086

Qy 2850 AAATTAAGTGGTGGTCAAAAAAGAAAGCTGTCATTAGGAATTGCTGTTCTTGGGAACCCA 2909
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Qy 2910 AAGATACTGCTGCTAGATGAACCAACAGCTGGAATGACCCCTGTTCTCGACATATTGTA 2969
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Db 2147 AAGATACTCCTGCTAGACGAGCCTACAGCAGGAATGGGCTACCCCTGCTCTCCGCCATATTGTT 2206

Qy 2970 TGGAATCTTTTAAAATACAGAAAGCCAATCGGGTGACAGTGTTCAGTCACTTCATG 3029
          |||||||| |||||||||| |||||||||||||||||| |||||||||||||||||
Db 2207 TGGAATCTTCTAAAGTCTAAAGATATAGAAAGGCTAACAGAGTGACCGTGTTTAGTGTTACTTCACTTCATG 2266

Qy 3030 GATGAAGCTGACATTCTTGCGATAGGAGAAAGCTGTGATATCACAAGGAATGTGAAAATGT 3089
          |||||||| |||||||||| |||| |||||||| |||| ||| |||||||||||||| |||
Db 2267 GATGAGGCTGACATTCTTGCCGACAGGAGAAAGCTGTCATATCACAAGGAATGCTGAAGTGT 2326

Qy 3090 GTTGGTTCTTCAATGTTCCTCAAAGTAAAAGTAAATGGGGGATCGGCTACCGCCTCATGTAC 3149
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Db 2327 GTTGGTTCTTCAATTTCCTAAAGAGTAAAGAGTAAATGGGAATCGGCTACCGCCCTCAGCATGTAT 2386

Qy 3150 ATAGACAAATATTGTGCCACAGAATCTCTTTCTTCACTGGTTAAACACATATACCTTGA 3209
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Db 2387 ATAGACAGATACTGTGCCACAGAGTCACCTGTCCGTCCGGTTAGGCAGCACATACCCGCA 2446

Qy 3210 GCTACTTTATTACAACAGAATGACCAAACAACTTGTGTATAGTTGTCCTTTGCCTTCAAGGACATG 3269

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Db   3527 GGACTGTGATTTTATCCTGCAAAATTCTTCGTGTGTGGTGTTTGCCTCATTGCTTATGTG 3586
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Qy   4350 CCATCAGTTATTCTGTTCACTTATATTGCTTCTTCACCTTTAAGAAAAATTTAAATACC 4409
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Qy   4410 AAAGAATTTGGTCATTATCATTCGTGGCAGCGTGNCTTGTATTGCAATCACTGAA 4469
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Db   3647 AAGGAATTTGGTCATTATCATTCGTGACCGCCGGTTGGCTTGTCGTGGCAATCACGGAA 3706

Qy   4470 ATAACTTTCTTTATGGGATACACACAATTGCAACTATTCTTCATTGTCCTTTTGTATCATC 4529
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Qy   4530 ATTCCAATCTATCCACTTCAGGTTGCCTGATTTCTTCATAAAGATTTCTTGGAAGAAT 4589
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Db   3767 ATTCCAATCTACCCTCTCCTGGGTTGTCTGATTTCTTCATAAAGGGTTCTTGGAAGAAT 3826

Qy   4590 GTAC 4593
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Db   3827 ATGC 3830
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RESULT 3

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LOCUS       AK034961                1529 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 12 days embryo embryonic body between diaphragm region
            and neck cDNA, RIKEN full-length enriched library, clone:9430067009
            product:ATP-BINDING CASSETTE PROTEIN homolog [Homo sapiens], full
            insert sequence.
ACCESSION   AK034961
VERSION     AK034961.1  GI:26330331
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,M.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system-384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
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Qy   2447 GCCGCGCTACTGACGCAGAATGACCAGCAGCTCGTGTACAGCCTGCCCTTTCAAAGACATG 2506
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Db   3270 GACAAATTTCAGGTTGTTTCTGCCCTAGACAGTCATTCAAATTGGGTGTCATTTCT 3329
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Qy   2507 GACAAATTTCAGGCTGTTGTTTCTGCTCTAGACATTCATTCAAACCTGGGTGTTATTTCT 2566

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Db   3390 ATTGACCAAGCAGATTATAGTGTATTTACTCAGCACAGCCACTGGAGAGAAATGGATTCA 3449
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Db   3450 AAATCTTTGATGAAATGGAACAGAGAGCTTACTTATCCTTCTGAAAACCAAGGCTTCTCTA 3509
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Qy   2687 AAATCCTTTGATGAAATGGAACAGAGAGTTTACTTATCCTTCTGAAAACGAAAGCTTCTTCA 2746

Db   3510 GTGAGCCACCATGAGCCCTTTGGAAACAACAGATGTATACAATAGCAAAGTTTCATTCTTT 3569
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Qy   2747 GTGAGCCACCATGAGCCTCTGGAAGCAGCAAGTTGCTACGATTGCAAAGTTTCATTCCTC 2806

Db   3570 ACCTTGAAACGTGAAAGTAAATCAGTGAGATCAGTGTTGCTTCTGCTTTTAATTTTTTTC 3629
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Qy   2807 TCATTGAAACGAGAAAGCAAATCAGTGCGCGCTGTGTTGCTTCTGCTTCGCTTTTAATTTTTTT 2866

Db   3630 ACAGTTCAGATTTTATGTTTTTTGGTTCATCACTCTTTTAAAAATGCTGTGTGTTCCCATC 3689
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Qy   2867 GCAGTTCAGATTTTATGTTTTTTCTCCATCATTCTTTTAAAAATGCTGTGGTTCCCATC 2926

Db   3690 AAACTTGTTCCAGACTTATATTTCTAAAACCCAGAGACAAACCACATAAATACAAAACA 3749
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Qy   2927 AAACCTCGTTCCAGACTTGTATTTCCTAAAGCCTGGAGATAAACCTCATAAAATACAAAACA 2986

Db   3750 AGTCGTGCTTCTCAAAATTCTGCTGACTCCAGATACGATCTTATTAGCTTTTTCACA 3809
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Db   3810 AGCCAGAACATAATGGTGACGATGATTAATGACAGTGATATGTATCCGTGGCTCCCCAT 3869
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Qy   3047 CACCAGAACATAATGGTGCGCAATGTTAATGACAGTGACTATCGTCTGCGTCGTCCTCAC 3106

Db   3870 AGTGCGGCTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAAC 3929
               |||| || ||||||||||| |||||||||||| || |||| |||||| |||||||||||
Qy   3107 AGTGCGGCTCTCAATGTGGTGCGTTCTGAAAAGGACTATGTTTTTCGCTGTTTTCAAC 3166

Db   3930 AGTACTATGGTTTATTCTTCTTACCTATATTAGTTGAATATCATTAGTAACTACTCATCTTTAT 3989
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Db   3990 CATTTAAATGTGACTGAAACCATCCAGAATCTCGAGTACCCCATTCTTTCAAGAAATTACT 4049
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Db   4050 GATATAGTTTTTAAAATGAGCTGTATTTCAGCTGTAGGTTTGCTTGGAATCATTGTTACT 4109
               |||||  ||||||||||||||| ||||||  |||||||||||| |||||||||||||||
Qy   3287 GACATTGTTTTTAAAATGAGCTATATTTGATTGTTGATGCTGCGGAAGTCATTTATCATCAT 3346

Db   4110 GCAATGCCACCCTACTTTGCCATGGAAATGCAGAGAATCATAAGATCAAAGCTTATACT 4169
               ||||||||||||||||||||||||| ||||||||||||||||||| |||||||||||||
Qy   3347 GCAATGCCACCCTACTTTGCCATGGAAATGCAGAGAATCATAAGATCAAAGCTTATACT 3406

Db   4170 CAACTTAAACTTTCAGGCCTTTTTGCCATCGACTCTTTGGATTGGACAAGCTGTTGTTGAT 4229
               |||||||||||| ||||| ||||| |||||||||||||||||||||||||||||||||||
Qy   3407 CAACTTAAACTTTTTCGGGTTCTTTTGCCATCAGCCTATTGGGTTGGACAAGCTGTTGTGGAT 3466

Db   4230 ATCCCCTTATTTTTATCATTCTATTTGATGCTAGGAAGCTTACTGTGCATTCATTAT 4289
               ||||||  ||| | ||| ||| ||| |||||||||  |||| |||||||| ||||||
Qy   3467 ATTCCCTTGTTTTTTGTTGTTCGATTTGATGCTGCGGGAAGTTTTATTTGCATTCATCAT 3526

Db   4290 GGATTATATTTTTATACTGTAAAGTTCCTTGCGTGGTTTTTTGCCTTATTGGTTATGTT 4349
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JOURNAL   of 60,770 full-length cDNAs
REFERENCE Nature 420, 563-573 (2002)
           6 (bases 1 to 1529)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
           Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
           Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
           Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
           Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
           Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
           Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
           Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
           Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
           Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
           Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
           Muramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
           Physical and Chemical Research (RIKEN) Laboratory for Genome
           Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
           RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
           Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
           URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
           Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
           Encyclopedia Project of Genome Exploration Research Group in Riken
           Genomic Sciences Center and Genome Science Laboratory in RIKEN.
           Division of Experimental Animal Research in Riken contributed to
           prepare mouse tissues.
           Please visit our web site for further details.
           URL:http://genome.gsc.riken.jp/
           URL:http://fantom.gsc.riken.jp/.
FEATURES   Location/Qualifiers
     source   1..1529
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
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                     /db_xref="taxon:10090"
                     /clone="9430067009"
                     /tissue_type="embryonic body between diaphragm region and
                     neck"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="12 days embryo"
                     61..>1527
                     /note="unnamed protein product; ATP-BINDING CASSETTE
                     PROTEIN homolog [Homo sapiens] (SPTR|CAB93535, evidence:
                     FASTY, 89.4%ID, 76.5%length, match=3750)
                     putative"
                     /codon_start=1
     CDS   /protein_id="BAC28896.1"
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                     /translation="MEQSLLILSETKASSVSTMSLWKQVSTIAKFHFLSLKRESKSV
                     RAVLLLLIFFAVQIFMFFLHHSFKNAVVPIKLVPDLYFLKPGDKPHKYXTSLLLQNS
                     TDSDINGLIEFFAHQNIMVAMPNDSDYVSAAPHSAALNVRSEKDYVFSAVFNSTMVY
                     CLPVMMNIISNYYLYHLNVTEAIQTWSTPFIQEITDIVFKIELYFQAALLGIIVTAMP
                     PYFAMENAENHKIKAYTQLKLSGLLPSAYWVGQAVVDIPLFFVLILMLGSLFAFHHG
                     LYFYPAKFLAVVFCLIAYVPSVILFTYIASFTFKKILNTKEFWSPIYSVALACVAIT
                     ETTFFLQYAVTAVFHYTFCIAIPIYPLLGCLISFIKGSWKNMPKNENTYNPWDRLLVA
                     VIMPYLQCILMFLLLQHYEKIHGGRSIRKDPFFRALSQKAKNKKFPEPPINEDEDEDV
                     KAERLKVKELMGCQCCEEKPAIMVCNLHKEYDDKDFLH"
ORIGIN

Query Match   18.5%; Score 1209.6; DB 3; Length 1529;
Best Local Similarity   86.9%; Pred. No. 1.6e-242;
Matches 1329; Conservative   0; Mismatches 200; Indels   0; Gaps   0;

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Qy   3405 TATAGTGTATTACTCAGCAGCCACTGAGGAGGAAGAAATGGATTCAAAATCTTTGATGAA 3464
          |||||||||||| |||||||| || |||||||||||||| |||||||||| |||||||||
Db      1 TATAGTGTATTACACAGCAGCCGCGGGAGGAGGAAGAAACAGATTCAAAATCCTTTGATGAA 60

Qy   3465 ATGGAACAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCCTCAGTGAGCACCATGAGC 3524
          |||||||||||| |||||||||||||||||||||| ||||| |||||||||||||||||||
Db     61 ATGGAACAGAGTTTACTTATTCTTTCATTCTGAAACCAAAGCTTCTTCAGTGAGCACCATGAGC 120
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Qy   3525 CTTTGAAACAACAGATGTATACAATAGCAATAGCAAAGTTCATTTCTTTACCTGAAACGTGAA 3584
          ||||  |||  | |||| ||| |  |||| ||  ||  ||||||||||| |||||| || ||||
Db    121 CTCTGGAAGCAGCAGCAAGTGTCTACGATGTCCATCATTCCTCTCATTGAAACGAGAA 180

Qy   3585 AGTAAATCAGTGAGATCAGTGTCTTTCGCTTCTGCTTTTAATTTTTTTCACAGTTCAGATTTT 3644
          || ||||||||| | | ||| ||| |||| ||||||||||||||||||  |||||||||||||
Db    181 AGCAAATCAGTGCGCGCTGTGTGCTCTGCTTTTAATTTTTTTGCAGTTCAGATTTT 240

Qy   3645 ATGTTTTTGGGTCATCACTCTTTTAAAAAATGCTGTGGTCCCATCAAACTTGTTCCAGAC 3704
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Db    241 ATGTTTTTCCATCATTCTTTTAAAAATCTTTAAAAATGCTGTGGTTCCCATCAAACTCGTTCCAGAC 300

Qy   3705 TTATATTTTCTAAAACCTGGAGACAAAACCACATAAAATACAAATACAACAAGCCTGCTTCAA 3764
          || ||||| |||||| ||| |||| ||| | |||||| ||||| | ||||||||||||||||
Db    301 TTGTATTTCCTAAAGCCTGAGATAAACCTCATAAATACAAACAAGCAACAAGCCTGCTTCAA 360

Qy   3765 AATTCCGCTGACTCAGATATCAGTGATCTTATTAGCTTTTCAACAGCCAGAGAACACATAATG 3824
          ||||| | |||||||||||||| || ||||||| || ||||| ||| ||||| |||||||||
Db    361 AATTCTACTGACTCAGATATCAATGGTCTTATTGAGTTTTTTGCACACCAGAACATAATG 420

Qy   3825 GTGACCATGATTAATGACAGTGACTATGTGCTGCTGCCTCCCATAGTGCGGCGTTAAAT 3884
          ||| | ||| ||||||||||||||| |||||||||||||| |||||||| ||  || ||
Db    421 GTGGCAATGTTAATGACAGTGACCTATGTGCTGCTGCCTCACAGTGCGGCTCTCAAT 480

Qy   3885 GTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTAT 3944
          ||| ||| ||| ||||||||||||||||| | |||||||||||||||||||||||||||
Db    481 GTGGTGCGTTCTGAAAAGGACTATGTTTTTTCGTGCTGTTTTCAACAGTACTATGGTTAT 540

Qy   3945 TCTTTACCTATATTAGTGGAATATCATTAGTAACTACTATCTTATCATTAAATGTGACT 4004
          | ||| || | | || |  ||| |||| |||||||||||||| |||||||||||||||||
Db    541 TGTTTGCCAGTCATGATGAACATCAGTAGTAACTACTATCTTTATCATTAAATGTGACT 600

Qy   4005 GAACCATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGATATAGTTTTTAAA 4064
          || ||||||||| ||||||||||| || ||||||||||||||||| || |||||||||
Db    601 GAAGCCATCCAGACCTGGAGTACCCCGTTCATTCAAGAAATTACTGACATTGTTTTTAAA 660

Qy   4065 ATTGAGCTGTATTTTCAAGCAGCTTGCTTGGAATCATTGTTACTGCAATGCCACCTAC 4124
          ||||||||| |||||||||||| ||||||||||||||||||||||||||||||||||||
Db    661 ATTGAGCTATATTTTCAAGCAGTTTGCTTGGAATCATTGTTACTGCAATGCCACCTAC 720

Qy   4125 TTTGCCATGGAAAATGCAGAGAATCATAAAGATCAAAGCTTATACTCAACTTAAACTTTCA 4184
          |||||||||||||||||||||||||||||||||||||||||| | |||||||||||||| |
Db    721 TTTGCCATGGAAAATGCAGAGAATCATAAAGATCAAAGCTTATATCTCAACTTAAACTTTCG 780

Qy   4185 GGTCTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCCTTATTTTT 4244
          ||||||| |||| || | |||||| ||||||||||||||| |||| |||| | |||||
Db    781 GGTCTTTTGCCATCAGCCTATTGGGTTGGACAAGCTGTTGTGTGGATATTCCCTTGTTTTTT 840

Qy   4245 ATCATTCTTATTTTGTGATGCTGAGGAAGCTTACTGCATTCATTATGGATTATATTTTAT 4304
          | ||| ||| ||||| |||||| |||||  ||| |||||| || || | | |||||||||
Db    841 GTTGTTCTGATTTTGATGCTGGGAAGTTTATTGCATTTCATCATGACTGTATTTTTAT 900

Qy   4305 ACTGTAAAGTTCCTTGCGTGTGGTTTTTGCCTATTGGTTATGTTCATCAGTTATTCTG 4364
          | ||| || ||||| || ||| | ||| ||||| || || |||| ||||| |||||||
Db    901 CCTGCAAAATTCTTGCCTGTTTTCATTACACCTTCTGCATAGTGCCCTCCGTCATTCTG 960

Qy   4365 TTCACTTATATTGCCTTCTTTCACCTTAAGAAAAATTTAAATACCAAGAATTTGGTCA 4424
          ||||| || || || ||| ||||| || ||||||||||||||||||||||||||||||
Db    961 TTCACGTACATAGCTTCGTTCACTTTCAAGAAAAATTTAAATACCAAGAATTTGGTCA 1020

Qy   4425 TTTATCTATTCTGTGGCAGCCGGTTGNCTTGACCGGCATTGGCTTCTTTATG 4484
          ||| ||||||||||| | | ||  || |||| || || |||| || |||||
Db   1021 TTTATCTATTCTGTGACCCGCCATTGGCTTGTGTGGCAATCACGGAAACAACTTTCTTTTCTG 1080

Qy   4485 GGATACACAATTGCAACTATTCTTCATTATGCCTTTGTATCATCATCCAATCATCATCCA 4544
          |||| |||| || | || || ||||||||| || || ||||||||||||||||||||||
Db   1081 CAATATGCAGTTACGGCTGTCTTTCATTACACCTTCTGCATAGTGCCCATTCATCATCCA 1140

Qy   4545 CTTCTAGGTTGCCTGGTCGATTTTCTTTTTCATAAAGATTTCTTGGAAGAATGTACGAAAAATGTG 4604
          || || ||||| ||| | ||||||| ||| ||||||| ||||||||||||||| ||||||||| ||
Db   1141 CTCCTGGGTTGTCTGATTTCTTTCTCATAAAGGGTTCTTGGAAGAATATGCCAAAAAATGAG 1200
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Qy  4966  TCTCTTTCTGTGTGAAAAAGGAGAGATCTAGGACTATTGGTCCAAATGGTGCTGGCA  5025
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TCTCTTTCTGTGTGAAAAAGGAGAGATCTAGGACTATTGGTCCAAATGGTGCTGGCA   240

Qy  5026  AAAGCACAATTATTAATATTCGGTTGGTGATATTGAGGCAGATCAATAAGA         5085
          |||||||||||||||||||||||||||  |||||||||| || ||  ||||
Db   241  AAAGCACAATTATTAATATTCGGTTAGTGATATTGAACCAGCTCAGGCCAGTATTT     300

Qy  5086  TAGGAGATTATTCTTCAGAGACAAGTGAAGTGATGATGATCGAAGTGTATGGGTTACT   5145
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  TAGGAGATTATTCTTCAGAGACAAGTGAAGTGATGATGATCGAAGTGTATGGGTTACT   360

Qy  5146  GTCCTCAGATAAACCCTTTGTGGCCAGATACTACATTGCAGGAACATTTGAAATTTATG  5205
          ||||||||| |||||||||||||||||||||||||||||||||||||||||| ||||
Db   361  GTCCTCAGATAAACCCTTTGTGGCCAGATACTACATTGCAGGAACATTTGAAATTTATG  420

Qy  5206  GAGCTGTCAAAGGAATGAGTGCAAGTGACATGAACATGAAGAAGTCATAAGTCGAATAACACATG  5265
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   421  GAGCTGTCAAAGGAATGAGTGCAAGTGACATGAACATGAAGAAGTCATAAGTCGAATAACACATG  480

Qy  5266  CACTTGATTTAAAAGAACATCTTCAGAGAGACTGTAAAGAAACTACCTGCAGGAATCCAAAC  5325
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Db   481  CACTTGATTTAAAAGAACATCTTCAGAGAGACTGTAAAGAAACTACCTGCNAGGAATCAA   540

Qy  5326  GAAAGTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAAC      5385
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Db   541  CGAAAGTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAAC    600

Qy  5386  CATCTACAGGTATGGATCCCAAA--GCCAAACAGCACATGGCGGCAGCAATTCGAACTGC   5443
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Db   601  CATCTACAGGTCTGGATCCCAAATGCCAAACAGCACATGGCATGCAATTCGAACTGC     660

Qy  5444  ATTTAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGGC   5503
          ||                                              ||
Db   661  AT--------NNAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGGC   711

Qy  5504  TGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTGTCTAAGATGTATCGGAACAGTACA  5563
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   712  TGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTGTCTAAGATGTATCGGAACAGTACA  771

Qy  5564  ACATCTAAAGAGTAAATTGGAAAAGGCTACTTTTTGGAAATAAATAAA--GGACTGGA  5622
          |||||||||||||||||||||||||||||||||    ||||||||||||
Db   772  ACATCAAAGAGTAAATTGGAAAAG--NACTTTTTGGAAATTAAATAAAGGACTGGA    829

Qy  5623  TAGAAAACCTAGAAG-TAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCA  5681
          |||||||||||||||  |||||||||||||||||||||||||||||||||||||||||||
Db   830  TAGAAAACCTAGAAGCTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCA   889

Qy  5682  AGCCGTCAGGAAAGTTTTCTCATTTGGCTTTATAAATTCCTAAGGAAGATGTTCAG     5741
          ||||||||  |||||||||||||||||||||  |||||||  ||||||||||||||
Db   890  AGCCGTCA-GAAAGTTTTCTCATTTGGCTTTCTAAAATTAATTAAGGAAGATGTTCAG     948

Qy  5742  TCCCTTTCACAATCTTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTGAAGAA  5801
          ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db   949  TCCCTTTCCCAATCTTTTTTTAAGCTGGAAGAAGCTAAACATGC-TTTGCCATTGAAGAA  1007

Qy  5802  TATAGCTTTTCTCAAGCAATTGGAACAGGTTTTTGTAGAACTCACTAAAGACAACAAGAG  5861
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Db  1008  TATAGC-TTTTCTCAAGCAATTGGAACAGGTTTTTGTAGAACTCACTAAAGACAACAAGAG  1066

Qy  5862  GAGGAAGATATAGTTGTGAACTTAAACAGCACTTGGTGGAACAACACAAGAA         5921
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  1067  GAGGAAGATAATAGTTGTGAACTTAAACAGCACTTTGGT-GGAACGAACAAGAGA        1125

Qy  5922  GATAGAGTAGTATTTTGAATTTGTATTGTTCGGTCTGCTTACTGGGACTTCTTTCTTTT   5981
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1126  GATAGAGTAGTATTTTGAATTTGTATTGTTCGGTCTGCTTACTGGGACTTCTTTCTTTTT  1185

Qy  5982  CACTTAATTTAACTTGGTTAAAAAGTTTTTTATTGGAATGGTAACTGGCGACAACCAG   6041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1186  CACTTAATTTTAACTTGGTTAAAAAGTTTTTTATTGGAATGGTAACTGGCGACAACCAG    1245

Qy  6042  AACGCACTCGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGTGTGTTTGCTT   6101
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Qy  4605  GACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTTACCTGCCAGTGT  4664
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Db  1201  AATACCTACAATCCCTGGGATAGAGACTTTTAGTTGTCTGTAATCATGCCCTACCTGCCAGTGT  1260

Qy  4665  GTACTGTGGATTTCCTCTTACAATACTACTGAGAAAAAAATATGGAGGCAGATCAATAAGA  4724
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Db  1261  ATACTGTGGATTTCCTCTTACAACACTACATGAGAAAATACATGGAGGCAGATCTTATAAGA  1320

Qy  4725  AAAGATCCCTTTTCAGAAAACCTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGACCA   4784
          |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  AAGGATCCATTTTCAGGGCCCTTCACCAAAAGGCCAAAAATAAGAAGTTCCAGAACCA   1380

Qy  4785  CCAGACAATGAGGATGAAGATGTCAAAGCTCAAAGACTAAAGGTCAAAGAGCTG     4844
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CCCATCAATGAGGATGAAGATGAAGATGTCAAAGACTGAAAGACTGAAAGAGAGCTG    1440

Qy  4845  ATGGGTTGCCAGTGTTGTGTGAGGAGAAACCATCCATTATGTGTCAGCAATTTGCATAAAGAAA  4904
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  ATGGGTTGCCAGTGTTGTGTGAGGAGAAGCCAGCCATTATGTGTGCATTTGCATTTGCATAAAGAG  1500

Qy  4905  TATGATGACAAGAAAGAGATTTTCTTTC      4933
          ||||||||||||||||||||||||||||
Db  1501  TATGATGACAAGAAAGAGATTTTCTTCATTC  1529
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RESULT 4
U66672
LOCUS       U66672                  1346 bp    mRNA    linear   HTC 23-JUL-2001
DEFINITION  Homo sapiens clone EST90625 mRNA sequence.
ACCESSION   U66672
VERSION     U66672.1  GI:1906557
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1346)
  AUTHORS   Allikmets,R., Gerrard,B., Hutchinson,A. and Dean,M.
  TITLE     Characterization of the human ABC superfamily: isolation and
            mapping of 21 new genes using the expressed sequence tags database
  JOURNAL   Hum. Mol. Genet. 5 (10), 1649-1655 (1996)
  MEDLINE   97049974
   PUBMED   8894702
REFERENCE   2  (bases 1 to 1346)
  AUTHORS   Allikmets,R., Gerrard,B. and Dean,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1996) Human Genetics Section, National Cancer
            Institute, NCI-FCRDC, Frederick, MD 21702, USA
FEATURES             Location/Qualifiers
     source          1..1346
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="EST90625"
                     /note="similar to ATP-binding cassette transporter"
ORIGIN

Query Match             18.1%;  Score 1182;  DB 3;  Length 1346;
Best Local Similarity   96.5%;  Pred. No. 9.5e-237;
Matches 1306;  Conservative  0;  Mismatches 29;  Indels 19;  Gaps 9;

Qy  4786  CAGACAATGAGGATGAAGATGAAGATGTCAAAGTCAAAGACTGAAAGTCAAAGAGCTGA   4845
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     1  CAGACAATGAGGATGAAGATGAAGATGTCAAAGTCAAAGACTTAAAGTCAAAGAGCTGA     60

Qy  4846  TGGGTTGCCAGTGTTGTGTGAGGAGAAACCATCCATTATGTGTCAGCAATTTGCATAAAGAAT  4905
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TGGGTTGCCAGTGTTGTGTGAGGAGAAACCATCCATTATGTGTCAGCAATTTGCATAAAGAAT   120

Qy  4906  ATGATGACAAGAAAGAGATTTTCTTTCTTTCCAAGAAAAAGTGGCCAACTAAATACA   4965
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  ATGATGACAAGAAAGAGATTTTCTTTCTTTCCAAGAAAAAGTGGCCAACTAAATACA    180
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Db   1246 AACGGCACTCGAAATTTTCTAAGCTCCCTTAATTGAAATGCTGGTGGTTGTGTGTTTGCTT 1305
               ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6102 TTCTTTAAATAAAACGTATGTATAATTAAGTGAA 6135
               ||||||||||||||||||||||||||||||
Db   1306 TTCTTTAAATAAAACGTATGTATAATTAAGTGAA 1339
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SLRRLNIAIEVDAFGTRNGTDDPSYNGAIIVSGDEKDHRFSIACNTKRLNCFPVLLDV
ISNGLLGIFNSSHIQTDRSTFPEEHMDYEYGRSNTFFWIPMAASFTPYIAMSSIGD
YKKKAHSQLRIGSLHYPSAYWFGQALVDVSLYFLILLMQIMDYIFSPEEIIFIIQNLL
IQVVIFSIVATDLNEYGFGLGLFFWHHVNTSLHIDWLSIHFF"
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ORIGIN

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Query Match         15.0%;    Score 978.2;  DB 3;    Length 6017;
Best Local Similarity   53.4%;    Pred. No. 6.2e-194;
Matches 2580;  Conservative    0;  Mismatches 2044;   Indels 206;   Gaps 17;
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Qy  1068 AAGAATTACTTAATTAAATGCAGAACCAAAAGAGAGTAGTGTTCAGGAAATTCTTTTTCCA 1127
              ||||| ||  ||||  ||    | |||| |||||
Db     1 AAGAACTGTCTCAAAAAATGAGAATGAAAAGACAGACCTTGTTGGAATGGCTCTTTTCA 60

Qy  1128 CTATTTTTTTA---TTTGGTTAATATTAATTAATTAGCATGATGATGCATCCAAATAAGAAATAT 1184
              |||| ||       || ||  |||| ||  ||  | |||||||||||| |  || |  |
Db    61 TTTCTTCTGTACTGTTCGTGTACCTATTTTTCTCCAATTACATCAAGTCATGACACT 120

Qy  1185 GAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGAGTTACTCTTTCTAATCTAATT 1244
              |||| || | || || | ||||| | |  | | |||||| ||| ||  || ||  | |
Db   121 CCTCAAATGTCTTCAATGGATCTGGGACGTGTAGATAGTTTAATGATACTAATTATTGTT 180

Qy  1245 CTTGGATATACTCCAGTGACTAATTACAAGCAGCATCAAGCAGAAAGTGTCTACTGAT 1304
              | ||| |  | |  | || |  ||| | |  ||||   |||| |||  ||| | || |
Db   181 ATTGCATTTGCACCTGAATCCAAAACTACCCAAGAGATAATGAACAAAGTGGCTTCAGCC 240

Qy  1305 CATCTACCTGATGTCATATTACTGAAGAATATACAAATGAAAAAGAAAATGTTAACATCC 1364
              ||  | |  |  | ||  |  |||| | | |||  |||| ||  | | || |||  |||
Db   241 CCATTCCTAAAAGGAGGAACAATCATGGGGTGGCCTGATGAAAAAAAGCATGGATGAATTG 300

Qy  1365 AGTCTCCTCAAGCCGAGCAACTTGTGAGGTGTGGTTTCAAGACTCCATGTCCTATGAA 1424
              || ||||  ||  | || ||| ||| |||| |||| ||||| ||||| | |||| |||
Db   301 GATTTGAACATTCAATAGACGCGCGTGAGAGTCATCTTTACTGATATACCTTCTCTACCAT 360

Qy  1425 CTTCGTTTTTTCCTG---ATATGATTCCAGTATCTTCTATTATATATGGATTCAAGAGCT 1481
              | ||| ||||| ||     | || ||  || ||||| || | | |||||  ||||||| ||
Db   361 TTGAAGTTTTCTTGGGACCATAGAATCCCATGATGAAGAAGATATTACCTTTGTTGCC 420

Qy  1482 GGCTGTTCAAAATCA-----------TGTGAGGCGTGCTCAGTACTGGTCCTCCAGGT 1526
              ||  |||| |  ||            |||| | | ||  | ||||  |||||   |||
Db   421 CACTGTCAAGCAGTGAATGAAAAATGAAGTGTGAAGGTGCAGAGTTCTGGGAGAAGGC 480

Qy  1527 TTCACAGTTTACAGCATCATCCATGATGCTGCCATTATACAGTTGAGACGATCCATGTTCT 1586
              |||| |||| ||||| || | ||| ||||  |||||| ||||| || |  |||  |||||
Db   481 TTTGTAGCTTTTCAAGCTGCCATTAATGCTGCATCACAGAAATCGGCAACAAATCATTCA 540

Qy  1587 CTTTGGAAGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAAAACTGCTGTGTTGAGAA 1646
              | ||| ||| ||||| ||| || |  ||||| ||| |||| || ||| ||||| ||  |||
Db   541 GTGATGGAACCAGCTGAGTCAGTTACTGTGACATATGGTGTACATATGAAGATTACCTTTGTT 600

Qy  1647 ATAGATACCTTTCCCGAGGAGTAATTTAAATAACCTAGTTATATACCTTTTCTCCATTTTT 1706
              | | || || |  | ||| |  || |  | | ||  |||| | || || || | |  |||
Db   601 CAAGGAGGAGGTGCAACTGATTTTTTCATTTCTTTCATTATTTCTTTTCTTCTTTACATTT 660

Qy  1707 GGATACTTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAAATAAAGAATTTTA 1766
              ||| || || || ||| | || | || | |  || ||||  | ||||| | |||
Db   661 ATATACATGTATCAGTCAAT--GTTACACAAGAAAGACAATACATTACGTCATTGATG 717

Qy  1767 AAGATAATGGGACTTCATGATACTGCCTTTGGCTTTCCTGGTTCTTCTCTATACAAGT 1826
              ||| | |||| || ||||| |  |||| ||| | |||||| |||| | | |||||||
Db   718 ACAATGATGGGACTCCGAGTCAGCATCCGGCTTTCTGGGGTTTGATGTATGGTGGC 777

Qy  1827 TTAATTTTCTTATGTCTCCCTTCTATGGCAGTCATTGCAGCAGCTTCTTGTTATATTCCT 1886
              ||| ||||| | | || | |  || || | | | |||||| |||  || || |  ||||
Db   778 TTCATCCCATCATGGCCACTTTAATGGCTGTCCTTATTGTAAAATCTGCACAAATTGTCTC 837

Qy  1887 CAAAGTAGCAGCATTGTGATATTTCTGCTTTTTTCCTTTATGGATTATCATCTGTATTT 1946
              |||| ||| | | | | || || | ||| || || | | ||| | | ||| |||  ||
Db   838 CTGACTGGTTTTGTGATGGTCTTCACCCTCTTTCTCCTTGTTGGCCTGTCTTTGATAACT 897

Qy  1947 TTTGCTTAATGCTGCACACCTCTTTTAAAAAATCAAAACAAAACATGTGGGAATAGTTGAATTT 2006
              ||| ||  ||| || ||||| || | | |  | | ||||  |||| | || ||||| | |||
Db   898 TTAGCTTCCCTGATGAGTGTGTTGATAAAGAAACCTTTCCTTACGGGCGTTGGTTGTGTT 957
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RESULT 5

CR627382

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LOCUS       CR627382                6017 bp    mRNA    linear   HTC 03-AUG-2004
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686F2450 (from clone DKFZp686F2450).
ACCESSION   CR627382
VERSION     CR627382.1  GI:50949859
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6017)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  CONSRTM   The German cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (03-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by Medigenomix (Martinsried/Germany) within the cDNA
            sequencing consortium of the German Genome Project.
            This clone (DKFZp686F2450) is available at the RZPD Deutsches
            Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
            Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686F2450
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
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                     /clone="DKFZp686F2450"
                     /tissue_type="amygdala"
                     /clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
                     DH10B; sites SfiIA + SfiIB"
                     /dev_stage="adult"
                     /note="ATP-binding cassette A9, N-terminus truncated,
                     differentially spliced"
     gene            1..6017
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                     TFIYYVSVNVTQERQYITSLMTMMGLRESAFWLSWGLMYAGFIPIMATLMALIVKSAQ
                     IVLTGFMVFLFLLVGLSLITLAPLMSVLIKKFPLTGLVFLLIVFWGILGFPALY
                     THIPAFLEWTLCLLSPPAFTVGMAQLIHLDYDVNSNAHLDSSQNPYLIIATLFMIVFD
                     TLLYLVILTLYPFDKILPAEYGHRCSPLFFLKSCFWPGHGRANHVVLENETDSDPTPNDC
                     FEEVSPEFCGKEAIRIRNLKKEYAGKCERVEALKGVVFDIYEGQITALLGHSGAGKTT
                     LLNILSGLSVPTSGSVTVYNHTLSRMADIENISKFTGFCPQSNVOFGFLTVKENLRLF
                     AKIKGILPHEVKEKVQRVVQELEMENIQDILAQNLSGGQNRKLTFGIAILGDPQVLLL
                     DEPTAGLDPLSRHRIWNLLKEGKSDRVILFSTQFMDEADILADRKVFISNGKLKCAGS
                     SLFLKKKWGIGYHLSLHLNERCDPESITSLVKQHISDAKLTAQSEEKLVYILPLERTN
                     KFPELYRLDRCSNQGIEDYGVSITTINEVFLKLEGKSTIDESDIGIWGOLQTDGAKD
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Qy  2007  TTTGTTACTGTGGCTTTGGATTATTGGCCTTATGATAATCCTCATAGAAAGTTTTCCC  2066
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Db   958  CTCCTTATTGTCTTTTGGGGGATCCTGGGATTCCCAGCCATTGTATACACA---TCTTCCT  1014

Qy  2067  AAATCGTTAGTGTGGCTTTTCAGTCCTTCTGTCTCTACTTTGTGATTGGTGTATTGCA  2126
              |||||||  ||||| | ||||    |||   |||  |||||||  ||||| ||| |
Db  1015  GCATTTTTGGAATGGACTTTGTGTCTTCCTTAGCCCCTTGCCTTCACTGTTGGGATGGCC  1074

Qy  2127  CAGGTCATGCATTGAGAAGATTTAAATGAAGGTGCTTCATTTTCAAATTGACTGCGAGGC  2186
              || |||  | ||||||| ||||||   | |||| | |||| | ||| ||| ||| |
Db  1075  CAGCTTATACATTTGGACTATGATGTGAATTCTAATGCCCACTGGATTCTTCACAAAAT  1134

Qy  2187  CCATATCCTCTAATTATTACAATTATCATGCTCACACTTAATAGTAGTATATTCTATGTCCTC  2246
              ||||||| ||  | |||| |  |||||| | ||| || | |||||||| | ||
Db  1135  CCATACCTCATAATAGCTACTCTCTTTCATGTTGGTTTTGACACCCTTCGTATTTGGTA  1194

Qy  2247  TTGGCGTCTATCTGATCAAGTCATTCCAGGGAATTGGCTTACCGGAGATCATCTTTA  2306
              |||||| |   ||| ||| ||||| | ||||  ||| ||  |||| ||||| |
Db  1195  TTGACATTATATTTGACAAAAATTTGCCCGCGTGAATATGGACATCGATGTTCTCCCTTG  1254

Qy  2307  TATTTTCTGAAGCCTTCATATTGGTCAAAGAGTAAAGAAATTATGAGGAGTTATCAGAG  2366
              ||||||  |||||  | ||| ||| ||||||||||  ||| |||||||||| ||||||
Db  1255  TTTTTCCTGAAATCCTGTTTTTGGTTTCAACACGGAACAGGCTAATCATGTGGTCCTGAG  1314

Qy  2367  GGCAATGTTAATGGAAAATATTAGTTTTAGTAGTTTTGAAATTATTGAGCCAGTTTCTTCAGAATTT  2426
              ||| |||||  | |||| |||  |||||   |||||  |||| |||| | |||| ||||
Db  1315  AATGAAACAGATTCTGATCCTACACCTAATGACTGTTTTGAACCAGTGTCTCCAGAATTC  1374

Qy  2427  GTAGGAAAAGAAGCCATAAGAATTAGTGTATTCAGAAGACATACAGAAAGAGGGTGAA  2486
              |||||||||  | ||||    |||||| ||   ||| |||||| | |||||| ||||
Db  1375  TGTGGGAAGGAAGCCATCGAAATCTTTAAAAAGAATCATGTGCAGGAAGTGTGAG  1434

Qy  2487  AATGTGGAGGCTTTGAGAAATTGTCATTTGACATTATGAGGGTCAGATTACTGCCTTA  2546
              |  |||| | | || |||  || | |||| |||||||| | || ||  ||| | ||
Db  1435  AGAGTAGAAGCTTTGAAAGGTGTGGTGTTGACATATATGAAGGCCAGGCACCTGCCCCTC  1494

Qy  2547  CTTGGCCCAGTGCAACAGGAAAGAGTACATTTGTGGGACTCTGCCCA  2606
              |||||| ||||| |||||  |||||| || |||  |||| || ||||
Db  1495  CTTGGTCACAGTGGAGCTGGAGAAAAACTCCCTGTTAAACATACTACCCCTGTGTAAAAACTGTTAAACATACTGGGGTTGTCAGTT  1554

Qy  2607  CCTTCTGATGGGTTGCATCTATATATGGACAGAGTCTCAGAAATAGATGAAATGTTT  2666
              |||| |||| || | |||| ||||||| |||||||| | |||| ||||||||| |||
Db  1555  CCAACATCAGGTTCAGTCAGTTCCTATATCACACTGTCTATATATGACAGAGTGGCTGATATAGAA  1614

Qy  2667  GAAGCAAGACTACTGCTCGTCATTGGCATTGTCCACAGTTAGATATACACTTGATGTTTTGACA  2726
              | ||||| |  ||||| |  |||||| |||||  ||||| | |||||| | |||| ||||
Db  1615  AATATCAGCAAGTTCACTGGATTTTGTTCCAAATCCAATGTGCAATTGGATTTCTCACT  1674

Qy  2727  GTAGAAGAAATTTATCAATTTGGCTTCAATCAAAGGGATACCAGCCAACAATATAATA  2786
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Db  1675  GTGAAAGAAAACCTCAGGCTGTTGTTGCTAAAATAAAAGGGATTTGCCACATGAAGTGGAG  1734

Qy  2787  CAAGAAGTGCAGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGCT  2846
              ||| ||||  | |||||||   |||||   |||| ||| |||||||||||  | ||| ||
Db  1735  AAAGAGGTACAACGAGTTGTACAGGAATTAGAAATGGAAAATGAAAAGATTTCAGA  1794

Qy  2847  GTTTTCAACAGTACTATGGTTTATTCTTTACCCATATATTAGTAACATCATTAGTAACTAC  3980
              |  ||||| ||  |||  |||| | ||| |||  |||| || |  |||||| ||||||
Db  1795  GCAATGTAATACAAAACGGCTGAATTGCTTTCCTCCTGGATGTCATTAGCAATGGA  1854

Qy  2907  CCAAAGATACTGCTCTAGATGCAATGAAACAGCTGGATGAAAAAGAAGATGGGAAC  2966
              |||||| ||||| ||  ||||   || |   | |||||||||||| |||||||||||||||
Db  1855  CCTCAAGTTTTGCTATTGGATGAACCGACCCGATCCTCTTTCAAGGCACCGA  1914

Qy  2967  GTATGGAATCTTAAAATACAGAAAAAGCCAATCGGGTGACAGTGTTTCAGTPACTCATTTC  3026
              |||| ||| ||  |||| |   |||||| ||| || |||||| ||||  | || | |
Db  1915  ATATGGAATCTCCTGAAAGAGGGGAATCAGAACAGAGGTAATTCTCTTCAGCACCCAGTTT  1974

Qy  3027  ATGGATGAAGCTGACATTCTTGACGATAGGAAAGCTGTGATATCACAAAGGAATGCTGAAA  3086
              |||| |||||||| |||||  || ||| | |||  |||||  || ||  |||||||||||||
Db  1975  ATAGATGAGGCTGACATTCTCGCGCAGAGGAAGGTGTTCATAATCCATAGGGAAGCTGAAG  2034
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Qy  3087  TGTGTTGGTCTTCTTCAAATGTCCTCAAAAGTAAATGGGGATCGGCTACCGCCTGAGCATG  3146
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Db  2035  TGTGCAGGCGCTTCTCCTGTTCCTTAAGAAGAAGAAATGGGCATAGGCCTACCATTTAGTTTG  2094

Qy  3147  TACATAGACAAATATTGTGCCACAGAATCTCTTTCTTCACTGGTTAAACAACATATACCT  3206
              || |||||||| |   || ||| || || || | |  | |||||||| | ||||||| |
Db  2095  CATCTGAATGAAAGGTGTGATCCAGAGAGTATAACATCACTGGTTAAGCAGCACATCTCT  2154

Qy  3207  GGAGCTACTTATTACAACAGATGACCAACAACTGTGTATGAGCTTGCCTTCAAGGAC  3266
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Db  2155  GATGCCAAATTGACAGCACAAGTGAAGAAAAAACTTGTATATAATTTGCCTTTGAAAGG  2214

Qy  3267  ATGGACAAAATTTCAGGTTTGTTTTCTCGCCCTAGACAGTCATTCAAATTGGGTGTCATT  3326
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Db  2215  ACAAACAAATTTCCAGAACTTTACAGGGATCTTGATAGAGTTCTAACCAAGGCATTGAG  2274

Qy  3327  TCTTATGGTGTTTCATGACGACTTTGGAAGACGTATTTTTAAAGCTAGGAAGTTGAAGCA  3386
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Db  2275  GATTATGGTGTTTCCATAACAACTTTGAATGAGGTGTTTCTGAAATTAGAAGAAAAAATCA  2334

Qy  3387  GAAATTGACCAAGCAGATTATAGTGTATTTACTCAGCGCACTCGGAGGAGAAATGGAT  3446
              ||||||  || || |  |   ||| ||| |||| || | |||||||||||||  ||||
Db  2335  ACTATTGATGAATCAGATATTGGGGACAATTACAAACTGATGGGCAAAAGAT  2394

Qy  3447  TCAAAATCTTTTGATGAAATGGAACAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCT  3506
              ||||| ||  |   | ||| || ||  | |||| ||| | || ||||| | |||| |
Db  2395  ATAGGAAGCCCTGTTGAGCTGGAACAAGTTTTGTCTTCCTCCACGAAACAAGGAAAAC-  2453

Qy  3507  CTAGTGCACCATGAGCCGTTGGAAACAACAGATGTATCAATAGCAAAAGTTCATTTC  3566
              ||||| | |  | |||  ||  ||||||| |  ||| |||||||||| |  || |||||
Db  2454  --AATCAGTGCGTGCGCGCTCGGAGGCAGCAGCGCTCGTGCAATAGCAAAAGTTCGCTTC  2511

Qy  3567  TTTACCTTGAAACGTGAAAGTAAATCAGTGAATCAGTTGCTTCTGCGTTTTAATTTTT  3626
              | |  | |  | | ||  | ||| ||||||  ||| | | | || |||| ||||||
Db  2512  CTAAAGTTAAAGAACAAGAAAAAGCCTGTGGACTATATTATTGCTTTTTTGGTTTTAGC  2571

Qy  3627  TTCACAGTTCAGATTTTTATGTTTTGGTTCATCACTCTTTAAAAATCGTGTGGTTCCC  3686
              ||  |  ||  | |   | |||| |  |||||| ||| ||  || | |||| ||||
Db  2572  TTTATCCCTCCAACTTTTGGAACATCTATTCTACGAGTCATATCACATATCGAAAAGTT---ACCCG  2628

Qy  3687  ATCAAACTGTTCCAGACTTATATTTTCTAAAACCTGGAGACAAACCACATAAATACAAA  3746
              || |||||| ||  || | | || | |  |||||| |||  ||||||| |||||||||
Db  2629  TGGGACTGTCTCCAAATCATCAATAAGACTCAGCAGGTCAACAACCCACCAGGATCCTCTG  2688

Qy  3747  ACAAGTCTGCTTCTGCCAAGTGATTAAGCAGCATGATCCAGTGATCTTATTAGCTTTTTC  3806
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Db  2689  ACCCATTACTGGTCATCAATAAGACAGGGTCAACCATTGATAACTTTTTACATTCACTG  2748

Qy  3807  ACAAGCCAGAAC------ATAATGTGACGATGATTAATGACAGTGACTGACTATCCGTG  3860
              |  | ||| |||       | || | | |  |  |||| ||| | ||||| ||  | ||
Db  2749  AGGCGACTGAACATAGCTATAGAAGGTGATGCCTTTGGAACTAGAAATGGCACAGATGAC  2808

Qy  3861  GCTCCCCATAGTGCGGCTTTAAATGTGATGCATTCAGGTGCATCTGTCTGTGTTTTGCAGCT  3920
              || |  || |  |  ||| | |||  |  ||| | |  | | | |||| |||||| |
Db  2809  CCATCTTACAATGGTACTCATTGTGTCTGTCAGTGATGAGAAAAGATCCACGACGTCATTT  2868

Qy  3921  GTTTTCAACAGTACTATGGTTTATTCTTTACCTATATTAGTAATATCATTAGTAACTAC  3980
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Db  2869  GCATGTAATACAAAAACGGCTGAATTGCTTTCCTCCTGGAGTCATTAGCAATGGA  2928

Qy  3981  TATCTTTATCATTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTTCAA  4040
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Db  2929  CTACTTGGAGTTTTTAATTCGTCAGAACACATTTGACTACTAACACCTTTCTTCTGATACCG  2988

Qy  4041  GAAATTACTGATATAGTTTTAAAATTGAAGCTGTATTTCAAGCAGCTTTGCTTGGAATC  4100
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Db  2989  GA-----GCATATGGATTATGGATATGGTACCGAAGTAACACCTTTCTTCTGATACCG  3042

Qy  4101  ATTGTTACTGCAATGCCACCTTACTTTGCCATGGAAAAATGCGAGAATCATAAGATCAAA  4160
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Db  3043  ATGGCAGCCTCTTTCACTCCATACATTGCAATGCAATGCAGCAGCATTGGTGACTACAAAAAAAAA  3102

Qy  4161  GCTTATACTGCAACTTAACTTTCAGGTCTTTGCCATCTGCATTGGATTGGACCAAGCT  4220
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RESULT 6
CD250953
LOCUS   CD250953   850 bp   mRNA   linear   EST 22-MAY-2003
DEFINITION AGENCOURT 14211041 NIH_MGC_179 Homo sapiens cDNA clone
            IMAGE:30385589 5', mRNA sequence.
ACCESSION   CD250953
VERSION   CD250953.1 GI:31011419
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 850)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM452 row: o column: 06
            High quality sequence stop: 719.

FEATURES
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                    /note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV
                    (destroyed); Site 2: NotI; Library is oligo-dT primed and
                    directionally cloned (EcoRV site is destroyed upon
                    cloning). Average insert size 1.1 kb. Library was
                    constructed by (Invitrogen). Note: this is a NIH_MGC
                    Library."

ORIGIN

Query Match   12.8%;   Score 837;   DB 6;   Length 850;
Best Local Similarity 99.8%;   Pred. No. 1.8e-164;
Matches 848; Conservative   0; Mismatches 1; Indels 1; Gaps 1;

Qy   5014 ATGGTGCTGCAAAAGCACAATTATTAATA-TTCTGGTTGGTGATATTGAACCAACTTCA 5072
           |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   1 ATGGTGCTGCAAAAGCACAATTATTAATAATTCTGGTTGGTGATATTGAACCAACTTCA 60

Qy   5073 GGCCAGGTATTTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGAAGATGATTCACTGAAG 5132
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Db   61 GGCCAGGTATTTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGAAGATGATTCACTGAAG 120

Qy   5133 TGTATGGGTACTGTCCTCAGATAAACCCTTGTGGGCCAGATACTACATTGCAGGAGGACAT 5192
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Db   121 TGTATGGGTACTGTCCTCAGATAAACCCTTGTGGGCCAGATACTACATTGCAGGAGGAACAT 180

Qy   5193 TTTCAAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAAGAAGTCATAAGT 5252
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Db   181 TTTCAAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAAGAAGTCATAAGT 240

Qy   5253 CGAATAACACATGCACTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCT 5312
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Db   241 CGAATAACACATGCACTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCT 300

Qy   5313 GCAGGAATCAAACGAAAGTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACT 5372
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Db   301 GCAGGAATCAAACGAAAGTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACT 360

Qy   5373 TTGCTAGTGAACCATCTACACAGGTATGGATCCCAAAGCCAAACAGACACATGTGGCGAGCA 5432
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Db   361 TTGCTAGTGAACCATCTACACAGGTATGGATCCCAAAGCCAAACAGACACATGTGGCGAGCA 420

Qy   5433 ATTCGAACTGCATTAAAACAGAAAACAGAAAGCGGGTCGTATTCTGACCACTCACTATATGGAG 5492
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Db   421 ATTCGAACTGCATTAAAACAGAAAACAGAAAGCGGGTCTATTCTGACCACTCACTATATGGAG 480

Qy   5493 GAGGCAGAGGCGTCTGTCTGTGATCGAGTAGTCATCATGTGTCTGGGCAGTTAAGAGTATC 5552
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Db   481 GAGGCAGAGGCGTCTGTCTGTGATCGAGTAGTCATCATGTGTCTGGGCAGTTAAGAGTATC 540

Qy   5553 GGAACAGTACACACATCTAAAGAATAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTG 5612
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Db   541 GGAACAGTACACACATCTAAAGAATAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTG 600

Qy   5613 AAGGACTGGATAGAAAACCTAGAAGTAGTTTTTCTTCATTTTGGCTTAAAGAGAAATTCAGTATATTTTC 5672
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Db   601 AAGGACTGGATAGAAAACCTAGAAGTAGTTTTTCTTCATTTTGGCTTAAAGAGAAATTCAGTATATTTTC 660

Qy   5673 CCAAATGCAAGCCGTCAGGAAAGTTTTTTTCTTTATTTTGGCTTATAAAATTCCTAAGGAA 5732
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Db   661 CCAAATGCAAGCCGTCAGGAAAGTTTTTTTCTTTATTTTGGCTTATAAAATTCCTAANGAA 720

Qy   5733 GATGTTCAGTCCTTCACAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCC 5792
           ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   721 GATGTTCAGTCCTTCACAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCC 780

RESULT 7
CD629433/c
LOCUS   CD629433   560461651 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION   560461651 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629433
VERSION   CD629433.1 GI:4027699
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 838)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J.T., Au-Young,J. and Stuve,L.L.
  TITLE   Circular rapid amplification of cDNA ends for high-throughput
             extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT   Contact: Fu GK
             Incyte Genomics, Inc.
             3160 Porter Dr., Palo Alto, CA 94304, USA
             Tel: 650854102
             Email: gfu@incyte.com.
FEATURES   Location/Qualifiers
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ORIGIN

Query Match   12.1%;   Score 789.2;   DB 6;   Length 838;
Best Local Similarity 98.7%;   Pred. No. 1.9e-154;
Matches 827; Conservative   0; Mismatches 8; Indels 3; Gaps 3;

Qy   3396 CAAGCAGATTATAGTGTATTACTC-AGCAGCCACTGGAGGAAGAAATGGATTCAAAATC 3454
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   838 CAAGCAGATTATAGTGTATTAACTCAAGCAGCCACTGGAGGAAGAAATGGATTCGAAATC 779

Qy   3455 TTTTGATGAAATGGAACAGAGCTTACTT-ATTCTTCTGAAACCAAGGCTTCTCTAGTGA 3513
           |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   778 TTTTGATGAAATGGAACAGAGCTTACTTGATTCTTCTGAAACCAAGGCTGCTCTAGTGA 719

Qy   3514 GCACCATGAGCCTTTGGAAACAACAGATGTATACAACAGATGTATACAACAGATGTATC 3572
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||-ACC
Db   718 GCACCATGAGCCTTTGGAAACAACAGATGTATACAACAGATGTATACAACAGATGTGACC 659

Qy   3573 TTGAAACGTGAAAGTAAATCAGTGAGATCAGTGAGATCAGTGCTTTTAATTTTTTTCACA 3632
           ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   658 TTGAAACGTGAAAGTAAATCAGTGAGATCAGTGAGATCAGTGCTTTTAATTTTTTTTCACA 599

Qy   3633 GTTCAGATTTTATGTTTTGGTTCATCACTCTTTAAAAATGCTGGTTCCCATCAAA 3692
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   598 GTTCAGATTTTATGTTTTGGTTCATCACTCTTTAAAAATGCTGGTTCCCATCAAA 539

Qy   3693 CTTGTTCCGACTTATATTTCTAAAACCTGGAGACAAACCACCATAAATACAAAACAAGT 3752
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   538 CTTGTTCCGACTTATATTTCTAAAACCTGGAGACAAACCACCACATAAATACAAAACAAGT 479

Qy   3753 CTGCTTCTTCAAAATTCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGC 3812
           ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   478 CTGCTTCTTCAAAATTCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGC 419

Qy   3813 CAGAACATAATGGTGACGATGATAATGACAGTGACTATGATCCCCATAGT 3872
           |||||||||||||||||||||||||||||||||||||||||||||||||||

```
                    College of Medicine); available through Life
                    Technologies."

ORIGIN

        Query Match         11.7%;   Score 761.4;  DB 5;    Length 872;
        Best Local Similarity  97.9%;   Pred. No. 1.3e-148;
        Matches 825;   Conservative  0; Mismatches 11;  Indels  7;  Gaps  5;

Qy    4970  TTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGTCAGTTGTTTCAAATGTGCTCGCAAAAG  5029
            ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       1  TTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGTCAAATGTGCTGGCAAAAG    60

Qy    5030  CACAATTATTAATATTCTGGTTGGTGATATTGAACCACTTCAGGCCAGGTATTTTTAGG  5089
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  CACAATTATTAATATTCTGGTTGGTGATATTGAACCACTTCAGGCCAGGTATTTTTAGG   120

Qy    5090  AGATTATTCTTCAGAGACAAGTGAAGATGATGATCACTGAAGTGTATGGGTTACTGTCC  5149
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  AGATTATTCTTCAGAGACAAGTGAAGATGATGATCACTGAAGTGTATGGGTTACTGTCC   180

Qy    5150  TCAGATAAACCCTTGTGGGCCAGATACTACATTTGAAATTTATGAGC  5209
            |||||||||||||||||||||||||||||||||||||||||||||||
Db     181  TCAGATAAACCCTTGTGGGCCAGATACTACATTTGAAATTTATGAGC   240

Qy    5210  TGTCAAGGAATGAGTGCAAGTGACATGAAAGAAGTCATAAGTCGAATAACAACATGCACT  5269
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  TGTCAAGGAATGAGTGCAAGTGACATGAAAGAAGTCATAAGTCGAATAACAACATGCACT   300

Qy    5270  TGATTTAAAGAACATCTTCAGAGACTGTAAGAAAACTACCTGCAGGAATCAAACGAAA  5329
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  TGATTTAAAGAACATCTTCAGAGACTGTAAGAAAACTACCTGCAGGAATCAAACGAAA   360

Qy    5330  GTTGTGTTTTGCTCAAGTATGCTAGGGAATCCTCAGATTACTTGCTAGATGAACCATC  5389
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  GTTGTGTTTTGCTCAAGTATGCTAGGGAATCCTCAGATTACTTGCTAGATGAACCATC   420

Qy    5390  TCACGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTGCAACTGCATTTAA  5449
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  TCACGGTATGGATCCCAAAGCCAAACAGCACACGTGGCGAGCAATTGCAACTGCATTTAA   480

Qy    5450  AAACAGAAAGCGGGCTGCATTCTGACCACTCCACTATATGGAGGAGGCAGAGGCTGTCTG  5509
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  AAACAGAAAGCGGGCTGCATTCTGACCACTCCACTATATGGAGGAGGCAGAGGCTGTCTG   540

Qy    5510  TGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCT  5569
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  TGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCT   600

Qy    5570  AAAGAGTAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTGAAGGACTGGATAGAAAA  5629
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  AAAGAGTAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTGAAGGACTGGATAGAAAA   660

Qy    5630  CCTGAGAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAG-CCGTC  5688
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db     661  CCTAGAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCAGCCCGTC   720

Qy    5689  AGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATT-CCTAAGGAAGATGTTCAGT-CCCT  5746
            |||||||||||||||||||||||||||||||||||  |||||||||||||||||||| ||||
Db     721  AGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCCTAAGGAAGATGTTCAGTCCCCT   780

Qy    5747  TTCACAATCTTTTTTAA---GCTGGAAGAAGCTAAACAT-GCTTTTGCCATTGAAGAAT  5802
            |||||||||||||||||     |||||||||||||||| ||||||||||||||||||||
Db     781  TTCACAATCTTTTTTAAGCCTGGAAGGAAGGCTAAACATGGCTTTTGCCATTGGAGAGA   840

Qy    5803  ATA  5805
            |||
Db     841  ATA  843


RESULT 9
BC029426
LOCUS        BC029426                 809 bp    mRNA    linear   HTC 19-NOV-2003
DEFINITION   Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 5,
```

[left column — rotated, bottom portion]

```
Db     418  CAGAACATATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCCATAGT  359

Qy    3873  GCGGCTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTGCAGTGTTTCAACAGT  3932
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358  GCGGCTTTAAATGTGGTGCATTCAGAAAAGGACTATGTTTTGCAGTGTTTCAACAGT  299

Qy    3933  ACTATGGTTTATTCTTACCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCAT  3992
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298  ACTATGGTTTATTCTTACCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCAT  239

Qy    3993  TTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGAT  4052
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238  TTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGAT  179

Qy    4053  ATAGTTTTTAAAATTGAGCGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCA  4112
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178  ATAGTTTTTAAAATTGAGCGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCA  119

Qy    4113  ATGCCACCTTACTTTGCCATGGAAAATCCAGAGAATCATAAGATCAAAGCTTATACTCAA  4172
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     118  ATGCCACCTTACTTTGCCATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATACTCAA  59

Qy    4173  CTTAAACTTTCAGGTCTTTTGCCATCTGCATATTGGATTGGAATGGACAAGCTGTGTTGATA  4230
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      58  CTTAAACTTTCAGGTCTTTTGCCATCTGCATATTGGATTGGAATGGACAAGCTGTGTTGATA  1


RESULT 8
BQ722933
LOCUS        BQ722933                 872 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION   AGENCOURT_8100461 Lupski_sympathetic_trunk Homo sapiens cDNA clone
             IMAGE:6190464 5', mRNA sequence.
ACCESSION    BQ722933
VERSION      BQ722933.1  GI:21861819
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 872)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM13589  row: f  column: 01
             High quality sequence stop: 717.
FEATURES             Location/Qualifiers
     source          1..872
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6190464"
                     /sex="male"
                     /tissue_type="sympathetic trunk"
                     /dev_stage="adult, 16 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski sympathetic trunk"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCACGCGTCG-3' and
                     5'-GACTAGTTCTAGATCGGCACGCGAGCGGCCGCCCT(15)-3'.. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
```

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ACCESSION   BC029426
VERSION     BC029426.1  GI:20809520
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 809)
AUTHORS     Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE       Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE     22388257
PUBMED      12477932
REFERENCE   2  (bases 1 to 809)
AUTHORS     Strausberg,R.
TITLE       Direct Submission
JOURNAL     Submitted (01-MAY-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site:   http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 41 Row: 1 Column: 5
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 27262625
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
     source          1..809
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4723522"
                     /tissue_type="Liver"
                     /clone_lib="NIH_MGC_76"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-LIB"
ORIGIN
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mRNA (cDNA clone IMAGE:4723522), containing frame-shift errors.

```
Qy    994  AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA  1053
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     38  AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA  97

Qy   1054  GAACACTTCACTGAAGAATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGG  1113
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98  GAACACTTCACTGAAGAATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGG  157

Qy   1114  AAATTCTTTTCCACTATTTTTTTATTGGTTAATATAGAACTCAATCCTATGGACATGCATGATGCATCCAA  1173
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158  AAATTCTTTTCCACTATTTTTTTATTGGTTAATATAGAACTCAATCCTATGGACATGCATGATGCATCCAA  217

Qy   1174  ATAAGAAATATGAAGAAGTGCTAATATAGAACTCAATCCTATGGACAAGTTACTCTTT  1233
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    218  ATAAGAAATATGAAGAAGTGCTAATATAGAACTCAATCCTATGGACAAGTTACTCTTT  277

Qy   1234  CTAATCTAATTCTTGGATATCCCAGTGACTAATATTACAGCAGCATCATGCAGAAAG  1293
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    278  CTAATCTAATTCTTGGATATCCCAGTGACTAATATTACAGCAGCATCATGCAGAAAG  337

Qy   1294  TGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAGAAA  1353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    338  TGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAGAAA  397

Qy   1354  TGTTAACATCCAGTCTCTCAAGCCGAGCACTTGTAGGTGTGGTTTCAAAGACTCCA  1413
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    398  TGTTAACATCCAGTCTCTCAAGCCGAGCACTTGTAGGTGTGGTTTCAAAGACTCCA  457

Qy   1414  TGTCCATGAACTTCGTTTTTTCCTGATATGATTCCAGTATCTTCTATTTATATGGATT  1473
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    458  TGTCCATGAACTTCGTTTTTTCCTGATATGATTCCAGTATCTTCTATTTATATGGATT  517

Qy   1474  CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCGTCAGTACTGGTTCCTCAGGTTTTCACAG  1533
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    518  CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCGTCAGTACTGGTTCCTCAGGTTTTCACAG  577

Qy   1534  TTTTACAAGCATCCATAGAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGA  1593
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    578  TTTTACAAGCATCCATAGAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGA  637

Qy   1594  AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATA  1653
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    638  AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATA  697

Qy   1654  CCTTTCCCGAGGAGTAATTTAATATACCTAGTTATATACCTAGTTATAGCATTTTCACCTTTGGATACT  1713
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    698  CCTTTCCCGAGGAGTAATTTAATATACCTAGTTATATACCTAGTTATAGCATTTTCACCTTTGGATACT  757

Qy   1714  TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAATAAAAGAA  1760
           |||||||||||||||||||||||||||||||
Db    758  TTTTGGCAATTCATATCGTAGCAGCAAAAAAAAAAAAAAAAAAA  804
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RESULT 10
AY414282
LOCUS       AY414282        4620 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Homo sapiens ABCA9 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY414282
VERSION     AY414282.1  GI:39770244
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4620)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE       Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
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Query Match         11.7%;  Score 760.6;  DB 3;  Length 809;
Best Local Similarity   99.5%;  Pred. No. 1.9e-148;
Matches  763;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;
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JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED    14671302
REFERENCE 2 (bases 1 to 4620)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
          Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
          Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
          Adams,M.D. and Cargill,M.
TITLE     Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
          them based on alignment.
FEATURES           Location/Qualifiers
     source        1..4620
                   /organism="Homo sapiens"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:9606"
     gene          <1..>4620
                   /gene="ABCA9"
                   /locus_tag="HCMS172"
ORIGIN

Query Match    11.5%;    Score 751;  DB 9;  Length 4620;
Best Local Similarity  50.2%;   Pred. No. 2.5e-146;
Matches 2433;  Conservative   0;  Mismatches 2071;  Indels 346;  Gaps  19;

Qy  1047 CAGACCAGAACACTTCTACTGAAGAATTACTTAATTAAATGCAGAACCAAAAAGAGTAGT 1106
              ||| | ||| ||||| |  ||||  ||  || |  || | |||| |  | | || |
Db    31 CAAACATGGGCTCTTCTCTGCAAGAACTGTCTCAAAAAATGGAGAATGAAAGACAGACC    90

Qy  1107 GTTCAGGAAATTCTTTTCCACTATTTTTTA--TTTTGGTTAATATTAATTAATTAGCATG 1163
              || | ||  |||| ||| ||  || |    |  |  | ||| || |  |  |  |
Db    91 TTGTTGGATGGCTCTTTTCATTTCTTCTGGTACTGTTTCTGTACCTATTTTCTCCAAT   150

Qy  1164 ATGCATCCAAATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAG 1223
              ||  |  || | || | |  |  | || |  |||  |  | | ||  |  ||| |||
Db   151 TTACATCAAGTTCATGACACTCCCTCAAATGTCTTCAATGTCTTCAAATTTTGCCCGTGAATAT   210

Qy  1224 TTTACTCTTTCTAATCTAATTCTTCCAGTGGATAATACTCCAGTGACTACTAACAGCAGCATC 1283
              || | || |  |  || |  |||  || ||  | ||  |  | ||| |  ||| | ||
Db   211 TTTAATGATACTAATTAATTGTATTGCATTTGCACCTGAAATCAATCCAAAACTACCCAAGAGATA   270

Qy  1284 ATGCAGAAAGTGTCTACTGATCATCTACCTGATGTCATAAT-ACTGAAGAATATACAAAT 1343
              |||| ||| | || | ||  |  || | || || | ||  ||| ||  | |  ||||
Db   271 ATGAACAAAGTGGCTTCAGCCCCATTCCTAAAAGGAAGAACAATCATGGGGTGGCCTGAT   330

Qy  1344 GAAAAAGAAAATGTAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTC 1403
              ||||| |||||| |||   |||  || ||  |  |  || |||  ||| || | | ||
Db   331 GAAAAAAGCATGGATGAATTGGAATTCAATATTCAATAGACCCAGTGAGAGTCATCTTT   390

Qy  1404 AAAGACTCCATGTCCTATGAACTTCGTTTTTTTCCTG--ATATGATTCCAGTATCCTCT 1460
              ||| ||| |||| | ||| |  ||||| |||| |||  | | ||||| | || ||||
Db   391 ACTGATACCTTCTCTCCACCATTGGAAGTTTCTTCTTGGGGACATTAGAATCCCCATGATGAAA   450

Qy  1461 ATTTATATGGATTCAAGAGCTGGCTGTCAAAATCA-------TGTGAGGGCT 1505
              ||||| ||| || ||| ||||| | | |||||||       ||||| |||
Db   451 GAGCACAGAGACCATTCAGCTCACTGTCAAGCAGTGAATGAAAATGAAGTGTGAAGGT   510

Qy  1506 GCTCAGTACTGGCTCCTCAGGTTCACAGTTTACAGAGATGCTGCCATTATA 1565
              |||  | ||| | ||| || || || | ||||| |  |  ||  |||||||
Db   511 TCAGAGTTCTCGGGAGAAAGGCTTTGTAGCTTTCAAGCTGCCATTAATGCTGCTATCATA   570

Qy  1566 CAGTTGAAGACCAATGTTTCTCTTGGAAGGAGCTGGAGTCAACTAAAGCTGTTATTATG 1625
              |||| || || || | ||| || ||  | || ||  | |  | || | || || ||||
Db   571 GAAATCGCAACAATCATTCAGTGATGATGAACAGCTGATGTCAGTTACTGGTGTACATATG   630

Qy  1626 GGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCCGAGGAGTAATTTAATATACCTA 1685
              ||| || || | || | | |||||| || || || | ||||| || |  | | ||||
Db   631 AAGATATTACCTTTTGTGTGCCCAAGGAGGAGTTGCAACTGATGATTTTTCATTTTCTTTGC   690

Qy  1686 GTTATAGCATTTCACCTTTTGGATACTTTTGGCAAGTCAGTAGCAGAAAAAGAA 1733
              || |  ||| || ||| || || |  |  | | | ||| || |  | | |||
Db   691 ATTATTCTTTTTCTACATTTATATACATGATCAGTCAAT--GTTAACAAGACAAGAAAGA   747

Qy  1746 AAAAAATAAAGAAGAATTTTAAGATAATGGGACTTCATGATACTGCCTTTTGGCTTTCC 1805
              ||| ||| ||| ||  | | ||| |||| |||||||  || |  | | | ||| | |
Db   748 CAATACATTACGTCATTGATGACAATGATGGGACTCCGAGAGTCAGCATTCTGGCTTTCC   807

Qy  1806 TGGGTTCTTCTATATACAAGTTAATTTTCTTATGTCCTTCTTATGTCAGTCATTGCG 1865
              ||| || | || | | | | ||  | | || || | |||  ||| | | | || ||
Db   808 TGGGGTTGATGTATGCTGGCTTCATCCTTATCATGGCCACTTTAATGGCTCTTATTGTA   867

Qy  1866 ACAGCTTCTTTGTTATTCCTCAAAGTAGCAGCATTGTGATATTTCTGCTTTTTTTCCTT 1925
              ||  |  || || | |  ||  || |  | || | || || | || || || |||
Db   868 AAATCTGCACAAATGTCGTCCTGACTCGGTTTGTGATGGTCTTCACCCTCTTTCTCCTC   927

Qy  1926 TATGGATTATCATCTGTATTTTTGCTTAATGCTGACACCCTCTTTTAAAAAATCAAAA 1985
              |||  | | || || |||  || |||| |||| ||   || |||  ||||| | |||
Db   928 TATGCCCTGTCTTTGATAACTTTAGCTTTCCTGATGAGTGTGTTGATAAAGAAACCTTTC   987

Qy  1986 CATGTGGAATAGTTGAATTTTTGTTACTGCGCTTTGGCTTTGGCCTTATGATA 2045
              | ||| | |  || || || | | || |  ||| || || |  ||||| || |
Db   988 CTTACGGGCTTGGTTGGTGTGTTCTCCTTAATTGTCTTATTGTCTTTTGGGGGATCCTGG 1047

Qy  2046 ATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCAGTCCTTTCTGTCACTGT 2105
              || |  || |||||  ||  ||| | | ||| ||| ||  |||| | || |  | | |
Db  1048 TTGTATACACA---TCTTCCTGCATTTTGGAATGGACTTGTGTCTTTCTTAGCCCCTTT 1104

Qy  2106 ACTTTTGTGATTGGTATTGCACAGGTCATGCATTAGAAGATTTAATGAAGGTGCTTCA 2165
              || | || | ||| ||| | ||| |  | | ||| ||| |||||| |  ||| || ||
Db  1105 GCCTTCACTGTTGGGGATGGCCCAGCTTATCACATTGGACTATGATGTGAATTCTAATGCC 1164

Qy  2166 TTTTCAAATTGACTGCAGGCCCATATCCTCTAATTATTACAATTATCATGTGCACACTT 2225
              ||| | |||||| || || |||  |  | ||| |||| ||| ||| |  |  | || ||
Db  1165 CACTTGGATTCTTCACAAAATCCATACCTACCTCATAATAGCTACTCTTTTCATGTTGGTTTTT 1224

Qy  2226 AATAGTATATTCTATGTCCCTTGGCTGTCTAATATAGAACTCAATCCTATGGACAAG 2285
              ||| | | || ||||  | || || || | |||| ||| | || ||  ||| |||
Db  1225 GACACCCTTCTGTATTGGTATTGGACATTATATTTGACAAAATTTTGCCCGTGAATAT 1284

Qy  2286 GGCTTACGGAGATCATCTTATATTTTCTGAGGCCTTCATATTGGTCAAGAGTAAAAGA 2345
              || | | || | || | ||| | | ||| ||  ||  ||| | || ||  | || |||
Db  1285 GGACATCGATGTCTCCCCTGTTTTTTCCTGAAATCCTGTTTTTGGTTCAACCAGGAGG 1344

Qy  2346 AATTATGAGGAGTTATCAGAGGCAATGTAATGGAATATTAGTTTTAGTGAAATTATT 2405
              ||| || | ||| | |||| || |  ||| | |||| |  |||| | ||| |||||
Db  1345 GCTAATCATGTGGTCCTTGAGATGAAACAGATTCGATCCTCACACCTAATGACTGTTTT 1404

Qy  2406 GAGCCAGTTCTTCAGAATTGTGAGGAAAAGAAGCCATAAGAATTAGTGGTATTCAGAAG 2465
              || |||| | || |||  |  |  |||  | || || | | |  | ||| | |||| ||
Db  1405 GAACCAGTGTCTCCAGAATTCTGTGGAAAGAAGCCATCAGCCCCAGTG---------- 1453

Qy  2466 ACATACAGAAAGAGAGGGTGAAAATGTGGAAATTTGTCATTTGACATATAT 2525
              |  ||  | ||| ||| |||||  ||| | |  ||| ||| ||| |||||
Db  1454 ------------------------------------TGGTGTTTGACATATAT 1470

Qy  2526 GAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGACAGGAAGAGTACATTGATGAAT 2585
              || | |||| || || ||  | | || |  |||| | ||  |||  | || | ||  |
Db  1471 GAAGGCCAGATCACTGCCCTCCTTGGTCACAGTGGAGCTGGAAAAAACTACCCTGTTAAAC 1530

Qy  2586 ATTCTTTTGTGGACTCTGCCCACCTTCTGATGGTTTGCATCTATATGGACACAGAGTC 2645
              ||| | || | ||| | |   ||| | |||| | |||  | ||||||| |  ||||||
Db  1531 ATACTTAGTGGGTTGTCAGTTCAACATCAGGTTCAGTCACTGCTCTATAATCACACACTT 1590

Qy  2646 TCAGAAATGATGATGAAATGTTGAAGCAGAGAAAAATGATTGGCATTGTCCACAGTTGAGAT 2705
              || | || || || | | ||| |||| || | | |||| ||| | |  |  ||| |||||
Db  1591 TCAAGAAATGGCTGATAGAAAATATCACAAGTTCACTGGATTTTGCCCACAATCCAAT 1650

Qy  2706 ATACACTTTGATGTTTTGACAGTAGAAGAGAAGAAAATTTATCAATTTGGCTTCAATCAAAGGG 2765
              ||||| |||| |||| || || | ||| || ||  | | |  || | |  || |||||||||
Db  1651 GTGCAATTTGGATTTCTCACTGTGAAAGAAAACCTCAGGCTGTTGCTAAAATAAAAAGGG 1710

Qy  2766 ATACCAGCCAACAATATAATACAAGAAGTGCAGAAGGTTTACTAGATTTAGACATGCAG 2825
              ||        |||  | | |||  ||| |  | || |  | || | | |  |  |
Db  1711 AT----------TTTGCCCACATGAGTGTGGAA 1733
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Qy  2826 ACTATCAAAGATAACCAAGCTAAAAAATTAAGTGTGGTCAAAAAGAAAGCTGTCATTA 2885
Db  1734 -------------------------------------------------------- 1733

Qy  2886 GGAATTGCTGTTCTGGGAACCCAAAGATACTGCTGTAGATGAACCAGCTGGAATG 2945
Db  1734 ----------------AGAGGTTTGCTATTGGATGAACCGACTGCGGATTG 1770

Qy  2946 GACCCCTGTTCTCGACATATTGTATGGAATCTTTAAAATACAGAAAAGCCAATCGGGTG 3005
Db  1771 GATCCTCCTTCAAGGCACCGAATATGGAATCTCCTGAAAGAGGGGAAATCAGACAGAGTA 1830

Qy  3006 ACAGTGTTCAGTACTCATTTCATTGATGAAGCTGACATTCTTGCAGATAGGAAAGCTGTG 3065
Db  1831 ATTCTTCTCAGCACCCAGTTTATAGATGAGGCTGACATTCTGCGGACAGGAAGGTGTTC 1890

Qy  3066 ATATCACAAGGAATGCTGAAAGTGTGTTGGTTCCTCAATGTCCTCAAAAGTAAATGGGGG 3125
Db  1891 ATATCCAATGGGAAGCTGAAGTGTGGCAGCCTCTTCTCCGTTCCTGTTCCTTAAGAAGAAATGGGGC 1950

Qy  3126 ATCGGCTACCGCCTGAGCATGTGACATAGACAAATATTGTGCCACAGAGAATCTCTTTCTTCA 3185
Db  1951 ATAGGCTACCATTTAAGTTTGCATCTGAATGAAAGGTGTGATCCAGAGAGTATAACATCA 2010

Qy  3186 CTGGTTAAACAACATATACCTGGAGCTACTTATTACACAGAATGACCAACAACTGTG 3245
Db  2011 CTGGTTAAGCAGCAGCATCTGATGCCCAAATTGACAGCACAAAGTGAAGAAAAACTTGTA 2070

Qy  3246 TATAGCTTGCCTTTCAAGGACATGACAGTTTTCAGTTTGTGTTTTCTGCCCTAGACAGT 3305
Db  2071 TATATTTTTGCCTTTGGAAAGGACAAAACAAATTTCCAGNNNNNNNNNNNNNNNNNNNN 2130

Qy  3306 CATTCAAAATTGGGTGTCATTTCTATGGTGTTCCATGACGACTTGGAAGACGTATTT 3365
Db  2131 TGTTCTACCAAGGCATTGAGGATTTGTGTTTCCATAACAACTTTGAATGAGGTGTTT 2190

Qy  3366 TTAAAGCTAGAAGTTGAAGCAGAAAATTGACCAAGCAGATTATAGTGTATTTACTCAGCAG 3425
Db  2191 CTGAAAATTAGAAGGAAAATCAACTATTGATGAATCAGTATTGGGGACAATTA 2250

Qy  3426 CCACTGGAGGAAGGAAGAAAATGGATTCAAAAATCTTTTGATGAAAATGGAACAGAGCTTACTTATT 3485
Db  2251 CAAACTGATGGGGCAAAAGATATTAGAAGCCTTGTTGTGAGCTGGAACAAGTTTTGTCTTCC 2310

Qy  3486 CTTTCTGAAACCAAGGCTTCTCTCTAGTGAGCACCATGAGCCTTTGGAAACACAGATGTAT 3545
Db  2311 TTCCACGAAACAAGGAAAAC---AATCAGTGGCGTGGCGCTGGCGCCAGCAGGTCTGT 2367

Qy  3546 ACAATAGGACAAAGTTTCATTTCTTTACCTGAAACGTGAAAGTAAATCAGTGAAGATCAGTG 3605
Db  2368 GCAATAGGAAAAGTTCGCTTCCTAAAGTTAAAGAAAGAAAAAGCCTGTGGACTATA 2427

Qy  3606 TTGCTTCTGCTTTTAATTTTTTTCCACAGTTGGAGATTTTTAATGTTTTTGGTTCATCATCACTCT 3665
Db  2428 TTATTGCTTTTTGGTATTAGCTTATCCCTGAACTTTTGGACATCTATTCTACGAGTCA 2487

Qy  3666 TTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTTATATTTTCTAAAACCTGGA 3725
Db  2488 TATCAGAAAAGT---TACCCGTGGGAACTGTCTCCAAATACTTCCTCTCACCAGGA 2544

Qy  3726 GACAAACCACATAAATACAAAACAAGTCGCTTCTTCAAAATTCTGCTGACTCAGATATC 3785
Db  2545 CAACAACCACAGGATCCCTGACCATCCATTTTACTGGTCATCAATAAGACAGGGTCAACCATT 2604

Qy  3786 AGTGATCTTATTAGCTTTTTCACAGGCCAGACATAATGGTGACGATGATTAATGACAGT 3845
Db  2605 GATAACTTTTTACATTTACACTGGAGCGGCAGACACTAGCTATAGAGAAGTGGAATGCCTTTGGA 2664

Qy  3846 GACTATGTATCCGTGGCTCCCCATAGTGCGGCTTAAATGTGATGCATTCAGAAAAGGAC 3905
Db  2665 ACTAGAAATGGCACAGATGACCCATCTTACAATGGTGCTCATCATTGTCAGGTGATGAA 2724

Qy  3906 TATGTTTTTGCAGCTGTGTTTCAACAGTACTACTAGGTTTATTCTTTACCTATTAGTAGTGAAT 3965
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Db  2725 AAGNNNNNNNNNNNNNNNNNNNNNNNN 2784

Qy  3966 ATCATTAGTAACTACTACTATCTTTATCATTAAATGTGACTGAAACCATCCAGATCTGGAGT 4025
Db  2785 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2844

Qy  4026 ACCCCATTCTTCAAGAAATTACTGATATAGTTTTAAAATGAGCTGTATTTCAAGCA 4085
Db  2845 NNNNNNNNNNNNNNNGAGCATATGGATTATGAGTATGGTACCGAAGTAACACC 2904

Qy  4086 GCTTTGCTTGGAAATCATTGTTACTGCAATGCCACCTTACTTGCCATGGAAAATGCAGAG 4145
Db  2905 TTCTTCTGGATACCGGCGAGCCTCTTCACTCCATACATTGCAATGCAGCAGCATTGGT 2964

Qy  4146 AATCATAAGATCAAAGCTATACTCAGTCTTCAGTCTTTGCCATCTGCATAT 4205
Db  2965 GACTACAAAAAAAAGCTCATTCCCCAGCTACGGATTTCAGCCCTTCTGCATAC 3024

Qy  4206 TGGATTGGACAAGCTGTGTTGGTGAAATCCCCTTATTTTTATCATTCTTATTTGATGC-- 4263
Db  3025 TGGTTTGGCCAAGCACTGGTGGATGTTTCCCGTACTTTTTGATCTCCTGCTAATGCAA 3084

Qy  4264 --TAGGAAGCTTACTGGCATTCATTATGGATTATATATTTTATACTGTAAAGTTCCTTGC 4321
Db  3085 ATAATGGATTATATTTTTAGGCCCAGGAGGATTATATTATA-ATTCAAAACCTGTTAAT 3143

Qy  4322 TGTGGTTTTGCCTATTGGTTATGTTCCATCAGTTATTCGTTCACTATATTGCTTC 4381
Db  3144 TCAAATCCTGTGTAGTAGTTGGCTATGTCATGTCCATCTCGTTTTCTTGACATATGTGATTTC 3203

Qy  4382 TTTCACCTTTAAGAAAAATTTTAAATACCAAAGAATTTTGGTCATTTATTCTATTGTGGC 4441
Db  3204 ATTCATTTTTCGCAATGGGACAAAAAAATAGTGGCATTTGGTCATTTTTTCTTCT----- 3256

Qy  4442 AGCGTTGNCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGATACACAATTGCAAC 4501
Db  3257 ---------------------TAATTGTGGTCATCTTCTCGATAGTTGCTAC 3287

Qy  4502 TATTCTTCATTATGCCTTTTGTATCATCATCCAATCTATCCACTTCTAGGTTGCCTGAT 4561
Db  3288 TGATCTAAATGA-------------------------------------------- 3299

Qy  4562 TTCTTTCATAAAGATTTCTTGGGAGAATGTACGAAAAAATGTGGACACCTATAATCCATG 4621
Db  3300 ------ATATGGATTTCAGGGCTATTTTTCAGGGCTATTTTTGGCACCATGTTAATAACCTCCCTTCACAT 3352

Qy  4622 GGATAGGCTTCAGTAGCTGTTATAT-CGCCTTACCTGCCAGTGTGTACTGTGACTTTTCC 4680
Db  3353 TGATTTGGCTCTCTATTCATTTTTCTGAGCCTTACCTTCATTTTCATTTTCTTTTCA 3412

Qy  4681 TCTTACAATACTATGCAGAAAAATATGGAGGCAGATCAATAGAAAAGATCCCTTTTCA 4740
Db  3413 TTCTCGGATGCCTAGAACTGCAGGAAGAAACTAATGAGAAGAGGATCCTGTGTTCA 3472

Qy  4741 GAAACCTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGACCACCAGCAATGAGGATG 4800
Db  3473 GAATTTCTCCAA-----GAAGCAACGCTATTTTTCCAAACCCGAAGGAG 3526

Qy  4801 AAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAATAAAGAAGTATAATGACAGAAAAG 4860
Db  3527 AGGAGGAAGATATCCAGATCCAGATGGTCGAAATGAGGAGAAGATATGCAGGCAAAAAGA 3586

Qy  4861 GTGAGGAGAAACATCCATTATGGTCAGCAATTGCATAAAGAATATGAGTCAAGAAAG 4920
Db  3587 TTGATGAGACACCCGTCATCATTGCCAGCTGTCTACGGAAGGAATATCACTCTTCGTGTGA 3646

Qy  4921 ATTTTCTTCTTCAAGAAAAGTAAAGAATGGCAACTAAATACATCTCTTTCTTGTGTGA 4980
Db  3647 AAAATTGCTTTTCTAAAAGGAAGAAAAAATTGCCACAAGAAATGTCTCTTTTTGT---- 3702

Qy  4981 AAAAAGGAGAGATCTTAGGACTATTGGGTGCTGCAAAAGCACAATTATTA 5040
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TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2334 row: c column: 01
            High quality sequence stop: 537.

FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6101304"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_82"
                     /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccattaggcc); Site_2: SfiI (ggccattaggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C, G, or T). Average insert size
                     1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech Laboratories (Palo
                     Alto, CA)."

ORIGIN
Query Match   11.4%; Score 741.4; DB 5; Length 773;
Best Local Similarity 98.4%; Pred. No. 2e-144;
Matches 759; Conservative 0; Mismatches 11; Indels 11; Gaps 1;

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Qy   5323 AACGAAAGTTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTGCTAGATG 5382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 AACGAAAGTTGTGTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTGCTAGATG 62

Qy   5383 AACCATCTACAGGTATGGATCCCAAAGCCAAAACGACACATGTGCGAGCAATTCGAACTG 5442
          ||||||||||||||||||||||| |||||| |||||||||||||||||||||||||||||
Db     63 AACCATCTACAGGTATGGATCCCAAAGCCAAAACGACACATGTGCGAGCAATTCGAACTG 122

Qy   5443 CATTTAAAACACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGG 5502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 CATTTAAAACACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGG 182

Qy   5503 CTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGCAGTTATCGGAACAGTAC 5562
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 CTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGCAGTTATCGGAACAGTAC 242

Qy   5563 AACATCTAAAGAGTAAATTGGAAAAAGGCTACTTTTTGGAAATTAAATTGAAGGACTGGA 5622
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 AACATCTAAAGAGTAAATTGGAAAAAGGCTACTTTTTGGAAATTAAATTGAAGGACTGGA 302

Qy   5623 TAGAAAACCTAGAAGTAGAACCGCCTTCAAAGAGAAAATTCAGTATATTTTCCCAAATGCAA 5682
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Db    303 TAGAAAACCTAGAAGTAGAACCGCCTTCAAAGAGAAAATTCAGTATATTTTCCCAAATGCAA 362

Qy   5683 GCCGTCAGGAAAGTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGT 5742
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Db    363 GCCGTCAGGAAAGTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGT 422

Qy   5743 CCCTTTCACAATCTTTTTTAAGCTGGAAGAGCTAAACATGCTTTTGCCATTGAAGAAT 5802
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 CCCTTTCACAATCTTTTTTAAGCTGGAAGAGCTAAACATGCTTTTGCCATTGAAGAAT 482

Qy   5803 ATAGCTTTTCTCAAGCAACATTGGAACCAGAGCAGGTTTTGTAGAACTCACTAAAGAACAAGAGG 5862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    483 ATAGCTTTTCTCAAGCAACATTGGAACCAGAGCAGGTTTTGTAGAACTCACTAAAGAACAAGAGG 542
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Db   3703 -------GAAGTTATAGGACGACTGTAGGACACAATGAGGACTGGTAAAGTACAACATTA 3754
Qy   5041 ATATTCTGGTTGGTGATATGAACCAACTTCAGGCCAGGTATTTTAGGAGATTATTCTT 5100

Db   3755 AGATGATAACTGGAGACACAAAACCAACTGCAGGACAGGTGATTTTGAAAGGG------- 3807
Qy   5101 CAGAGACAAGTGAAGATGAAGATGATTCACTGAAGTGTACTGTTACTGTCCTCAGATAAACC 5160

Db   3808 -------AGCGGTGGAGGGGAACCCCTGGGCTTCCTGGGGTACTGCCCTCAGGAGAATG 3859
Qy   5161 CTTTGTGGCCAGATACTACATTGAGGAACATTTATGGAGCTGTCAAAGGAA 5220

Db   3860 CGCTGTGGGCCCAACCTGACAGTGAGGCAGCACCTGGAGGTGTACGCTGCGCGTGAAAGGTC 3919
Qy   5221 TGAGTGCAAGTGACATGAACATGAAGAAGTCATAAGTGGAATAACACATGCACTGATTTAAAAG 5280

Db   3920 TCAGGAAAAGGGGACACGCAATGATCGCCATCACACGGTTAGTGGATGCGCTCAAGCTGCAGG 3979
Qy   5281 AACACTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAGTTGTGTTTG 5340

Db   3980 ACCAGTGAAGGCTGAGGTCCCGTGCAGAGGACTTGTCAGAGGGGAATAAAGCGAAGGCTGCTTTG 4039
Qy   5341 CTCTAAGTATGCTAGGGAATCCTCAGATTACTTGCTAGATGTGAACCATCTACAGGTATGG 5400

Db   4040 TGCTAGCATCCTGGGGACCCGTCAGTGTGCTTCTGATGTGTGCTCTGATGAGCCGTCGACCCGGATGG 4099
Qy   5401 ATCCCAAAGCCAAAACGACACATGTGCGACCAATTCGAATTCGAATCTTAAAACACAGAAAGC 5460

Db   4100 ACCCGAGGGGCAGCAGCAAATGTGCAGTGAATTCGGGCCCACCTTTAGAAACACCGGAGA 4159
Qy   5461 GGGCTGCTATTCTGACCACTCACTATATGGAGGAGGGCAGAGGCTGTCTGTGATCGAGTAG 5520

Db   4160 GGGGGCGCCCTCCCTGACCACCCACTACGCGCAGAGGCGGAGGGCTGAGGCCGGTGTGGGACCGAGTGG 4219
Qy   5521 CTATCATGGTGTCTCGGGCAGTTAAGCATGTGATCGGAACAGTGATATCGGAACATCTAAAGAGTAAAT 5580

Db   4220 CCATCATGGTGTCAGGAGAAGCTGAGAGATGTATTGGTTCATCCAACACCTGAAAAAGCAAAT 4279
Qy   5581 TTGGAAAAAGGCTACTTTTTGGAAATTAAATTGGAAGGACTAGGAGTAG 5640

Db   4280 TTGGCAAGACTACCTGCTGGAGATGAAGCTGAAGAACCTGGCACAAA-------TGG 4330
Qy   5641 ACCGGCTTCAAAGAGAAAATTCAGTATATTTTCCCAAATGCAAGCCGGTCAGGAAAGTTTTT 5700

Db   4331 AGCCCCTCCATGCAGAGATCCTGAGGCTTTTTCCCCCAGGCTGCTCAGCAGGAAAGGTTCT 4390
Qy   5701 CTTCTATTTTGGCTTATAAAAATTCCTAAGGAAGATGTTCAGTCCCTTTCACAATCTTTTT 5760

Db   4391 CCTCCCGATGGTCTATAAGTTGCCTGTTGAAGATGTCGGACCTTTATCACAGGCTTTTCT 4450
Qy   5761 TTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTGAAGAAATATAGCTTTTCTCAAGCAA 5820

Db   4451 TCAAATTAGAGATAGTTAAACAGAGTTCGACCTGGAGGAGTACAGCCTCTCACAGTCTA 4510
Qy   5821 CATTGGAACAGTTTTTGTAGAACTCACTAAAGAAGAGGAAGAT 5870

Db   4511 CCCTGGAGCAGGTTTTCCTGGAGCTCTCCAAGGAGCAGCAGGAGCTGGGTGAT 4560
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RESULT 11
BQ441353

LOCUS   BQ441353   773 bp   mRNA   linear   EST 24-MAY-2002
DEFINITION AGENCOURT_7838430 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6101304
            5', mRNA sequence.
ACCESSION   BQ441353
VERSION   BQ441353.1 GI:21180429
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 773)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.

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Qy    5863  AGGAAGATATAGTTGTGGAACTTAAACAGCACACTTGGTGGAACGAACAACAAGAAG  5922
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Db     543  AGGAAGATATAGTTGTGGAACTTTAAACAGCACACTTGGTGGAACGAACAACAAGAAG   602

Qy    5923  ATAGAGTAGTAGTATTTTGAATTGTATTGTTCGGTCTGCTTCGGTCTGCTTCTTTCTTTCTTTTC  5982
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     603  ATAGAGTAGTATTTTGAATTGTATTGTTCGGTCTGCTTCGGTCTGCTTCTTTCTTTTC   662

Qy    5983  ACTTAATTTTAACTTGGTTAAAAAGTTTTTTATTGGAATGGTAACTGGAGAACCAAGA  6042
            ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db     663  ACTTAATTTT-ACTTGGTTTAAAAGTTTTTTATTGGAATGGTAACTGGAGAACCCAGA   721

Qy    6043  ACGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGTTGTGTG  6093
            |||||||||||||||||||||||||||||||||||||| ||| |||||
Db     722  ACGCACTTGAAATTTTTCAAGCTCCCCTAATTGAAATGCTGGGGGGTTGGGGG   772
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RESULT 12
CD629439/c
LOCUS   CD629439   874 bp   mRNA   linear   EST 12-JAN-2004
DEFINITION   5604627JJ1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629439
VERSION   CD629439.1 GI:40277705
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 874)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE   Circular rapid amplification of cDNA ends for high-throughput
             extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT   Contact: Fu GK
             Incyte Genomics, Inc.
             3160 Porter Dr., Palo Alto, CA 94304, USA
             Tel: 650854102
             Email: gfu@incyte.com.
FEATURES   Location/Qualifiers
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ORIGIN

Query Match   11.3%;   Score 740.2; DB 6; Length 874;
Best Local Similarity   95.8%;   Pred. No. 3.6e-144;
Matches   846;   Conservative   0;   Mismatches   28;   Indels   9;   Gaps   8;

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Qy    3348  ACTTTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTAT  3407
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Db     874  ACTTTGGAAAACTAATTTTTAAA--CTAAATTGAACCAGAAATTGACCACCAGATAAT   817

Qy    3408  AGTGTATTACTCAGCAGCCACTGGAGGAGAAATGAGATTCAAAATCTTTGATGAAATG  3467
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Db     816  AGTGTATTACTCACCACCACCACCTGGAGGAGAAATGAGATTCAAAATCTTTGATGAAATG   757

Qy    3468  GAACAGAGCTTACTTATTCTTTCTGAAACCAAGCCTTCTCAGTGAGCACCATGAGCCTT  3527
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Db     756  GAACAGACTTTACTTATTCTTTCTGAAACCAA-GCTGCTCAGTGA-CACCATGAACCTTT   699

Qy    3528  TGGAAACAACAGATGTATACAATAGCAAAGTTCATTCTTTTACCTTGAAACGTGAAAGT  3587
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Db     698  TGGAAACAACAGATGTATACAATACACAAGTTTCATTCTTTTACCTTGAAACGTGAAAGT   639

Qy    3588  AAATCAGTGAGATCAGTGCTTCGCTTTTAATTTTTTTCACAGTTCAGATTTTTATG  3647
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Qy    3648  TTTTTGGTTCATCACTCTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTA  3707
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Db     3707
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Db     578  TTTTTGGTTCATCACTCTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTA  519
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Qy    3708  TATTTTCTAAAACCTGGAGACAAACCACCATAAATACAAACAAGTCTGCTTCTCAAAGG  3767
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Db     518  TATTTTCTAAAACCTGGAGAC-AACCACCATAAATAC-AAACAAGTCTGCTTCTCAAAAT   461

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Db     400  ACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGGCTTAAATGTG   341

Qy    3888  ATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTACTACTAGTGTTATTCT  3947
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Qy    4008  ACCATCCAGATCTGGAGTACCCCATTCTTCAAGAAATTACTGATATAGTTTTAAAATT  4067
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Db     220  ACCATCCAGATCTGGAGTACCCCATTCTTCAAGAAATTACTGATATAGTTTTAAAATT   161

Qy    4068  GAGCTGTATTTCAAGCAGCTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTT  4127
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Qy    4128  GCCATGAAAATGCAGAATCATAAGATCAAAGCTTATATCCACTAAACTTTCAGGT  4187
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DEFINITION   5604640JJ1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629443
VERSION   CD629443.1 GI:40277709
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 912)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE   Circular rapid amplification of cDNA ends for high-throughput
             extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT   Contact: Fu GK
             Incyte Genomics, Inc.
             3160 Porter Dr., Palo Alto, CA 94304, USA
             Tel: 650854102
             Email: gfu@incyte.com.
FEATURES   Location/Qualifiers
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Matches   869;   Conservative   0;   Mismatches   17;   Indels   12;   Gaps   11;

REFERENCE   1 (bases 1 to 747)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE   Normalization and subtraction: two approaches to facilitate gene
              discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED   8889548
COMMENT   Contact: McCray, PB
              McCray Lab
              University of Iowa
              2024 University of Iowa Med Labs,.Iowa City, IA 52242, USA
              Tel: 319 356 4866
              Fax: 319 356 7171
              Email: paul-mccray@uiowa.edu
              Tissue Procurement: Dr. M. J. Welsh, University of Iowa
              cDNA library preparation: Dr. M. Bento Soares, University of Iowa
              cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
              DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
              Clone Distribution: Researchers may obtain clones from Research
              Genetics (www.resgen.com) or from Open Biosystems
              (www.openbiosystems.com).
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                     /clone_lib="UI-CF-DU1"
                     /note="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-DU1 is a normalized cDNA library containing the
                     following tissue(s): Primary Lung Epithelial Cells The
                     library was constructed according to Bonaldo, Lennon and
                     Soares, Genome Research, 6:791-806, 1996. First strand
                     cDNA synthesis was primed with an oligo-dT primer
                     containing a Not I site. Double stranded cDNA was ligated
                     to an EcoR I adaptor, digested with Not I, and cloned
                     directionally into pT7T3-Pac vector. The oligonucleotide
                     used to prime the synthesis of first-strand cDNA contains
                     a library tag sequence that is located between the Not I
                     site and the (dT)18 tail. The sequence tag for this
                     library is GGCTGTAGGC.
                     TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
                     TAG_LIB=UI-CF-DU1
                     TAG_SEQ=GGCTGTAGGC"
ORIGIN

Query Match   11.2%; Score 731; DB 5; Length 747;
Best Local Similarity   100.0%; Pred. No. 3e-142;
Matches   731; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy 5465 TGCTATTCTGACCACTCACTATATGGAGGAGCAGAGGCGTGTCGTGTGATCGAGTAGCTAT 5524
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Db 687 TGCTATTC-GACCACTCACTATATGGAGGAGCAGAGGCGTGTCTGTGATCGAGTAGCTAT 628

Qy 5525 CATGGTGTCTGGGCAGTAAGATGTATCGGACAGTACAACATCTAAAGAGTAAATTGG 5584
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Qy 3337 TTTCCATGACGACTTTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTGACC 3396
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Qy 3397 AAGCAGATTATAGTGTATTACTCAGCAGCCACTGGAGAGAAATGGATTCAAAAATCTT 3456
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Db 852 AAGCAGATTATAGTGTATTACTCA--CACCACTGGAGAGAAATGGATTCAAAAATCTT 795

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Db 735 ACCATGAGCCCTTGGAAACTAACAACAGATGTATACAATA-CAAAGTTCATTTCTTTACCTT 677

Qy 3575 GAAACGTGAAAGTAAATGCGAGATCAGTGTCTTCGCTTTAATTTTTTTCACAGT 3634
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Db 676 GAAACGTGAAAGTAAATGCGAGATCAGTGTCTTCGCTTTAATTTTTTTTCACAGT 617

Qy 3635 TCAGATTTTTATGTTTTGGTTCATCACTCTTTAAAAAATGCGTGGTTCCCATCAAACT 3694
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Db 139 GCCACCTTACTTTGCCATGGAAAATGCAGAGAATCATAAGATC-AAGCTTATACTCAACT 81

Qy 4175 TAAACTTTCAGGTCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTGTTTGATATC 4232
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RESULT 14
BU686259/c
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DEFINITION UI-CF-DU1-adn-m-03-0-UI.s1 UI-CF-DU1 Homo sapiens cDNA clone
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ACCESSION   BU686259
VERSION   BU686259.1 GI:23540987
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
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/clone_lib="Transcript Finishing Unit (TFU)"
/note="This sequence corresponds to an RT-PCR fragment
generated within the Transcript Finishing Initiative
(TFI), which is devoted to the characterization of new
human transcripts. Using the genomic sequence as a
scaffold for EST mapping and clustering we have performed
RT-PCR to bridge gaps between EST clusters that are likely
to be derived from the same genes. Each pair of EST
clusters selected for experimental validation was
designated a single Transcript Finishing Unit (TFU). In
this way we are able to confirm the membership of ESTs
from different clusters to a common transcript and to
provide intervening sequence information."

ORIGIN

Query Match   11.2%;   Score 729; DB 6; Length 730;
Best Local Similarity 99.9%;   Pred. No. 7.9e-142;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4440 GCAGCGGTGNCTGTATTGCAATCACTGAAATAACTTCTTATGGATACACAATTGCA 4499
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Qy 4980 AAAAAGGAGAGATCTTAGGACTATTGGGTCTGGCAAAGGCACAATTATT 5039
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Db   541 AAAAAGGAGAGATCTTAGGACTATTGGGTCTGGCAAAGGCACAATTATT   600

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Qy 5100 TCAGAGACAAGTGAAGATGATGATTCACTGAAGTGTATGGGTTACTGTCCTCAGATAAAC 5159
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Qy 5765 GCTGGAAGAAGCTAAACATGCTTTGCCATTGAAGAATATAGCTTTCTCAAGCAACATT 5824
Db   387 GCTGGAAGAAGCTAAACATGCTTTGCCATTGAAGAATATAGCTTTCTCAAGCAACATT   328
Qy 5825 GGACAGGTTTTGTAGAACTCACTAAAGAACAAGAGGAGGAAGATAATAGTTGTGGAAC 5884
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Db   267 TTTAAACAGCACACTTTGGTGGGAACGAACACAAGAACAAGAGTAGTATTTGAATTG   208
Qy 5945 TATTGTTCGGTCGTCGCTTACTGGGACTTCTTCTTCTTTCACTTAATTTAACTTGGTTTA 6004
Db   207 TATTGTTCGGTCGTCGCTTACTGGGACTTCTTCTTCTTTCACTTAATTTAACTTGGTTTA   148
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Qy 6065 CTCCTTAATTGAAATGCTGTGGTTGTGTTTTGCTTTTCTTTTAAATAAAACGTATGTAT 6124
Db   87 CTCCTTAATTGAAATGCTGTGGTTGTGTTTTGCTTTTCTTTTAAATAAAACGTATGTAT   28
Qy 6125 AATTAAGTGAA 6135
Db   27 AATTAAGTGAA   17

RESULT 15
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LOCUS   CF272622   730 bp   mRNA   linear   EST 31-JUL-2004
DEFINITION TFU00182 Transcript Finishing Unit (TFU) Homo sapiens cDNA, mRNA
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ACCESSION   CF272622
VERSION   CF272622.1 GI:50872859
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 730)
AUTHORS   The Transcript Finishing Consortium
            http://200.18.51.201/transcript/.
TITLE   A transcript finishing initiative for closing gaps in the human
            transcriptome
JOURNAL   Genome Res. 14 (7), 1413-1423 (2004)
COMMENT   Contact: Anamaria Aranha Camargo
            Laboratory of Molecular Biology and Genomics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente, 109, 4th floor-01509-010 SP Brazil
            Tel: (55) 011 33882248
            Fax: (55) 011 32077001
            Email: anamaria@compbio.ludwig.org.br
            RT-PCR fragment amplified from a pool of cDNAs prepared from tumor
            cell lines.
            PCR Primers
            FORWARD: gccacaaaggcttatctgag
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                 GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    December  4, 2004, 06:19:06 ; Search time 469 Seconds
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Scoring table:  IDENTITY_NUC
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Searched:       824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters:      1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
             1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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1	318	4.9	485	4	US-09-621-976-409	Sequence 409, App
2	159.2	2.4	5894	3	US-08-665-259-24	Sequence 24, Appl
3	159.2	2.4	5894	3	US-08-762-500-24	Sequence 24, Appl
4	159.2	2.4	6525	4	US-08-762-500-74	Sequence 74, Appl
5	137.6	2.1	7860	4	US-09-526-193A-2	Sequence 2, Appli
6	121.8	1.9	8037	4	US-09-774-528-209	Sequence 209, App
7	108.6	1.7	6705	4	US-09-032-438C-5	Sequence 5, Appli
8	108.6	1.7	6819	4	US-09-032-438C-2	Sequence 2, Appli
9	108.6	1.7	7488	4	US-09-032-438C-1	Sequence 1, Appli
10	105.6	1.6	786431	4	US-09-751-389-3	Sequence 3, Appli
11	103.4	1.6	1064	3	US-08-858-207A-88	Sequence 88, Appl
12	92.2	1.4	954	4	US-09-583-110-2618	Sequence 2618, Ap
13	92.2	1.4	5625	4	US-08-961-527-1	Sequence 1, Appli
14	83.8	1.3	450	4	US-09-621-976-2582	Sequence 2582, Ap
15	83.4	1.3	463	4	US-09-621-976-2581	Sequence 2581, Ap
16	83.4	1.3	478	4	US-09-621-976-2583	Sequence 2583, Ap
17	80.6	1.2	795	4	US-08-961-527-264	Sequence 264, App
18	79.6	1.2	750	4	US-09-583-110-876	Sequence 876, App
c 19	77.8	1.2	8536	4	US-08-956-171E-278	Sequence 278, App
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21	77.2	1.2	696	3	US-09-134-001C-987	Sequence 987, Ap
22	76.8	1.2	3044	4	US-09-710-279-4290	Sequence 4290, Ap
c 23	75.8	1.2	1026	3	US-09-134-001C-1205	Sequence 1205, Ap
24	75.8	1.2	1026	4	US-09-107-279-3201	Sequence 3201, Ap
25	75	1.1	774	4	US-09-107-532A-412	Sequence 412, Appl
26	74.6	1.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
27	74.6	1.1	1664976	4	US-09-692-570-1	Sequence 1, Appli
28	72.2	1.1	768	4	US-09-107-532A-1681	Sequence 1681, Ap
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c 32	71	1.1	1664976	4	US-09-692-570-1	Sequence 1, Appli
33	70.4	1.1	747	4	US-09-710-279-3217	Sequence 3217, Ap
34	70.4	1.1	4089	4	US-09-710-279-4203	Sequence 4203, Ap
35	69.8	1.1	990	4	US-09-107-532A-1190	Sequence 1190, Ap
36	69.8	1.1	28626	4	US-09-596-002-15	Sequence 15, Appl
37	69.2	1.1	969	2	US-09-107-532A-1008	Sequence 1008, Ap
c 38	68.4	1.0	19124	2	US-08-487-826B-13	Sequence 13, Appl
39	68	1.0	7963	4	US-08-956-171E-168	Sequence 168, App
c 40	68	1.0	7963	4	US-08-781-986A-168	Sequence 168, App
c 41	67.4	1.0	1011	4	US-09-583-110-366	Sequence 366, App
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43	66.2	1.0	714	4	US-09-134-000C-1821	Sequence 1821, Ap
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c 45	65.8	1.0	4848	4	US-08-961-527-185	Sequence 185, App

ALIGNMENTS

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RESULT 1
US-09-621-976-409

; Sequence 409, Application US/0921976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 409
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 185..484
US-09-621-976-409

Query Match             4.9%;  Score 318;  DB 4;  Length 485;
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Qy   1294 TGTCTACTGATCATCTAC 1311
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Best Local Similarity 48.0%; Pred. No. 1.2e-27;
Matches 554; Conservative 0; Mismatches 588; Indels 12; Gaps 3;

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Qy 2454 GGTATTCAGAAGACATACAGAAGAAGAAGAGGGTGAAAATGTGGAAGTGGAGGCTTTGAGAGAAATTTGTCA 2513

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APPLICANT:  Klinger, Katherine W.
TITLE OF INVENTION:  NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION:  COMPOSITIONS, METHODS OF MAKING AND USING SAME
NUMBER OF SEQUENCES:  83
CORRESPONDENCE ADDRESS:
   ADDRESSEE:  GENZYME CORPORATION
   STREET:  One Mountain Road
   CITY:  Framingham
   STATE:  Massachusetts
   COUNTRY:  United States of America
   ZIP:  01701
COMPUTER READABLE FORM:
   MEDIUM TYPE:  Floppy disk
   COMPUTER:  IBM PC compatible
   OPERATING SYSTEM:  PC-DOS/MS-DOS
   SOFTWARE:  Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICATION NUMBER:  US/08/762,500
   FILING DATE:  09-DEC-1996
   CLASSIFICATION:  435
PRIOR APPLICATION DATA:
   APPLICATION NUMBER:  US 08/665,259
   FILING DATE:  17-JUN-1996
PRIOR APPLICATION DATA:
   APPLICATION NUMBER:  PCT/US96/10469
   FILING DATE:  17-JUN-1996
ATTORNEY/AGENT INFORMATION:
   NAME:  Dugan, Deborah A.
   REGISTRATION NUMBER:  37,315
   REFERENCE/DOCKET NUMBER:  IG5-9.3
TELECOMMUNICATION INFORMATION:
   TELEPHONE:  (508) 872-8400
   TELEFAX:  (508) 872-5415
INFORMATION FOR SEQ ID NO:  24:
SEQUENCE CHARACTERISTICS:
   LENGTH:  5894 base pairs
   TYPE:  nucleic acid
   STRANDEDNESS:  single
   TOPOLOGY:  linear
MOLECULE TYPE:  cDNA
FEATURE:
   NAME/KEY:  CDS
   LOCATION:  2..5053
US-08-762-500-24:
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Query Match     2.4%;  Score 159.2;  DB 3;  Length 5894;
Best Local Similarity  48.0%;  Pred. No. 1.2e-27;
Matches  554;  Conservative    0;  Mismatches  588;  Indels  12;  Gaps      3;
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Qy   2274  CCAGGGGAATTTGGCTTACGGAGATCATCTTATATTTTCTGAAGGCCTTCATATTGGTCA  2333
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Db   1364  CCAGGGGCAGTTCGGCGTGCCTCAGCCTGGTACTTCTTCATCATGCCCTCCATTGGTGT  1423

Qy   2334  AAGAGTAAAAGAAATTATGAGGAGTTATCAGAGGGGCAATGTTAATGGAAAATTAGTTTT  2393
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Db   1424  GGGAAGCCCAGGAGCGGGTTGCAGGGAAGGAGAAGCAGTGACCCCGAGAAAGCACTC  1483

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Db   1484  AGAAACGAGTACTTTGAGCCGAGCCAGAGGACCTGG---TGGCGGGGATCAAGATCAAG  1540

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Db   1541  CACCTGTCCAAGGTGTTCAGGGTGTTCAGGGTTGGGAAATAAGGACAGGGCCGCCGTCTCA  1600

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Qy   2754  TCAATCAAAGGGATACCAGCCAACAATAATACAAGAAGTCAGAAGGTTTTACTAGAT  2813
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Db   1955  AAGCTTCCATCGACCCCTCATCGCAGGTTCCAAGGTGCTGTCTGATACTGGACGAGCCC  2014

Qy   2934  ACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGCAAATCTTTAAAATACAGAAAA  2993
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RESULT 4
US-08-762-500-74;
; Sequence 74, Application US/08762500
; Patent No. 6030806
GENERAL INFORMATION:
   APPLICANT:  Landes, Gregory M.
   APPLICANT:  Burn, Timothy C.
   APPLICANT:  Connors, Timothy D.
   APPLICANT:  Dackowski, William R.
   APPLICANT:  Van Raay, Terence J.
   APPLICANT:  Klinger, Katherine W.
   TITLE OF INVENTION:  NOVEL HUMAN CHROMOSOME 16 GENES,
   TITLE OF INVENTION:  COMPOSITIONS, METHODS OF MAKING AND USING SAME
   NUMBER OF SEQUENCES:  83
   CORRESPONDENCE ADDRESS:
   ADDRESSEE:  GENZYME CORPORATION
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Qy  2814  TTAGACATGCAGCTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGTCAAAAAGA  2873
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Db  2826  CAGAAATACCGTGCCGGCTATCACATGACCGCTGGGTGAAGGAGCCGCACTGCAACCCGGAA  2885
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Db  2886  GACATCTCCCAGCTGGTCCACCACGTGCCCAACGTGCGCGCTGGAGGACAGCGCTGGG  2945
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Qy  3294  GCCCTAGACAGTCATTCAAATTTGGGTGTCATTTC---TTATGGTGTTTCATGACGACT  3350
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Db  3006  AAACTGGAGAAGAAGCAGAAAGAGTGGGCATTGCCAGCTTTGGGCATCCATCACCACC  3065
          |||||||||||||||||||||||||||||||||||||||||||||
Qy  3351  TTGGAAGACGTATT  3364
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Db  3066  ATGGAGGAAGTCTT  3079
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RESULT 5
US-09-526-193A-2
; Sequence 2, Application US/0952193A
; Patent No. 6617122
; GENERAL INFORMATION:
;   APPLICANT: Hayden, Michael R.
;   APPLICANT: Brooks-Wilson, Angela R.
;   APPLICANT: Pimstone, Simon N.
;   TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
;   TITLE OF INVENTION: CHOLESTEROL LEVELS
;   FILE REFERENCE: 50110/002005
;   CURRENT APPLICATION NUMBER: US/09/526,193A
;   CURRENT FILING DATE: 2000-03-15
;   PRIOR APPLICATION NUMBER: 60/124,702
;   PRIOR FILING DATE: 1999-03-15
;   PRIOR APPLICATION NUMBER: 60/138,048
;   PRIOR FILING DATE: 1999-06-08
;   PRIOR APPLICATION NUMBER: 60/139,600
;   PRIOR FILING DATE: 1999-06-17
;   PRIOR APPLICATION NUMBER: 60/151,977
;   PRIOR FILING DATE: 1999-09-01
;   NUMBER OF SEQ ID NOS: 287

;   STREET: One Mountain Road
;   CITY: Framingham
;   STATE: Massachusetts
;   COUNTRY: United States of America
;   ZIP: 01701
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/762,500
;   FILING DATE: 09-DEC-1996
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/665,259
;   FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US96/10469
;   FILING DATE: 17-JUN-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Dugan, Deborah A.
;   REGISTRATION NUMBER: 37,315
;   REFERENCE/DOCKET NUMBER: IG5-9.3
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (508) 872-8400
;   TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 6525 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 573..5684
US-08-762-500-74:

Query Match   2.4%; Score 159.2; DB 3; Length 6525;
Best Local Similarity 48.0%; Pred. No. 1.2e-27;
Matches   554; Conservative 0; Mismatches 588; Indels 12; Gaps 3;

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Qy  2214  ATGCTCACACTTAATAGTATATTCTATGTCCTCTTGGCTGTCTATCCTTGATCAAGTCATT  2273
          |||||  |||||||||||||||||||  |||||||||||||||||||
Db  1935  ATGCTGCTGCTGGACTCTGTGCTTCTATGGCTGTGACCTGGTGACACTGGGTACAGGAGCCGTCTTC  1994
          |||||||||||||||||||||||||||
Qy  2274  CCAGGGGAATTGGCTACGGAGATCATCTTTATATTTCTGAAGCCTTCATATTGGTCA  2333
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Db  1995  CCAGGGGCAGTTCGGCGTGCCTCAGCCCTGGTACTTCTTCATCATGCCCCTCCATTGGTGT  2054
          |||||||||||||||||||||||||||||||||
Qy  2334  AAGAGTAAAAGAAAATTATGAGGAGTTATCAGAGGGCAATGTAATGAAAATTATTAGTTTT  2393
          ||||||||||||||||||||||||||||||||||||
Db  2055  GGGAAGCCAAGGGCGGGTTGCAGGGAGAAGAAGACAGTAGAAAGACCATAAGAATTAGT  2114
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Qy  2394  AGTGAAATTATTGAGCCAGTTTCTTCAGAATTTGTAGGAAAAGAAGCCATAAGAATTAGT  2453
          |||||||||||||||||||||||||||||||||
Db  2115  AGAAACGAGTACTTTGAGCCGAGCCAGAGGACCTGG---TGGCGGGGATCAAGATCAAG  2171
          |||||||||||||||||||||||||||||||||
Qy  2454  GGTATTCAGAAGACACATACAGAAAGAAGGTGAAAATGTGGAGGCTTTGAGAAATTTGTCA  2513
          |||||||||||||||||||||||||||||||
Db  2172  CACCTGTCCAAGGTGTTCAGGGTGGGAAATAAGGACAGAGGGCGGCCGTCAGAGACCTGAAC  2231
          ||||||||||||||||||||||||||||||||
Qy  2514  TTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAACAGGAAAGAGT  2573
          ||||||||||||||||||||||||||||||||
Db  2232  CTCAACCTGTACGAGGGACAGATCACCGTCCTGCTGGGCCAACGTGCCGGGAGACC  2291
          ||||||||||||||||||||||||||||||||
Qy  2574  ACATTGATGAATATTCTTTGTGGACTCGCCCACCTTCTGATGGGTTTGCATCTATATAT  2633
          ||||||||||||||||||||||||||||||||
Db  2292  ACCACCCTCTCCATGGCTCACAGGTCTCTTTCCCCCACCAGTGAAGCCATACATCAGC  2351
          |||||||||||||||||||||||||||||
Qy  2634  GGACACAGAGTCTCAGAAATAGATGAAAATGTTGAGCAAGAAAATGATTGGCATTTGT  2693
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-526-193A-2

Query Match　　　2.1%;　　Score 137.6;　DB 4;　Length 7860;
Best Local Similarity　52.7%;　Pred. No. 1.7e-22;
Matches 349;　Conservative 0;　Mismatches 304;　Indels　9;　Gaps　2;

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Qy   2492 GGAGGCTTTGAGAAATTTGTCATTTGACATATATGAGGTCAGATTACTTGCCTTACTTG 2551
          |||||| |||  || | || || ||||
Db   2813 GGTGGCTGTCGATGGCCTGGCACTGAATTTTATGAGGGCCAGATCACCTTCCTTCCTTGGG 2872

Qy   2552 CCACAGTGGAACAGAAAGAGTACATTCTTTGTGACTCGCCCACCTTC 2611
          |||||||||||||   || | ||
Db   2873 CCACAATGAGGCGGGAGAACGACCACCATGTCAATCCTGACCGGTTGTTCCCCCGAC 2932

Qy   2612 TGATGGGTTTGCATCTATATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGC 2671
                                       ||||||
Db   2933 CTCGGGGCACCGCCTCACATCCTGGGAAAAGACATTCGCTC------TGAGATGAGCACCAT 2986

Qy   2672 AAGAAAAATGATTGGCATTTGTCCACAGTTAGATATACACTTTGATGTTTTGACAGTAGA 2731
          |||||||  |||| |  ||
Db   2987 CCGGCAGAACCTGGGGGTCTGTCCCCAGCATAACGTGCTGTTTGACATGCTGACTGTCGA 3046

Qy   2732 AGAAAAATTTATCAATTTGGCTTCAATCAAAGGGATACCAGCCAACAATAATACAAGA 2791
          ||   || || |  || |||  ||  |||||
Db   3047 AGAACACATCTGGTTCTATGCCCGCTTGAAGGGCTCTCTGAAGAAGCACGTGAAGGCGGA 3106

Qy   2792 AGTGCAGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAA---GATAACCAAGCTAA 2848
          |  |||| ||  |||  ||
Db   3107 GATGGGAGCAGGAGATGGCCCTGGATGTTGGTTGCCATCAAGCAAGCTGAAAAGCAAAACAAG 3166

Qy   2849 AAAATTAAGTGGTGGTCAAAAAAGAAAGCTGTCAGTAGGAATTGCTGTTCTTCTTGGGAACCC 2908
          ||||
Db   3167 CCAGCTGTCAGTGGAATGCAGAGAAGCTATCTGTGGCCTTGTCGGGGGATC 3226

Qy   2909 AAAGATACTGCTGCTAGTGAACCAACAGCTGAATGACCCCTGTTCTCGACATATTGT 2968
          |  |  ||| ||
Db   3227 TAAGGTTGTCATTCTGGATGAACCACAGCTCGTGTGTGACCCTTACCTCCCGCAGGGGAAT 3286

Qy   2969 ATGGAATCTTTTAAAATACAGAAAAAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTCAT 3028
          |||||   |||
Db   3287 ATGGGAGCTGCTGCTGAAAATACCGACAAGGCCCGCACCCATTATTCTCTACACACCACAT 3346

Qy   3029 GGATGAAGCTGCTGCCACATTCTGCAGATAGGAGAAAGCTGTGATATCACAAGGAAATGC 3088
          || |||| ||||||||
Db   3347 GGATGAAGCGGCGACGTCCTGGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGCTG 3406

Qy   3089 TGTTGGTTCTTCAAATGTTCCTCAAAGTAAATGGGGATCGGCTACCCCCTGAGCATGTA 3148
          ||||||||  |||
Db   3407 TGTTGGGCTCTCCTGTTTCTGTTTCTGAAGACACCAGCTCAGCAGGGGAACAGGCCTCTGGT 3466

Qy   3149 CA 3150
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Db   3467 CA 3468
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RESULT 6
US-09-774-528-209
; Sequence 209, Application US/0974528
; Patent No. 674519
; GENERAL INFORMATION:
; APPLICANT: Tang, Y., Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.

; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619e1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 209
; LENGTH: 8037
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1654)..(7329)
US-09-774-528-209

Query Match　　　1.9%;　　Score 121.8;　DB 4;　Length 8037;
Best Local Similarity　49.9%;　Pred No. 9.6e-19;
Matches 337;　Conservative 0;　Mismatches 332;　Indels　6;　Gaps　1;

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Qy   2476 AGAAGGGTGAAAATGTGGAGGCTTTGAGAAATTTGTCATTTGACATATATGAGGGTCAGA 2535
          ||||    | ||
Db   2999 ACAAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGACCTCTACGAGAACCAGG 3058

Qy   2536 TTACTGCCTTACTTGCCACAGTGGAACAGGGCGGGCAAGAGTACATTGATGAATATTCTTGTG 2595
          |||   || | |||
Db   3059 TGGTCTCCTTCTTGGGCCACAAGGGCGGGCAAGACACCACCATGTCATCCTGACCG 3118

Qy   2596 GACTCTGCCACCTTCGATGGGTTGCATCTATATATGGACACAGAGTCTCAGAAATAG---- 2655
                                           ||| |
Db   3119 GCCTGTTCCCTCCACGTCGGGTTCCGCCACCATCTACGGCGCACGACATCCGACACG---- 3174

Qy   2656 ATGAAATGTTTGAAGCAAGAAAATGATTGGCATTTGTCCACAGTTAGATATACACTTTG 2715
                                 |||| |
Db   3175 --GAGATGGATGAGATCCGCAAGAACCTGGGCATGTGTCCGCCGCAGCACAATGTGCTCTTTG 3232

Qy   2716 ATGTTTGACAGTAGAAGAAGAAATTTATCAATTTGGCTTCAATCAAAGGGATACCAGCCA 2775
          |   ||||
Db   3233 ACCGGCTCACGGTGGAGGACACCATCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGG 3292

Qy   2776 ACAATAATAACAAGAAGTGCAGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAG 2835
          ||
Db   3293 AGGAGATCCGCAGAGATGGACAAGATGATCGAGGACCTGGAGTCTCTCAACAAGCGGC 3352

Qy   2836 ATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAAAGAAAGCTGTCATTAGGAATTGCTG 2895
                                 ||||
Db   3353 ACTCACTGGTCGTGTCCGGGCTCCGGTGTCCGTGGCCATCGTCCTGCCT 3412

Qy   2896 TTCTTGGGAACCCAAAGATACTGCTGCTAGTGAACCAACAGCTGAATGACCCCCTGTT 2955
          |     ||| |
Db   3413 TCGTGGGCGGGCTCTCGCCCCATCATCCTGGAACTCTTAAAATACAGAAAGCACCAGTG 3472

Qy   2956 CTCGACATATTGTATGGAATCTTTTAAAATACAGAAAAAAGCCAATCGGGTGACAGTGTTCA 3015
          |     |||| | ||
Db   3473 CGCGCCCGCCCATCTGGACCTCATCCTGAAGTACACAGAGGCTCCAGGTTA 3532

Qy   3016 GTACTCATTTCATGGATGAAGCTGACATTCTTGCAGATAGGAAAGCTGTGATATCACAAG 3075
          |||  ||  ||||
Db   3533 CCACCCACCACATGGATGAGGGCGACCTGCCTTGGGGACCTCCATGTCCCATCATCTCCCATG 3592

Qy   3076 GAATGCTGAAATGTGTTGGTTCTTCAATGTTCCTCAAAAGTAAATGGGGATCGGCTACCACC 3135
          |       || |  |
Db   3593 GGAAGCTCAAGTCGTGCGGCTCCCGCTCTCCGCTCTTCTCAAGGACGCACCTATGGCCACGGGTACC 3652

Qy   3136 GCCTGAGCATGTACA 3150
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Db   3653 GCCTCACGCTGGTCA 3667
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Db  6236  TCAGAGA---AGGGAGGGCTGTGGTCTCACATCCCACAGCATGGAAGAATGTGAGGCAC  6292
Qy  5506  TCTGTGATCGAGTAGCTATCATGGTGTCTCGGGCAGTTAAGGATGTATCGGAACAGTACAAC  5565
Db  6293  TGTGTACCCGCTGGCCATCATGGTAAAGGGCGCCTTTCGATGTATGGGCACCCATTCAGC  6352
Qy  5566  ATCTAAAGAGTAAATTGGAAAAGGCTACTTTTGGAAATTAAATTGAAGGACTCGATAG  5625
Db  6353  ATCTCAAGTCCAAATTGGAGATGGCTATATCGTCACAATTCGAGAATCAAATCCCGAAGG  6412
Qy  5626  AAAACCT  5632
Db  6413  ACGACCT  6419
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RESULT 8
US-09-032-438C-2
; Sequence 2, Application US/09032438C
; Patent No. 6713300
; GENERAL INFORMATION:
;   APPLICANT: Rattner, Amir
;   APPLICANT: Sun, Hui
;   APPLICANT: Lupski, James R.
;   APPLICANT: Nathans, Jeremy
;   APPLICANT: Anderson, Kent L.
;   APPLICANT: Leppert, Mark
;   APPLICANT: Dean, Michael
;   APPLICANT: Singh, Nanda
;   APPLICANT: Shroyer, No. 6713300h F.
;   APPLICANT: Smallwood, Philip M.
;   APPLICANT: Allikmets, Rando
;   APPLICANT: Lewis, Richard A.
;   APPLICANT: Li, Yixin
;   TITLE OF INVENTION: Nucleic Acid And Amino Acid Sequences For ATP-Binding Cassette
;   TITLE OF INVENTION: Transporter And Methods Of Screening For Agents That Modify
;   TITLE OF INVENTION: ATP-Binding Cassette Transporter
;   FILE REFERENCE: BYLR-0065
;   CURRENT APPLICATION NUMBER: US/09/032,438C
;   CURRENT FILING DATE: 1998-02-27
;   PRIOR APPLICATION NUMBER: US 60/039,388
;   PRIOR FILING DATE: 1997-02-27
;   NUMBER OF SEQ ID NOS: 120
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 6819
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-032-438C-2

Query Match   1.7%; Score 108.6; DB 4; Length 6819;
Best Local Similarity 49.8%; Pred. No. 1.2e-15;
Matches 332; Conservative   0; Mismatches 329; Indels 6; Gaps 2;

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Db  5873  TGTGTGTCGGAGTTCGCCCTGGAGTGCTTTGCCTCCTGGGAGTGAATGTGTGCCGGCA  5932
Qy  5026  AAAGCACAATTATTAATAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTT  5085
Db  5933  AACAACCACCATTCAAGATGCTCACTGGGACACCACAGTGACCTCAGGGGATGCCACCG  5992
Qy  5086  TAGGAGATTATTCTTCAGAGACAAGTGAAGATGATTCACTGAAGTGTATGGGTTACT  5145
Db  5993  TAGCAGGCAAGAGTATTTTAACCAATATTTCTGAAGTCCATCAAAA---TATGGGCTACT  6049
Qy  5146  GTCCTCAGATAAACCCTTGTGGCCAGATACTACATTGCAGGAACGAGGAACATTTGAAATTTATG  5205
Db  6050  GTCCTCAGTTGATGCAATCGATGAGCTGCTCACAGGACGAGGAACATCTTTACCTTTATG  6109
Qy  5206  GAGCTGTCAAAGGAATGAGTGTCAAGTGCAGTGCACTGAAAGAAGAAGTCATAAGTCGAATAACACATG  5265
Db  6110  CCCGGCTTCGAGGTGCTACCAGCGACAGAGAAATCGAAAAGGTTGCAAACTGCGAGTATTAAGA  6169
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RESULT 7
US-09-032-438C-5
; Sequence 5, Application US/09032438C
; Patent No. 6713300
; GENERAL INFORMATION:
;   APPLICANT: Rattner, Amir
;   APPLICANT: Sun, Hui
;   APPLICANT: Lupski, James R.
;   APPLICANT: Nathans, Jeremy
;   APPLICANT: Anderson, Kent L.
;   APPLICANT: Leppert, Mark
;   APPLICANT: Dean, Michael
;   APPLICANT: Singh, Nanda
;   APPLICANT: Shroyer, No. 6713300h F.
;   APPLICANT: Smallwood, Philip M.
;   APPLICANT: Allikmets, Rando
;   APPLICANT: Lewis, Richard A.
;   APPLICANT: Li, Yixin
;   TITLE OF INVENTION: Nucleic Acid And Amino Acid Sequences For ATP-Binding Cassette
;   TITLE OF INVENTION: Transporter And Methods Of Screening For Agents That Modify
;   TITLE OF INVENTION: ATP-Binding Cassette Transporter
;   FILE REFERENCE: BYLR-0065
;   CURRENT APPLICATION NUMBER: US/09/032,438C
;   CURRENT FILING DATE: 1998-02-27
;   PRIOR APPLICATION NUMBER: US 60/039,388
;   PRIOR FILING DATE: 1997-02-27
;   NUMBER OF SEQ ID NOS: 120
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 6705
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-032-438C-5

Query Match   1.7%; Score 108.6; DB 4; Length 6705;
Best Local Similarity 49.8%; Pred. No. 1.2e-15;
Matches 332; Conservative   0; Mismatches 329; Indels 6; Gaps 2;

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Qy  4966  TCTCTTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCTGGTGTGCTGGCA  5025
Db  5759  TGTGTGTCGGAGTTCGCCCTGGAGTGCTTTGCCTCCTGGGAGTGAATGTGTGCCGGCA  5818
Qy  5026  AAAGCACAATTATTAATAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTT  5085
Db  5819  AACAACCACCATTCAAGATGCTCACTGGGACACCACAGTGACCTCAGGGGATGCCACCG  5878
Qy  5086  TAGGAGATTATTCTTCAGAGACAAGTGAAGATGATTCACTGAAGTGTATGGGTTACT  5145
Db  5879  TAGCAGGCAAGAGTATTTTAACCAATATTTCTGAAGTCCATCAAAA---TATGGGCTACT  5935
Qy  5146  GTCCTCAGATAAACCCTTGTGTGGCCAGATACTACATTGCAGGAACGAGGAACATTTGAAATTTATG  5205
Db  5936  GTCCTCAGTTGATGCAATCGATGAGCTGCTCACAGGACGAGGAACATCTTTACCTTTATG  5995
Qy  5206  GAGCTGTCAAAGGAATGAGTGTACCAGCAGAGATCATGAAAGAAGAAGTCATAAGTCGAATAACACATG  5265
Db  5996  CCCGGGCTTCGAGGTGTACCAGCAGAAGAAATCGAAAAGTTGCAAACTACCTGCAAAGTTGCGAATATTAAGA  6055
Qy  5266  CACTTGATTTAAAGACAACATCTTCACCGCCGACTGTCTACGGCACGTCAGTGGGGCAACAAAC  5325
Db  6056  GCCTGGGCCTGCTCGTTTGCCTCTAAGTATGCTAGGAATATCCTCATTGGCTGCCCACCGCTCGGTGCCCACCGC  6115
Qy  5326  GAAAGTTGCGTTTGTTTTGCCTCAAGCTGACTTCAAGCTGACTTCTTGCTAGATGAAC  5385
Db  6116  GGAAACTCTCCACAGCCATCGCACTCAGCTGCTGCTCGCAATTCGAACTGCAT  6175
Qy  5386  CATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCAT  5445
Db  6176  CCACCAAGGGATGGACCCCCCGGCCACGCGCACGGCCGCCGTGCTTCGTGAACGTCATCGTCATCA  6235
Qy  5446  TTAAAAACAGAAACAGGCGGGCTGCTATTCTGACCCACTCACTATATGGAGGAGGAGGCTG  5505
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Qy  5266  CACTTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAGAACTACCTGCAGGATCAAAC  5325
Db  6170  GCCTGGGCCTGACTGTCTCACGCCGACTGCCTGGCACGTAGTGGGGCAACAAGC        6229
Qy  5326  GAAAGTTGTGTTTGCTCAAGTATGCTAGGAATCCTCAGATTACTTTGCTAGATGAAC     5385
Db  6230  GGAAACTCTCCACAGCCATCGCCACTCATTGGCTGCCCACCGCGTCGTGCTGGATGAGC    6289
Qy  5386  CATCTACACAGGTATGGATCCCAAAGCCAAACAGCACAGCATGTGGCGAGCAATTCGAACTGCAT  5445
Db  6290  CCACCACAGGGATGGACCCCCAGGCACGCCCCAGCGTCGTGGAACGTCATCGTGAGCGATCA  6349
Qy  5446  TTAAAAACAGAAGCGGGGCCGTGCTATTCTGACCACTCCACTATATGGAGGAGGCAGAGGCTG  5505
Db  6350  TCAGAGA--AGGGAGGGGCTGTGGTCCTCACATCCCACAGCATGGAAGAATGTGAGGCAC   6406
Qy  5506  TCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGATCGGAACAGTACAAC    5565
Db  6407  TGTGTACCCGGCTGGCCATCATCGGGTAAAGGCGCCTTTGCGATGTATGGGCACCATTCAGC 6466
Qy  5566  ATCTAAAGAGTAAATTGGAAAAAGGCTACTTTTGGAAATTAAATTGAAGGACTGGATAG    5625
Db  6467  ATCTCAAGTCCAAATTGGAGATGGCTATATCGTCACAATGAAGATCAAATCCCGAAGG     6526
Qy  5626  AAAACCT  5632
Db  6527  ACGACCT  6533
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Db  6521  AAACACCACCATTCAAGATGCTCACTGGGGACCACCAGTGACCTCAGGGATGCCACCG     6580
Qy  5086  TAGGAGATTATTCTTCAGAGACTGAAGCAGCAAGTGAGGATGATTCACTGAAGTGTATGGTTACT 5145
Db  6581  TAGCAGGCAAGAGATTATTTAACCAATATTTCTGAAGTCCATCAAAA---TATGGCTACT  6637
Qy  5146  GTCCTCAGATAAACCCTTTGTGGCCAGATACTACATTGCAGGAACATTTGAAATTTATG    5205
Db  6638  GTCCTCCAGTTGATGCAATCGATGAGCTGCTCACGAGGACGAACATCTTTACCTTTATG   6697
Qy  5206  GAGTGTCAAAGAATGAGTGCAAGTGACATGGAAAGAGTCATAAGTTGAATAACACATG    5265
Db  6698  CCCGGCTTCGAGTGTACCAGCAGAAGAAATCGAAAAGTTGCAAACTGGAGTATTAAGA    6757
Qy  5266  CACTTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAGAACTACCTGCAGGATCAAAC 5325
Db  6758  GCCTGGGCCTGACTGTCTCACGCCGACTGCCTGGCACGTAGTGGGGCAACAAGC       6817
Qy  5326  GAAAGTTGTGTTTGCTCAAGTATGCTAGGAATCCTCAGATTACTTTGCTAGATGAAC    5385
Db  6818  GGAAACTCTCCACAGCCATCGCCACTCATTGGCTGCCCACCGCGTCGTGCTGGATGAGC   6877
Qy  5386  CATCTACACAGGTATGGATCCCAAAGCCAAACAGCACAGCATGTGGCGAGCAATTCGAACTGCAT 5445
Db  6878  CCACCACAGGGATGGACCCCCAGGCACGCCCCAGCGTCGTGGAACGTCATCGTGAGCGATCA 6937
Qy  5446  TTAAAAACAGAAGCGGGGCTGTGCTATTCTGACCACTCCACTATATGGAGGAGGCAGAGGCTG 5505
Db  6938  TCAGAGA--AGGGAGGGGCTGTGGTCCTCACATCCCACAGCATGGAAGAATGTGAGGCAC   6994
Qy  5506  TCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGATCGGAACAGTACAAC   5565
Db  6995  TGTGTACCCGGCTGGCCATCATCGGGTAAAGGCGCCTTTGCGATGTATGGGCACCATTCAGC 7054
Qy  5566  ATCTAAAGAGTAAATTGGAAAAAGGCTACTTTTGGAAATTAAATTGAAGGACTGGATAG   5625
Db  7055  ATCTCAAGTCCAAATTGGAGATGGCTATATCGTCACAATGAAGATCAAATCCCGAAGG    7114
Qy  5626  AAAACCT  5632
Db  7115  ACGACCT  7121
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RESULT 9
US-09-032-438C-1
; Sequence 1, Application US/09032438C
; Patent No. 6713300
; GENERAL INFORMATION:
; APPLICANT: Rattner, Amir
; APPLICANT: Sun, Hui
; APPLICANT: Lupski, James R.
; APPLICANT: Nathans, Jeremy
; APPLICANT: Anderson, Kent L.
; APPLICANT: Leppert, Mark
; APPLICANT: Dean, Michael
; APPLICANT: Singh, Nanda
; APPLICANT: Shroyer, No. 6713300h F.
; APPLICANT: Smallwood, Phillip M.
; APPLICANT: Allikmets, Rando
; APPLICANT: Lewis, Richard A.
; APPLICANT: Li, Yixin
; TITLE OF INVENTION: Nucleic Acid And Amino Acid Sequences For ATP-Binding Cassette
; TITLE OF INVENTION: Transporter And Methods Of Screening For Agents That Modify
; TITLE OF INVENTION: ATP-Binding Cassette Transporter
; FILE REFERENCE: BYLR-0065
; CURRENT APPLICATION NUMBER: US/09/032,438C
; CURRENT FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: US 60/039,388
; PRIOR FILING DATE: 1997-02-27
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.2
US-09-032-438C-1
; SEQ ID NO 1
; LENGTH: 7488
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-032-438C-1

Query Match   1.7%; Score 108.6; DB 4; Length 7488;
Best Local Similarity 49.8%; Pred. No. 1.2e-15;
Matches 332; Conservative 0; Mismatches 329; Indels 6; Gaps 2;

RESULT 10
US-09-751-389-3
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001067
; CURRENT APPLICATION NUMBER: US/09/751,389
; CURRENT FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 786431
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(786431)
; OTHER INFORMATION: n = A, T, C or G
US-09-751-389-3

Query Match   1.6%; Score 105.6; DB 4; Length 786431;
Best Local Similarity 55.1%; Pred. No. 5.2e-14;
Matches 313; Conservative 0; Mismatches 244; Indels 11; Gaps 5;

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Qy   163  CTGGATTTGGACAGTGGCTGTCTGTCGTTGTTAGTTCATTTCTCAGCCTTTGTCACACTAATA  222
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Qy  4966  TCTCTTTCTGTGTGAAAAAAGGAGGAGATCTTAGGACTATTGGGTCCAAATGGTGCTGCA   5025
Db  6461  TGTGTGTCGGAGTTCGCCTGGAGAGTGCTTTGCCTCCTGGGAGTGAAATGGTGCCGGCA    6520
Qy  5026  AAAGCACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGCCAGGTATTT     5085
```

REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 1064 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-858-207A-88

Query Match   1.6%;   Score 103.4;   DB 3;   Length 1064;
Best Local Similarity 47.9%;   Pred. No. 8.9e-15;
Matches 328; Conservative 0; Mismatches 356; Indels 1; Gaps 1;

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Qy   4903 AATATGATGACAAGAAAGATTTCTTCTTTCAAGAAAAGTAAAGAAAGTGCAACTAAAT 4962
            ||| |||   ||| ||| ||  |||  || |||||||||||| ||||||||  ||
Db    143 AAAAGGGAGCCAAAAGTTCTTTATCCATCCGAAAAACAAATTTTGAAGCGGTTAAGG 202

Qy   4963 ACATCTTCTTCTGTGTGAAAAAGGAGATCTTAGGACTATTGGGTCAAATGGTGCTG 5022
            ||| |||   ||||||||  ||  ||||||||||||||||||||||||||||||
Db    203 ATTTATCGTTTGAGGTTCCAAAGGACAAATTTTAGGTTTATTGGTGCTAATGGGCAG 262

Qy   5023 GCAAAAGCACAATTATTAATATTCTGGTTGTGATATTGAACCAACTTCAGGCCAGGTAT 5082
            ||    |||||   ||    |||||    ||||| ||  ||||||||||||||||
Db    263 GTAAGTCAACAACGATTAAAATGTTGACAGGGATTTTAAAACCGACATCTGGTTTTGTC 322

Qy   5083 TTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATGATTCACTGAGTGTATGGGGT 5142
            ||| ||||  |||| ||| |||  || ||| ||||   ||| ||||||||
Db    323 GCATTAATGGGAAGATTCCTCAAGAAAATCGTCAGGATTATGTTAAGGATATTGGTGTTG 382

Qy   5143 ACTGTCCTCAGATAAAACCCTTTGTGCGCCAGATACTACATTGCAGGAACATTTCGAGGAA 5202
            |||||||||||||| ||| |||  |||| ||||  || |||| ||||
Db    383 TTTTTGGGCAACGCACCCAGCTTTGGTGGGATTTCGCTTACAGAGAGAAGTCATAAGTCGAATAAACAC 5262

Qy   5203 ATGGACTGTCAAAGGAATGAGTGCCCTGATGCAGTCAGTATTTCAAAAACGCATGAAATG 5262
            |||
Db    443 TAAAGAAATTTATGATGTCCCTGACTGTAAAGAACTGTAAAGAACTACCTGCAGGAATCA 5322

Qy   5263 ATGCACTTGATTTAAAAGAACATCTTCAGAGAGTCTGAAGAAAAATTTGACCATCATCAGTTCAAC 562
Db    503 ATGTTTTAGACTTGAAAGAGTTTATTAAGATCCTGCTCAGGAATCCTCAGATTACTTGCTCAGATG 5382

Qy   5323 AACGAAAGTGTGTTTGCTCTAAGTATGCTAAGTGTGTCTGGGCAGTTAAGATGTATCGGAACAGTAC 5562
Db    563 GTATGAGAGCGGATATTGCGCGCCTCCTTGCTCCACAATCCCAAAGTTCTTTTTTTTTTAGATG 622

Qy   5383 AACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCCGAGCAATTCGAACTG 5442
            ||| || |||   ||| ||||||||||| |||||||||| |||| ||| |||| |||
Db    623 AGCCGACCCATGGTTTTGGACCTTTCGGTTAAGGATAATATTCGTCGGCAATTACTCAGA 682

Qy   5443 CATTTAAAAACAGAAACCAGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGG 5502
Db    683 TCAATCAAGAGGAAGAAACTACCATTCTTTTGACCACTCACGATTTGAGTGATATTGA-G 741

Qy   5503 CTGTCTGTGATCGAGTAGCTATCATCGTGTCTGGGCAGTTAAGATGTATCGGAACAGTAC 5562
Db    742 CAATTTGTGATCGGATTTTCATGATTGATGACAAGGGCCAAGAGAGATTTTTGATGGAACAGTGA 801

Qy   5563 AACATCTAAAGAGTAAATTGGAAA 5587
            ||| |||  |||  | |||||
Db    802 GCCAACTCAAGGAGACCTTTGGTAA 826
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RESULT 12
US-09-583-110-2618
; Sequence 2618, Application US/0958110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.

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Db   404844 CTTGTCTGATACCTGGGTGCTGGTCTTCGGCCTAGTTCTTAAGTCTTCGGCATGTTAAATA 404903
              |||   ||| |||  |||  |||
Qy      223 GGATGGATTATGTCCAGCTTGGGAATTATTACCAGGAATTAAAACAACTTTTA 282
              ||||| ||||  |||| |||| |||||||||
Db   404904 GAATAGAATCCACATGTGCATTGGGAGTAAGCCCAAGAGTTCATAAACAAGTTTATG 404963
Qy      283 GAGTGCTTCCTGAG---CTCTCTTCTATTGTTCCCCCTTCTACTTTTGCTTCCCCTG 339
              ||| |||||    |||| ||| ||| ||| |||||
Db   404964 GATTGCTTTTCTCTAAGCTTCTCTGTCTCCCATGTTCTCCGGGTAGTTTCTCGTTTCCTCGT 405023
Qy      340 TGGCTGCTGTTCTATCCTCCAGCCAGGAGAGCT-AGTGTTATTTATTTCTCCATTGTGTTAC 398
              |||||||||||||||||  |||||||| |||| |||  ||||  |||||||||||
Db   405024 GGTTTCTCTTTAAGATCCCTTGGCAAGAAAGGCTGGAGGCTTTATTTATTTATTTCCTCCACTGTGCTGT 405083
Qy      399 ACACTTGTGCAGCTGCA---ACCACCATATCCAGGGCCCAATGTAGGAGGTAGAGAAGA 455
              |||||||||| ||  |||||||||  ||| |||| |||||||||||
Db   405084 GCCCTTCTGCAACTACATTCACTTCCAGGGCCATGTGAGGAGGAGGACAGAGAGAAAAAGA 405143
Qy      456 AAAGCAAAGGGATTGGCCTCATCCTCTTACAACGATAGTTCCATTGAATAGGAGAAAG 515
              ||| |||  ||| ||  |||||| |||||||| ||||  ||||||||
Db   405144 AACATAATGGAGGTTGACCCAACCCTCTTGGAACCACAGCTTCAGTGAACAAACAAGAAA 405203
Qy      516 GTTTCCTCCTCCAGAGTGTTGGCTGCGACTAGG--CTTTGTTACTGTAGTCGTGGCCCTG 573
              |||||||||||||||||||||||||  ||||||||  |||
Db   405204 ATTTACTTTCTTAAGAATTTCGGCTCCTCTGTGTTCCCCATTTCTGCCACCACCACCACCA 405263
Qy      574 TTACCATGGGATTGCTTGCATGTGGGATACAGGAGAATTCAGAAAGAAAAAGATTT 633
              ||||||  ||| ||| |||| ||||||||||||||||||  |||
Db   405264 TCACCATGTGATTGCTTGAGGACTGGGCAAGAGTAAGCAAGAAGAAAAACGGGTGG 405323
Qy      634 GCTATTTCTACAATTCTCCCTGAGCATTAAGACCCCTCCCTTGCCCATTCCTCAA--TTCAAA 691
              ||||| | |||||||||||||||||||| |||||||||||  || |||||  |||
Db   405324 GGAATTGCCACATTCTCTCTGAGCATTATGAGTTCTGAGCATTATGATTTTCCACCTCCTAAAGCTAAAT 405383
Qy      692 GCTAAGGCTTCTTCTGGAGCTGCCTCTG 719
              |||||||||||||||||||||||
Db   405384 GAGCAGGCTTGTCCTGGAGCTGTGTCTATG 405411
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RESULT 11
US-08-858-207A-88
; Sequence 88, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Stodola, Robert
; TITLE OF INVENTION: No. 63483281 Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,207A
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017670
; FILING DATE: 14-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R

; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US/60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2618
;   LENGTH: 954
;   TYPE: DNA
;   ORGANISM: Streptococcus pneumoniae
US-09-583-110-2618

Query Match   1.4%; Score 92.2; DB 4; Length 954;
Best Local Similarity 46.2%; Pred. No. 3.8e-12;
Matches 307; Conservative 0; Mismatches 358; Indels 0; Gaps 0;

Qy   4923 TTTCTTCTTTCAAGAAAAGTAAAGAAAATACATCTCTTCTGTGTGAAA 4982
          ||||| ||| ||| ||||||||||||| | | | | || |||||||
Db   46 TTTATTCATCCTGAAAAGCAGACCCTTTGAAGCGGTCAAGGATTCCA 105

Qy   4983 AAAGGAGAGATCTTAGGACTATTGGGTCTCCAAATGGTGCTGGCAAAAGCACAATTATTAAT 5042
          ||| ||| ||| ||||||| || ||| | |||||||| || || ||||| |||| |||| ||
Db   106 AAAGGGCAGATTTTAGGATTATCGGGCAAATGGTGCTGGGAAGTCGACAACCATTAAA 165

Qy   5043 ATTCTGGTTGGTGTATATTGAACCAACTTCAGGCCAGGTATTTTTAGGAGAGATTATTCTTCA 5102
          ||||| || || | ||| ||| |||||| || ||| | |||||| | |||| ||| || |||
Db   166 ATGCTGACAGGAGAATTTTGAAACCAACATCTCGTTTTTGTCGGATTAACGGCAAGAGTTCCC 225

Qy   5103 GAGACAAGTGAAGATGATGATTCACTGAAGTGTATGGGTTACTGTCCTCAGATAAACCCT 5162
          ||||||||||| || |||||||| |||| || |||||| ||| || || ||||||||||
Db   226 CAGGACAAATCGGCAAGATTATGTCAAAGATATTGGCGTAGTCTTTGGACAACGCACCCAG 285

Qy   5163 TTGTGGGCCAGATACTACATTGCAGGACCATTTGAAATTTATGGAGCTGTCAAGGAATG 5222
          ||||| ||||| ||| |||||| ||||| || || ||||| |||||| || ||||| ||
Db   286 CTATGGTGGGATTTGGCTCTGCGAAGAGACCTACACTGTCTTAAAAGAGATTTATGATGTG 345

Qy   5223 AGTGCAAGTGACATGAAAGAAGTCATAAGTCGAATAACACATGCACTTGATTTAAAAGAA 5282
          ||||||||||| |||||||||| ||||||| |||| || |||| ||||| |||| |||||
Db   346 CCAAACTCGCTCTTTCATCATAAGGCCATATATGGACTTTTTGAATGAAGTCGTTGTTTGCT 405

Qy   5283 CATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAGTTGTGTTTTGCT 5342
          |||||||||| || || ||||| || ||| || ||||| |||| ||||| ||| || ||
Db   406 TTTATCAAGGATCCCGTGCGGACTCTTTCACTGGGCGGGGATATTGCG 465

Qy   5343 CTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTCTAGATGAACCTTCACAGTATGGAT 5402
          ||||||||| ||||| |||||||||||| ||||| |||| || || | ||| ||| |||
Db   466 CTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTCTAGATGAACCATTCACAGTATGGAT 525

Db   526 GTTTCGGTTAAGGATAATATTCGTCGGGCAATTACTCAGATCAATCAAGAGGAGAAACT 585

Db   586 GCTGCTATTCTGACCACTCACTATATGGAGGAGGAGCAGAGCCTGTCTCGTGATCGAGTAGCT 645

Db   646 ACCATTCTTTGACCACTCACGATTTGAGTGTATATTGGACTGTGATTTGTGATCGGATTTTC 705

Qy   5583 GGAAA 5587
          |||||
Db   706 GGTAA 710

RESULT 13
US-08-961-527-1

Query Match   1.4%; Score 92.2; DB 4; Length 5625;
Best Local Similarity 46.2%; Pred. No. 8.4e-12;
Matches 307; Conservative 0; Mismatches 358; Indels 0; Gaps 0;

Qy   4923 TTTCTTCTTTCAAGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTCTGTGTGAAA 4982
          ||||| ||| ||| | ||||||||||||| | | | | || |||| ||||| |||||
Db   2132 TTTATTCATCCTGAAAAGCAGACCTTTGGGTCGGCGGTCAAGGATTTGACCTTTGAGGTTCCA 2191

Qy   4983 AAAGGAGAGATCTTAGGACTATTGGGTCTCCAAATGGTGCTGGCAAAAGCACAATTATTAAT 5042
          ||| ||| ||| ||||||| || ||| | ||||||| || || ||||| |||| || ||
Db   2192 AAAGGGCAGATTTTAGGATTATCGGGCAAATGGTGCTGGGAAGTCGACAACCATTAAA 2251

Qy   5043 ATTCTGGTTGGTGTATATTGAACCAACTTCAGGCCAGGTATTTTTAGGAGAGATTATTCTTCA 5102
          ||||| || || | ||| ||| |||||| || ||| | |||||| | |||| ||| || |||
Db   2252 ATGCTGACAGGAGAATTTTGAAACCAACAATCTCGTTTTTGTCGGATTAACGGCAAGAGTTCCC 2311

Qy   5103 GAGACAAGTGAAGATGATGATTCACTGAAGTGTATGGGTTACTGTCCTCAGATAAACCCT 5162
          ||||||||||| || |||||||| |||| || |||||| ||| || || ||||||||
Db   2312 CAGGACAAATCGGCAAGATTATGTCAAAGATATTGGCGTAGTCTTTGGACAACGCACCCAG 2371

Qy   5163 TTGTGGCCAGATACTACATTGCAGGAATCAAACGAAAGTTGTTTTTGCT 5222
          ||||| ||||| ||| |||||| |||| |||| ||||| ||| || ||
Db   2372 CTATGGTGGGATTTGGCTCTGCGAAGAGACCTACACTGTCTTAAAAGAGATTTATGATGTG 2431

Qy   5223 AGTGCAAGTGACATGAAAGAAGTCATAAGTCGAATAACATGGCCAGTATGGAT 5282
          ||||||||||| |||||| ||||| ||||| |||| || ||| || || |||
Db   2432 CCAGACTCGCTCTTTCATAAGGCTGTATAAGCGGTATGGGACTTGTTGGATTTGAAGGAC 2491

Qy   5283 CATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAGTTGTGTTTTGCT 5342
          ||||||||||| || || ||||| || ||| || ||||| |||| ||||| ||| |||||
Db   2492 TTTATCAAGGATCCCGTGCGGACTCTTTCACTGGGACACAGTGTATTGCG 2551

Qy   5343 CTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTCTAGATGAACCTTCACAGTATGGAT 5402
          ||||||||| ||||| ||||||||||| ||||| |||| || || | ||| ||| |||
Db   2552 CTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTCTAGATGAACCATTCACAGTATGGAT 5402

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Db    2552 GCCTCCTTGCTCCACAATCCCAAGGTTCTTTTTTTAGATGAGCCGACCATTGGTTTCGAC 2611
                ||||||    |||   |||   ||||||   ||

Qy    5403 CCCAAAGCCAAACAGCACATGTGCGCAGCAATTCGAACTGCATTTAAAAACAGAAAGCGG 5462

Db    2612 GTTTCGGTTAAGGATAATATTCGTCGGGCAATTACTCAGATCAATCAAGAGAGGAAGAAACT 2671

Qy    5463 GCTGCTATTCTGACCACTCACTATATGAGGAGGCAGAGGCTGTCTGTGATCGAGTAGCT 5522
                ||||||||||    ||||||     ||||||    ||||||

Db    2672 ACCATTCTTTTGACCACTCACGATTTGAGTGATATTGAGCAACTTGTGATCGGATTTTC 2731

Qy    5523 ATCATGGTGTCTCGGGCAGTTAAGATGTATCCGAACAGTACAACATCTAAAGAGTAAATTT 5582
                |||||    ||||||    ||||   |||

Db    2732 ATGATTGACAAGGGGCAAGAGATTTTTGATGGAACGGTGAGCCAACTCAAGGAGGACCTTT 2791

Qy    5583 GGAAA 5587
           |||||

Db    2792 GGTAA 2796
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RESULT 14

US-09-621-976-2582

; Sequence 2582, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2582
;　TYPE: DNA
;　LENGTH: 450
;　ORGANISM: Homo sapiens
;　FEATURE:
;　NAME/KEY: CDS
;　LOCATION: 69..308
US-09-621-976-2582

Query Match　　　1.3%;　　Score 83.8;　DB 4;　Length 450;
Best Local Similarity　60.2%;　Pred. No. 2.7e-10;
Matches 139;　Conservative　0;　Mismatches　92;　Indels　0;　Gaps　0;

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Qy    5693 AAGTTTTCTTCTTCTCATTTGGCTTATAAAATTCCTAAGGAAGAGATGTTCAGTCCTTTCACA 5752
                ||||||    |||||||    ||||   ||||||    ||||||

Db      74 AAAATATTCCTCTTTTAATGGCTATAAGTTAACCTGTGGAGGATGTCCACCCTCTATCTCG 133

Qy    5753 ATCTTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTTTC 5812
                ||    |||||||    |||    ||||||||    ||||||    ||

Db     134 GGCCTTTTTCAAGTTAGAGGCGATGAAACAGACCTTCAACCTGGAGGAATACAGCCCTCTC 193

Qy    5813 TCAAGCAACATTGGAACAGGTTTTTGTAGAACTCACTAAAGAACAAGAGGAGGAAGATAA 5872
                ||||||    ||||||    ||||   |||

Db     194 TCAGGCTACCTTGGAGCAGGTATTCTTAGAACTCTGTAAAGAGCAGGAGCTGGGAAATGT 253

Qy    5873 TAGTGTGTGGAACTTAAACAGCACACTTGGTGGGAACGAACCAAGAAGA 5923
                |||||    |||||

Db     254 TGATGATAAAATTGATACAACAGTTGAATGGAAACTTCTCCCACAGGAAGA 304
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RESULT 15

US-09-621-976-2581

; Sequence 2581, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2581
;　TYPE: DNA
;　LENGTH: 463
;　ORGANISM: Homo sapiens
;　FEATURE:
;　NAME/KEY: CDS
;　LOCATION: 110..328
US-09-621-976-2581

Query Match　　　1.3%;　　Score 83.4;　DB 4;　Length 463;
Best Local Similarity　60.3%;　Pred. No. 3.3e-10;
Matches 138;　Conservative　0;　Mismatches　91;　Indels　0;　Gaps　0;

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Qy    5695 GTTTTTCTTCTATTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCTTTCACAAT 5754
                ||||||    |||||||    ||||   ||||||    ||||||

Db      96 GATATTCCTCTTTAATGGCTATAAGTTACCTGTGGAGGATGTCCACCCTCTATCTCGGC 155

Qy    5755 CTTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTGCCATTGAAGAATATAGCTTTTCTC 5814
                ||    |||||||    |||    ||||||||    ||||||    ||

Db     156 CCTTTTTTCAAGTTAGAGGCGATGAAACAGACCTTCAACCTGGAGGAATACAGCCCTCTC 215

Qy    5815 AAGCAACATTGGAACAGGTTTTGTAGAACTCACTAAAGAACAAGAGGAGGAAGATAATA 5874
                ||||||    ||||||    ||||   |||

Db     216 AGGCTACCTTGGAGCAGGTATTCTTAGAACTCTGTAAAGAGCAGGAGCTGGGAAATGTTG 275

Qy    5875 GTTGTGGAACTTAAACAGCACACTTGGTGGGAACGAACGAACCAAGAAGA 5923
                |||||    |||||

Db     276 ATGATAAAATTGATACAACAGTTGAATGGAAACTTCTCCCACAGGAAGA 324
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Search completed: December　4, 2004, 19:42:59
Job time : 484 secs

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2004, 06:30:51 ; Search time 2950 Seconds
(without alignments)
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Title: US-10-005-338B-1
Perfect score: 6525
Sequence: 1 aaaatgttgatatttctct........ttgatcataataagtgaaat 6525

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3694831 seqs, 2747406616 residues

Total number of hits satisfying chosen parameters: 7389662

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	6524	100.0	6525	14	US-10-005-338B-1	Sequence 1, Appli
2	6122.8	93.8	6369	18	US-10-343-903-33	Sequence 33, Appl
3	5373.2	82.3	5475	13	US-10-090-458-4	Sequence 4, Appli
4	5255.8	80.5	5463	13	US-10-090-458-1	Sequence 1, Appli
5	5247.4	80.4	5262	9	US-09-971-121-5	Sequence 5, Appli
6	4918.4	75.4	4929	9	US-09-971-121-1	Sequence 1, Appli
7	4807.4	73.7	4917	13	US-10-090-458-3	Sequence 3, Appli
8	4754.8	72.9	4785	9	US-09-971-121-3	Sequence 3, Appli
9	3258.2	49.9	3347	16	US-10-108-260A-160	Sequence 160, App
10	3178	48.7	3268	15	US-10-094-749-984	Sequence 984, App
11	1789.4	27.4	3928	10	US-09-822-846-98	Sequence 98, Appl
12	1731.8	26.5	1943	16	US-10-108-260A-1424	Sequence 1424, Ap
13	1722.8	26.4	1818	15	US-10-204-887-32	Sequence 32, Appl
14	1543.8	23.7	1548	10	US-09-822-846-97	Sequence 97, Appl
15	1182	18.1	1346	9	US-09-962-436-337	Sequence 337, App
16	1182	18.1	1346	9	US-09-880-107-3406	Sequence 3406, Ap
17	1182	18.1	1346	9	US-09-954-531-1033	Sequence 1033, App
18	1182	18.1	1346	15	US-10-171-581-333	Sequence 333, App
19	1150.4	17.6	6181	14	US-10-005-338B-4	Sequence 4, Appli
20	1118.8	17.1	5981	14	US-10-005-338B-3	Sequence 3, Appli
21	1117.2	17.1	4875	13	US-10-090-454-3	Sequence 3, Appli
22	1117.2	17.1	5018	13	US-10-090-454-1	Sequence 1, Appli
23	1090.8	16.7	5296	14	US-10-005-338B-2	Sequence 2, Appli
24	1089.2	16.7	5211	17	US-10-467-685-36	Sequence 36, Appl
25	1086	16.6	4854	13	US-10-090-453A-3	Sequence 3, Appli
26	1086	16.6	5332	13	US-10-090-453A-1	Sequence 1, Appli
27	930.6	14.3	4727	16	US-10-332-447-56	Sequence 56, Appl
28	930.6	14.3	5149	18	US-10-343-902-60	Sequence 60, Appl
29	908.2	13.9	4766	15	US-10-093-463-199	Sequence 199, App
30	907.2	13.9	5677	18	US-10-788-792-45	Sequence 45, Appl
31	901.2	13.8	5065	18	US-10-343-903-35	Sequence 35, Appl
32	894.8	13.7	4798	15	US-10-093-463-197	Sequence 197, App
33	857.8	13.1	5622	18	US-10-343-903-42	Sequence 42, Appl
34	797.4	12.2	5175	16	US-10-085-198-37	Sequence 37, Appl
35	757.4	11.6	974	9	US-09-833-381-1085	Sequence 1085, Ap
36	670.4	10.3	740	15	US-10-242-355-968	Sequence 968, App
37	670.4	10.3	740	15	US-10-242-355-969	Sequence 969, App
38	651.4	10.0	2645	15	US-10-094-749-1290	Sequence 1290, Ap
39	600	9.2	668	15	US-10-242-355-970	Sequence 970, App
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41	475.4	7.3	477	9	US-09-867-701-10804	Sequence 10804, A
c 42	471.2	7.2	476	9	US-09-867-701-4362	Sequence 4362, Ap
43	459	7.0	465	16	US-10-242-535A-44227	Sequence 44227, A
44	459	7.0	465	16	US-10-085-783A-44227	Sequence 44227, A
45	452.8	6.9	456	16	US-10-242-535A-16105	Sequence 16105, A

ALIGNMENTS

RESULT 1
US-10-005-338B-1
; Sequence 1, Application US/10005338B
; Publication No. US20030044895A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLE, Patrice
; APPLICANT: ROSIER-MONTUS, Marie-Francoise
; APPLICANT: PRADES, Catherine
; APPLICANT: ARNOULD-REGUIGNE, Isabelle
; APPLICANT: DUVERGER, Nicolas
; APPLICANT: ALLIKMETS, Rando
; APPLICANT: DEAN, Michael
; TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCA5, ABCA6, ABCA9, AND ABCA10 GENE
; TITLE OF INVENTION: CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF
; FILE REFERENCE: ABCA5, 6, 9, 10
; CURRENT APPLICATION NUMBER: US/10/005,338B
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/263,231
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: FR 00403440.1
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 6525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 4449
; OTHER INFORMATION: n=unknown, may be a or g or c or t
US-10-005-338B-1

Query Match   100.0%; Score 6524; DB 14; Length 6525;
Best Local Similarity   100.0%; Pred. No. 0;

Matches 6525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     61 CTACCCACATTCTTGAACTGTAGTGTCATTTAGTTATTTTCAAAAACTTTTGCAG 120

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Qy    721 GGGCGGGTTCGGGAGATACCAAAGGAGAAAAAGTACCACTGTTGATATGGTGGTATTTCAA 780
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Qy   1141 TTTGGTTAATATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAGTGCCTAATA 1200
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Qy   1201 TAGAACTCAATCCATGGACAAGTTACTCTTCTAATCTAATCTTCTGATATACTCCAG 1260
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Qy  2821 TGCAGACTATCAAAGATAACCAAGCTAAAAAATAAGTGGTGGTCAAAAAGAAAGCTGT 2880
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Qy  3661 ACTCTTTAAAAATGCTGTGGTCCCATCAAAACTTGTTCCAGACTTATATTTTCTAAAAC 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 ACTCTTTAAAAATGCTGTGGTCCCATCAAAACTTGTTCCAGACTTATATTTTCTAAAAC 3720

Qy  3721 CTGGACAAACCACCATATAATACAAAAACAAGTCTGCTTCTTCAAAATTCTGCTGACTCAG 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 CTGGACAAACCACCATATAATACAAAAACAAGTCTGCTTCTTCAAAATTCTGCTGACTCAG 3780

Qy  3781 ATATCAGTGATCTTATTAGCTTATTAGCCAGAACATATGGTGACGATGATTAATG 3840
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Db  3781 ATATCAGTGATCTTATTAGCTTATTAGCCAGAACATATGGTGACGATGATTAATG 3840

Qy  3841 ACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGGCTTTAAATGTGATGCATTCAGAAA 3900
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Db  3841 ACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGGCTTTAAATGTGATGCATTCAGAAA 3900

Qy  3901 AGGACTATGTTTTGCAGTGTTTCAACAGTGTTTCAACAGTGTTATTCTTTACCTATATTAG 3960
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Db  3901 AGGACTATGTTTTGCAGTGTTTCAACAGTGTTTCAACAGTGTTATTCTTTACCTATATTAG 3960

Qy  3961 TGAATATCATTAGTAACTACTATCTTTATCATTTAAATGTGACTGAAACCATCCAGATCT 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961 TGAATATCATTAGTAACTACTATCTTTATCATTTAAATGTGACTGAAACCATCCAGATCT 4020

Qy  4021 GGAGTACCCCATTCTTTCAAGAAAATTACTGATATAGTTTAAAATTGAGCTGTATTTTC 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021 GGAGTACCCCATTCTTTCAAGAAAATTACTGATATAGTTTAAAATTGAGCTGTATTTTC 4080

Qy  4081 AAGCAGCTTGCTTGGAATCATTCATTGTTACTGCCACCTTACTTTGCCATGGAAAATG 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081 AAGCAGCTTGCTTGGAATCATTCATTGTTACTGCCACCTTACTTTGCCATGGAAAATG 4140

Qy  4141 CAGAGAATCATAGATCAAAGCTTAATACTCAACTCAACTTCAGGTCTTTTGCCATCTG 4200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141 CAGAGAATCATAGATCAAAGCTTAATACTCAACTCAACTTCAGGTCTTTTGCCATCTG 4200

Qy  4201 CATATTGGATTGGACAGCGTGTTGTGATATCCCCTTATTTTTATCATTCTTATTTTGA 4260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201 CATATTGGATTGGACAGCGTGTTGTGATATCCCCTTATTTTTATCATTCTTATTTTGA 4260

Qy  4261 TGCTAGGAAGCTTACTGGCATTCATTGGATTTTTATACTGTAAAGTTCCTTG 4320
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Db  4261 TGCTAGGAAGCTTACTGGCATTCATTGGATTTTTATACTGTAAAGTTCCTTG 4320

Qy  4321 CTGTGGTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTCGTTGTCACTTATATTGCTT 4380
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Db  4321 CTGTGGTTTTTGCCTATTGGTTATGTTCCATCAGTTATTCTGTTCACTATATTGCTT 4380

Qy  4381 CTTTCACCTTAAGAAAATTTAAATACCAAAGAATTTGGTCATTATCTATTCTGTGG 4440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4381 CTTTCACCTTAAGAAAATTTAAATACCAAAGAATTTGGTCATTATCTATTCTGTGG 4440

Qy  4441 CAGCGGTTGNCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGATTACACAATTGCAA 4500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4441 CAGCGGTTGNCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGATTACACAATTGCAA 4500

Qy  4501 CTATTCTTCATTATGCCTTTGTGATCATCAATCCAATCTATCCACTTCTAGGTTGCCTGA 4560
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Db  4501 CTATTCTTCATTATGCCTTTGTGATCATCAATCCAATCTATCCACTTCTAGGTTGCCTGA 4560

Qy  4561 TTTCTTCATAAAGATTTCTTGGAAGAATGTACGAAAAAAATGTGACACCTATAATCCAT 4620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4561 TTTCTTCATAAAGATTTCTTGGAAGAATGTACGAAAAAAATGTGACACCTATAATCCAT 4620

Qy  4621 GGGATAGGCTTTCAGTAGCTGTATATCGCCTTACCTGCAGTGTGTACTGTGGATTTTCC 4680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4621 GGGATAGGCTTTCAGTAGCTGTATATCGCCTTACCTGCAGTGTGTACTGTGGATTTTCC 4680

Qy  4681 TCCTACAATACTATGAGAAAAATATGAGGCAGATCAATAAGAAAGATCCCTTTTTCA 4740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4681 TCCTACAATACTATGAGAAAAATATGAGGCAGATCAATAAGAAAGATCCCTTTTTCA 4740

Qy  4741 GAAACCTTTCAACGAAGCTCAAAAATAGGAAGCTTCCAGAACCACCAGACAATGAGGATG 4800
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Db  4741 GAAACCTTTCAACGAAGCTCAAAAATAGGAAGCTTCCAGAACCACCAGACAATGAGGATG 4800

Qy  4801 AAGATGAAGATGTCAAAGCTCAAAAGTCGAAAGAAGACTAAAGTCAAAGAGTTGCCAGTGTT 4860
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Db  4801 AAGATGAAGATGTCAAAGCTCAAAAGTCGAAAGAAGACTAAAGTCAAAGAGTTGCCAGTGTT 4860

Qy  4861 GTGAGGAGAAACCATCCATTATGTGCAATTTGCATAAAGAATATGATGACAAGAAAG 4920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4861 GTGAGGAGAAACCATCCATTATGTGCAATTTGCATAAAGAATATGATGACAAGAAAG 4920

Qy  4921 ATTTTCTTCTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCGTGTGTGA 4980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4921 ATTTTCTTCTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCGTGTGTGA 4980

Qy  4981 AAAAAGGAGAGATCTTAGGACTATTGGGTGCTGCCAAATGTGCACATTATTA 5040
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Db  4981 AAAAAGGAGAGATCTTAGGACTATTGGGTGCTGCCAAATGTGCACATTATTA 5040

Qy  5041 ATATTCGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTTAGGAGATTATTCTT 5100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5041 ATATTCGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTTAGGAGATTATTCTT 5100

Qy  5101 CAGAGACAAGTGGCAAGTGACATGAAGATGAATCACTGAAGTGTATGGGTTACTGTCCTCAGATAAACC 5160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5101 CAGAGACAAGTGGCAAGTGACATGAAGATGAATCACTGAAGTGTATGGGTTACTGTCCTCAGATAAACC 5160

Qy  5161 CTTTGTGGCCAGATACTTAGGACTATTGCAGGAACATTTATGGAGCTGTCAAAGGAA 5220
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Db  5161 CTTTGTGTGGCCAGATACTTAGGACTATTGCAGGAACATTTATGGAGCTGTCAAAGGAA 5220

Qy  5221 TGAGTGCAAGTGACATGGAATCCTTCAGATTACTTTGCTAGATCAAGTGCAATTAACATGCACTTGATTTAAAAG 5280
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Db  5221 TGAGTGCAAGTGACATGGAATCCTTCAGATTACTTTGCTAGATCAAGTGCAATTAACATGCACTTGATTTAAAAG 5280

Qy  5281 AACATCTTCAGAAGACTTCGAGAAGACTGTAAAGAAACTACCTGCAGGAACATCTTAAACAGAAGT 5340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5281 AACATCTTCAGAAGACTTCGAGAAGACTGTAAAGAAACTACCTGCAGGAACATCTTAAACAGAAGT 5340

Qy  5341 CTCTAAGTATGCTAGGGAATCCTCAGATTACTTGCTAGATGGAACCATCTACAGGTATGG 5400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5341 CTCTAAGTATGCTAGGGAATCCTCAGATTACTTGCTAGATGGAACCATCTACAGGTATGG 5400

Qy  5401 ATCCCAAAGCCAAACACCAAACAGCACCACATGTGCGGCAGCAATTCGAACTGCATTTAAAAACAGAAAGC 5460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5401 ATCCCAAAGCCAAACACCAAACAGCACCACATGTGCGGCAGCAATTCGAACTGCATTTAAAAACAGAAAGC 5460
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Db  5461 GGGCTGCTATTCTGACCACTCACTATGTGAGGAGGCAGAGGCGCTGTCTGTGATCGAGTAG 5520
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Qy  5461 GGGCTGCTATTCTGACCACTCACTATGTGAGGAGGCAGAGGCGCTGTCTGTGATCGAGTAG 5520

Qy  5521 CTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTAAAGAGTAAAT 5580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5521 CTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTAAAGAGTAAAT 5580

Qy  5581 TTGGAAAAGGCTACTTTTGGAAATTAAATTAAATTGAAGGACTGGATAGAAAACCTAGAAGTAG 5640
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Db  5581 TTGGAAAAGGCTACTTTTGGAAATTAAATTAAATTGAAGGACTGGATAGAAAACCTAGAAGTAG 5640

Qy  5641 ACCGCCTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAGGAAAGTTTT 5700
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Db  5641 ACCGCCTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAGGAAAGTTTT 5700

Qy  5701 CTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTCACAATCTTTT 5760
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Db  5701 CTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTCACAATCTTTT 5760

Qy  5761 TTAAGCTGGAAGAAGCTAAACATGCTTTGCCATTGAAGAATATAGCTTTTCTCAAGCAA 5820
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Db  5761 TTAAGCTGGAAGAAGCTAAACATGCTTTGCCATTGAAGAATATAGCTTTTCTCAAGCAA 5820

Qy  5821 CATTGGAACAGGTTTTTGTAGAACTCACTAAAGAACAAGAGGAAGAGATAGAGTAGTTGTG 5880
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Db  5821 CATTGGAACAGGTTTTTGTAGAACTCACTAAAGAACAAGAGGAAGAGATAGAGTAGTTGTG 5880

Qy  5881 GAACTTTAAACAGCACACTTTGGTGGAACAAGCAACAAGAGAAGATAGAGTAGTATTTGAA 5940
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Db  5881 GAACTTTAAACAGCACACTTTGGTGGAACAAGCAACAAGAGAAGATAGAGTAGTATTTGAA 5940

Qy  5941 TTTGTATTGTTCGGTCGCTACTGGGACTTCTTTTCTTTTTCACTTAATTTTAACTTTGG 6000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5941 TTTGTATTGTTCGGTCGCTACTGGGACTTCTTTTCTTTTTCACTTAATTTTAACTTTGG 6000

Qy  6001 TTTAAAAAGTTTTTATTGGAATGTAACTGGAATGGAAACCACTTGAAATTTTTC 6060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6001 TTTAAAAAGTTTTTATTGGAATGTAACTGGAATGGAAACCACTTGAAATTTTTC 6060

Qy  6061 TAAGCTCCTTAATTGAAAATGCTGTGGTTTGTGTTTGCTTTTCTTTCTTTAATAAAACGTAT 6120
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Db  6061 TAAGCTCCTTAATTGAAAATGCTGTGGTTTGTGTTTGCTTTTCTTTCTTTAATAAAACGTAT 6120

Qy  6121 GTATAATTAAGTGAAGCTGCATGTTGTATTGTGAGTATATAGTTTGTATG 6180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6121 GTATAATTAAGTGAAGCTGCATGTTGTATTGTGAGTATATAGTTTGTATG 6180

Qy  6181 TCATCTTTTTCACCATTCAGAAACAGTGCTTCTGATTTGTGATTTGTAAGGAATTGTAAT 6240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6181 TCATCTTTTTCACCATTCAGAAACAGTGCTTCTGATTTGTGATTTGTAAGGAATTGTAAT 6240

Qy  6241 AGAATAGTTTATTTTAAGTTATCTTAAGTTATGCCATCTTCTTAAATAAGTAACGTA 6300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6241 AGAATAGTTTATTTTAAGTTATCTTAAGTTATGCCATCTTCTTAAATAAGTAACGTA 6300

Qy  6301 ATGTTCCAATCTAAATAAAAATAATACATAAAGATACAATAAAGC 6360
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Db  6301 ATGTTCCAATCTAAATAAAAATAATACATAAAGATACAATAAAGC 6360

Qy  6361 AATGTGAAAGTTTCTTGCTTCCTTTTAATTTCTAAAAAAGCCACTTGAATGGAAGT 6420
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Db  6361 AATGTGAAAGTTTCTTGCTTCCTTTTAATTTCTAAAAAAGCCACTTGAATGGAAGT 6420

Qy  6421 TGTCATCCGTAAAAGCTGAAGTGTAAGCACTGAGGAA 6480
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Db  6421 TGTCATCCGTAAAAGCTGAAGTGTAAGCACTGAGGAA 6480

Qy  6481 AGTTATATCCACTAGGTGGCAGTCATTGATCATAATAAGTGAAAT 6525
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Db  6481 AGTTATATCCACTAGGTGGCAGTCATTGATCATAATAAGTGAAAT 6525
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RESULT 2
US-10-343-903-33
; Sequence 33, Application US/10343903
; Publication No. US20040224911A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry;
; APPLICANT: THORNTON, Michael; RAMKUMAR, Jayalaxmi;
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda;
; APPLICANT: BAUGHN, Mariah R.; YANG, Junming;
; APPLICANT: YAO, Monique G.; LAL, Preeti G.;
; APPLICANT: CHAWLA, Narinder K.; GANDHI, Ameena R.;
; APPLICANT: HAFALIA, April J.A.; NGUYEN, Danniel B.;
; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
; APPLICANT: TRIBOULEY, Catherine M.; LU, Dyung Aina M.;
; APPLICANT: XU, Yuming; REDDY, Roopa;
; APPLICANT: HERNANDEZ, Roberto; BOROWSKY, Mark L.;
; APPLICANT: LO, Terence P.; LU, Yan;
; APPLICANT: POLICKY, Jennifer L.; GREENE, Barrie D.;
; APPLICANT: SANJANWALA, Madhusudan M.; RAUMANN, Brigette E.;
; APPLICANT: BURFORD, Neil; ISON, Craig H.;
; APPLICANT: LEE, Ernestine A.; DING, Li;
; APPLICANT: DAS, Debopriya; KALLICK, Deborah A.;
; APPLICANT: KHAN, Farrah A.; SEILHAMER, Jeffrey J.;
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0183 USN
; CURRENT APPLICATION NUMBER: US/10/343,903
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: PCT/US01/24217
; PRIOR APPLICATION FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/231,434
; PRIOR APPLICATION FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/230,067
; PRIOR APPLICATION FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/228,140
; PRIOR APPLICATION FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/226,410
; PRIOR APPLICATION FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/224,456
; PRIOR APPLICATION FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/223,269
; PRIOR APPLICATION FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 6369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2798241CB1
US-10-343-903-33

Query Match   93.8%; Score 6122.8; DB 18; Length 6369;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 6127; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

Qy   1 AAAATGTTGATATTTCTCCTTAGCAGGCTGTCAACCAGGTTAGGTTCAGGTCATAAGTTT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   228 AAAATGTTGATATTTCTCCTTAGCAGGCTGTCAACCAGGTTAGGTTCAGGTCATAAGTTT 287

Qy   61 CTACCCACATTCTTGAACTGTAGTTGTCATTGTTCATTTTAGTTTATTTTTCAAAAACTTTGCAG 120
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Qy   121 TACCTTTTTGGTCTGTCTGTGTGCCTTGCCAGTGAACAGTCTGGATTTGGACAGTGGT 180
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Db   348 TACCTTTTTGGTCTGTCTGTGTGCCTTGCCAGTGAACAGTCTGGATTTGGACAGTGGT 407

Qy   181 CTGTCTGTTAGTTCAGTTTCTCAAGCCTTTGTCACACTAATAGGATTGGATTTATGTATG 240
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Db   408 CTGTCTGTTAGTTCAGTTTCTCAAGCCTTTGTCACACTAATAGGATTGGATTTATGTATG 467

Qy   241 TCCAGCTTGGGAATTATTACACGGAGGATTAAAAACACTTTTAGAGTGCTTCCTGAGCTC 300
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Db   468 TCCAGCTTGGGAATTATTACACGGAGGATTAAAAACACTTTTAGAGTGCTTCCTGAGCTC 527

Qy   301 TCTTTCTATTGTTCCCCTTCACTTTTTGCTTCCCTGTGGCTGCTGTTTCTATCCTCC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   528 TCTTTCTATTGTTCCCCTTCTACTTTTTGCTTCCCTGTGGCTGCTGTTTCTATCCTCC 587

Qy   361 AGCCAGAGAGCTAGTGTTTATTTTCTCACATTGTGTGTACACACTTGTGCAGCTGCAACCAC 420
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Db   588 AGCCAGAGAGCTAGTGTTTATTTTCTCACATTGTGTGTACACACTTGTGCAGCTGCAACCAC 647

Qy   421 CATATCAGGGCCCAATGGTAGGAGGTAGAGAGAAAGCAAGAAGGATTGGCCTCATCC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   648 CATATCCAGGGCCCAATGGTAGGAGGTAGAGAGAAAGCAAGAAGGATTGGCCTCATCC 707

Qy   481 TCTTACAACGATAGTTCCATTGAATAGAGAGAGAAAGTTTTCCTGCCTCCAGAGTGTTGGCT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   708 TCTTACAACGATAGTTCCATTGAATAGAGAGAGAAAGTTTTCCTGCCTCCAGAGTGTTGGCT 767

Qy   541 GCACTAGGCTTTGTACTGTAGTCTGGCCCTGTTACCATGGATTGCTGCATGTGGGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   768 GCACTAGGCTTTGTACTGTAGTCTGGCCCTGTTACCATGGATTGCTGCATGTGGGG 827

Qy   601 ATACAGGAGAATTCAGAAAGAAAAGATTTGCTATTTCTACATTCTCCCTGAGCATT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   828 ATACAGGAGAATTCAGAAAGAAAAAGATTTGCTATTTCTACATTCTCCCTGAGCATT 887

Qy   661 AAGACCTCCCTGCCCATTCCAATTCCAATTCAAAGCTTCTTCTGGAGCTGCCTCTGT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   888 AAGACCTCCCTGCCCATTCCAATTCCAATTCAAAGCTTCTTCTGGAGCTGCCTCTGT 947

Qy   721 GGGCGGTTCGGGAGATACCAAAGGAGAAAAAGTACCACTGTGATATGGTGGTATTTCAA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   948 GGGCGGTTCGGGAGATACCAAAGGAGAAAAAGTACCACTGTGATATGGTGGTATTTCAA 1007

Qy   781 ATTCTGGTCTACCCATTCACATGCCTTGTTACTTTGTACTTTGTTTCAGAGCTGACAGATTGCTGCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1008 ATTCTGGTCTACCCATTCACATGCCTTGTTACTTTGTTACTTTGTTTCAGAGCTGACAGATTGCTGCT 1067

Qy   841 CCATGCAATTCGTCCAGTTTCCTAGAGAGACAGCTGGAGTATGCTTAATCCATCTTAC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1068 CCATGCAATTCGTCCAGTTTCCTAGAGAGACAGCTGGAGTATGCTTAATCCATCTTAC 1127

Qy   901 CTGGGACTGAAACAGCTGCTTATTTTGCCGTTAAAAATTACACAGTTTACTGCGTGGC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1128 CTGGGACTGAAACAGCTGCTTATTTTGCCGTTAAAAATTACACAGTTTACTGCGTGGC 1187

Qy   961 TCCGGGTTGTTGTTGTTTGTTTGTTTCCTCTTAATAGGTTTTATTCAGAAAACATGTCCACTG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1188 TCCGGGTTGTTGTTGTTTGTTTGTTTCCTCTTAATAGGTTTTATTCAGAAAACATGTCCACTG 1247

Qy   1021 CAATTAGGGAGGTAGGAGTTGGAGACAGCAGGACCAGAGACACTTCTACTGAAGAATTACTTAA 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1248 CAATTAGGGAGGTAGGAGTTGGAGACAGCAGGACCAGAGACACTTCTACTGAAGAATTACTTAA 1307

Qy   1081 TTAAATGCAGAACCAAAAGAGTAGTGTTCAGAAATTCTTTTCCACTATTTTTTTTAT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1308 TTAAATGCAGAACCAAAAGAGTAGTGTTCAGAAATTCTTTTCCACTATTTTTTTTAT 1367

Qy   1141 TTTGGTTAATATTAATTAGCATGATGCATCCAAATAAGAAGAAGTGCCTAATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1368 TTTGGTTAATATTAATTAGCATGATGCATCCAAATAAGAAGAAGTGCCTAATA 1427

Qy   1201 TAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATCTTCAATTCTTGGATATACTCCAG 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1428 TAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATCTTCAATTCTTGGATATACTCCAG 1487

Qy   1261 TGACTAATATTACAAGCAGCATCATGCGAGAAAGTGTCTACTGATCATCTACCTGATGTCA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1488 TGACTAATATTACAAGCAGCATCATGCGAGAAAGTGTCTACTGATCATCTACCTGATGTCA 1547

Qy   1321 TAATTACTGAAGAATATACAAATGAAAAGAAAATGTTAACATCCAGTCTCTCTAAGCCGA 1380

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Db  1548 TAATTACTGAAGATATACAAATGAAAAGAAGAATGTTAACATCCAGTCCTCTCAAGCCGA 1607
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1381 GCAACTTGTAGGTGTGGTTTTCAAAGACTCCATGTCCTATGAACTTCGTTTTTTTTCCTG 1440

Db  1608 GCAACTTGTAGGTGTGGTTTTCAAAGACTCCATGTCCTATGAACTTCGTTTTTTTTCCTG 1667
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1441 ATATGATTCCAGTATCTTCTATTTATATGATTCAAGAGCTGGCTGTTCAAAATCATGTG 1500

Db  1668 ATATGATTCCAGTATCTTCTATTTATATGATTCAAGAGCTGGCTGTTCAAAATCATGTG 1727
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1501 AGGCTGCTCAGTACTGGTCCTCAGGTTTCACAGTTTTACAAGCATCCATAGATGCTGCCA 1560

Db  1728 AGGCTGCTCAGTACTGGTCCTCAGGTTTCACAGTTTTACAAGCATCCATAGATGCTGCCA 1787
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Qy  1561 TTATACAGTTGAAGACCAATGTTCTCTTGGAAGGAGCTGGAGTCAACTAAAGCTGTTA 1620

Db  1788 TTATACAGTTGAAGACCAATGTTCTCTTGGAAGGAGCTGGAGTCAACTAAAGCTGTTA 1847
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Qy  1621 TTATGGGAGAAACTGCTGTTGTGTAGAAATAGATACCTTTCCCCGAGGAGTAATTTTAATAT 1680

Db  1848 TTATGGGAGAAACTGCTGTTGTGTAGAAATAGATACCTTTCCCCGAGGAGTAATTTTAATAT 1907
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Qy  1681 ACCTAGTTATAGACATTTCACCTTTGATACTTTTGGCAATTCATCGTAGCAGAAA 1740

Db  1908 ACCTAGTTATAGACATTTCACCTTTGATACTTTTGGCAATTCATCGTAGCAGAAA 1967
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Qy  1741 AAGAAAAATAAAAGATTTTTAAAGATAATGGGACTTCATGATACTGCCTTTTGGC 1800

Db  1968 AAGAAAAATAAAAGATTTTTAAAGATAATGGGACTTCATGATACTGCCTTTTGGC 2027
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Qy  1801 TTTCCTGGGTTCTTCTATATACAAGTTTAATTTTTCTTATGTCCCTTCTTATGGCAGTCA 1860

Db  2028 TTTCCTGGGTTCTTCTATATACAAGTTTAATTTTTCTTATGTCCCTTCTTATGGCAGTCA 2087
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Qy  1861 TTGGCACAGTTCTTTGTATTCTCAAAGTAGCAGCATTGATATTCTGCTTTTT 1920

Db  2088 TTGGCACAGTTCTTTGTATTCTCAAAGTAGCAGCATTGATATTCTGCTTTTT 2147
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Qy  1921 TCCTTTATGGATTATCATCGTATTTTTTGCTTTAATGCTGACACCTCTTTTTTAAAAAAT 1980

Db  2148 TCCTTTATGGATTATCATCGTATTTTTTGCTTTAATGCTGACACCTCTTTTTTAAAAAAT 2207
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Qy  1981 CAAAACATGGGAATAGTTGAATTTTTGTTACTGTGGCTTTTGGTTATTGGCCCTTA 2040

Db  2208 CAAAACATGGGAATAGTTGAATTTTTGTTACTGTGGCTTTTGGTTATTGGCCCTTA 2267
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Qy  2041 TGATAATCCTCATAGAAAGTTTCCTCCAAATCGTTAGTGTGGCCTTTCAGTCCTTTCTGTC 2100

Db  2268 TGATAATCCTCATAGAAAGTTTCCTCCAAATCGTTAGTGTGGCCTTTCAGTCCTTTCTGTC 2327
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Qy  2101 ACTGTACTTTGTGATTGGATTGGTATTGCACAGTTATTGCACAGGCCATTAGAAGATTTTAATGAAGT 2160

Db  2328 ACTGTACTTTGTGATTGGATTGGTATTGCACAGTTATTGCACAGGCCATTAGAAGATTTTAATGAAGT 2387
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2161 CTTCATTTTCAAATTGACTGCAGGCAGGATCCCATATCCTCTAATTATTACAATTATCATGCTCA 2220

Db  2388 CTTCATTTTCAAATTGACTGCAGGCAGGATCCCATATCCTCTAATTATTACAATTATCATGCTCA 2447
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Qy  2221 CACTTAATAGTATATTCTATGTCATGTATGTTGGCTCTCTGGCTCTGATCAAGTCATCATTCCAGGGG 2280

Db  2448 CACTTAATAGTATATTCTATGTCATGTATGTTGGCTCTCTGGCTCTGATCAAGTCATCATTCCAGGGG 2507
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Qy  2281 AATTTGGCTTACCGGAGAATCATCTTTATATTTCTGAAGCCTTCATATGGTCAAAGAGTA 2340

Db  2508 AATTTGGCTTACCGGAGAATCATCTTTATATTTCTGAAGCCTTCATATGGTCAAAGAGCA 2567
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Qy  2341 AAAGAAATTATGAGGAGTATATGAGGAGTTATCAGAGGCAATGTTAATGGAAATATAGTAGTTTTAGTGAAA 2400

Db  2568 AAAGAAATTATGAGGAGTATATGAGGAGTTATCAGAGGCAATGTTAATGGAAATATAGTAGTTTTAGTGAAA 2627
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Qy  2401 TTATTGAGCCAGTTCTTCAGAATTGTTGAGGAAAGAAGCCATAAGAAGAATTAGTGGTATTC 2460
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Db  2628 TTATTGAGCCAGTTCTTCAGAATTGTTGAGGAAAGAAGCCATAAGAAGAATTAGTGGTTATTC 2687
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Qy  2461 AGAAGACATACAGAAGAAGAAGGTGAAAAATGTGGAGGCTTTGAGAAATTGTCATTTGACA 2520

Db  2688 AGAAGACATACAGAAGAAGAAGGTGAAAAATGTGAAAATTTGTCATTTGACA 2747
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Qy  2521 TATATGAGGGTCAGATTCAGATTACTGCCTTACTGGCCCAGTGTGAACAGGAAGAGTACATTGA 2580

Db  2748 TATATGAGGGTCAGATTCAGATTACTGCCTTACTGGCCCACAGTGAACAGGAAGAGTACATTGA 2807
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Qy  2581 TGAATATTCTTGTGGACTCTGCCCACCTTCGTGATGGGTTTGCATCTATATGGACACA 2640

Db  2808 TGAATATTCTTGTGGACTCTGCCCACCTTCGTGATGGGTTTGCATCTATATGGACACA 2867
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Qy  2641 GAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGATTGGCATTTGTCCACAGT 2700

Db  2868 GAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGGCATTTGTCCACAGT 2927
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Qy  2701 TAGATATACACTTGATGTTTGACAGTAGAGAGAAAATTTATCAATTTTGGCTTCAATCA 2760

Db  2928 TAGATATACACTTGATGTTTGACAGTAGAGAGAAATTTATCAATTTTGGCTTCAATCA 2987
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Qy  2761 AAGGGATACCAGCCAACAATATAATCAAGAAGTGCAGAAGGTTTACTAGATTTAGACA 2820

Db  2988 AAGGGATACCAGCCAACAATATAATCAAGAAGTGCAGAAGGTTTACTAGATTTAGACA 3047
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Qy  2821 TGCAGACTATCAAAGATAACAAGAGTAAAAATTAAGTGGTGGTCAAAAAGAAAGCTGT 2880

Db  3048 TGCAGACTATCAAAGATAACAAGAGTAAAAATTAAGTGGTGGTCAAAAAGAAAGCTGT 3107
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Qy  2881 CATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTGCTCTAGATGAACCAACAGCTG 2940

Db  3108 CATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTGCTCTAGATGAACCAACAGCTG 3167
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Qy  2941 GAATGACCCCTGTTCTCGACATATGTGATGGAATCTTTAAAATACAGAAAAGCCAATC 3000

Db  3168 GAATGACCCCTGTTCTCGACATATGTGATGGAATCTTTAAAATCAGAAAAGCCAATC 3227
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Qy  3001 GGGTGACAGTGTTCAGTACTACTCATGAGAGCATGTACACATAGACAAAATATTGTGCCACAGATAGGAAAG 3060

Db  3228 GGGTGACAGTGTTCAGTACTACTCATGAGAGCATGTACACATAGACAAATATTGTGCCACAGATAGGAAAG 3287
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Qy  3061 CTGTGATATCACAAGGAATGCTGAAATGTGTTGGTTCCTCAAATGTTCCTCAAAAGTAAAT 3120

Db  3288 CTGTGATATCACAAGGAATGCTGAAATGTGTTGGTTCCTCAAATGTTCCTCAAAAGTAAAT 3347
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Qy  3121 GGGGATCGGCTACCGCCTGAGCATGTACCTGAGCATGTACACATAGACAAATATTGTGCCACAGATAGGAAAG 3180

Db  3348 GGGGATCGGCTACCGCCTGAGCATGTACCTGAGCATGTACACATAGACAAATATTGTGCCACAGATAGGAAAG 3407
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Qy  3181 CTTCACTGGTTAAACACAATACTGGAGCTACTTTATTACAACAGAATGACCACAACAAC 3240

Db  3408 CTTCACTGGTTAAACACAATACTGGAGCTACTTTATTACAACAGAATGACCACAACAAC 3467
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Qy  3241 TTGTGTATAGTCTTGCCTTGCCTTCAAGGACATGACAAATTTCAGGTTTGTTTCTGCCCTAG 3300

Db  3468 TTGTGTATAGTCTTGCCTTGCCTTCAAGGACATGACAAATTTCAGGTTTGTTTCTGCCCTAG 3527
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Qy  3301 ACAGTCATTCAAATTGGGTGTCATTCTATGTGTTCCATGACGACTTGGAAGACG 3360

Db  3528 ACAGTCATTCAAATTGGGTGTCATTCTATGTGTTCCATGACGACTTGGAAGACG 3587
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Qy  3361 TATTTTAAAGTGAAGTTAGAAGTTGAGCAAATTGACCAAGCAGATTATAGTGTATTTACTC 3420

Db  3588 TATTTTTAAAGTGAAGTTAGAAGTTGAGCAAATTGACCAAGCAGATTATAGTGTATTTACTC 3647
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Qy  3421 AGCAGCCACCTGGAGAAGAAATGGATTCAAAATCTTTGATGAAATGGAACGAGAGCTTAC 3480

Db  3648 AGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTGATGAAATGGAACGAGAGCTTAC 3707
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Qy  3481 TTATTCTTTCTGAAAACCAAGGCTTCTCCAGTGGAGCACCATGAGCACCAAGACAGA 3540

Db  3708 TTATTCTTTCTGAAAACCAAGGCTTCTCCAGTGGAGCACCATGAGCACCAAGAACAGA 3767
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Nucleotide sequence alignment (Qy vs Db) with numbered positions (columns at 3541–4847 and 4621–5760).

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Db  5928 CTTCCTATTTGGCTGGAAGAAGAGTGCTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTTCACAATCTTTTT  5987
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   277 ATAAGAAATATGAAGAGAGTGCTAATATAAGAACTCAATATAGAACTCATCCATGGACAAGTTACTCTTT  336

Qy  5761 TTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTTTCTCAAGCAA  5820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1234 CTAATCTAATTCTTGGATATACTCCAGTGACTAATATTACAGCAGCATCATGCGAGAAAG  1293

Db  5988 TTAAGCTGGAAGAAGCAAACATGCTTTTGCCATTGAAGAATATAGCTTTTCTCAAGCAA  6047
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Qy   337 CTAATCTAATTCTTGGATATACTCCAGTGACTAATATTACAGCAGCATCATGCGAGAAAG  396

Qy  5821 CATTGGAACACAGGTTTTTGTAGAACTCACTCAAAGAACACAGAGGAGGAAGATAATAGTGTG  5880
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Db  1294 TGTCTACTGATCATCTCACTGATGTCATAATTACTGAAGAATATACAGAAAAAGAAGAA  1353

Db  6048 CATTGGAACACAGGTTTTTGTAGAACTCACTCAAAGAACACAGAGGAGGAAGATAATAGTGTG  6107
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Qy   397 TGTCTACTGATCATCTCACTGATGTCATAATTACTGAAGAATATACAGAAAAAGAAGAA  456

Qy  5881 GAACTTAAACAGCACACACTTTGGTGGGAACGAACACAAGAACAGAGTAGTATTTGAA  5940
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Db  1354 TGTTAACATCCAGTCTCTCTAAGCCAGCAACTTGTAGGTGTGGTTTCAAAGACTCCA  1413

Db  6108 GAACTTAAACAGCACACACTTTGGTGGGAACGAACACAAGAACAGAGTAGTATTTGAA  6167
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Qy   457 TGTTAACATCCAGTCTCTCTAAGCCAGCAACTTGTAGGTGTGGTTTCAAAGACTCCA  516

Qy  5941 TTTGTATTGTTCCGGTCTGCTCGCCTACTGGGACTTCCTTCTTTCTTTCTTTCACTTAATTTAACTTTGG  6000
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Db  1414 TGTCCTATGACTTCGGTTTTTTCTGATAGATGATTCCAGTATCTTCTATTTATATGGATT  1473

Db  6168 TTTGTATTGTTCCGGTCTGCTCGCCTACTGGGACTTCCTTCTTTCTTTCTTTCACTTAATTTAACTTTGG  6227
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Qy   517 TGTCCTATGACTTCGGTTTTTTCTGATAGATGATTCCAGTATCTTCTATTTATATGGATT  576

Qy  6001 TTTAAAAAGTTTTTTATTGGAATGGTAACTGAATCGGAGAACCAAGAACGCACTTGAAATTTTTC  6060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1474 CAAGAGCTGGCTGTCAAAATCATGTGAGCGCTGCTCAGTACTGGTCCTCAGGTTCCACAG  1533

Db  6228 TTTAAAAAGTTTTTTATTGGAATGGTAACTGAATCGGAGAACCAAGAACGCACTTGAAATTTTTC  6287
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Qy   577 CAAGAGCTGGCTGTCAAAATCATGTGAGCGCTGCTCAGTACTGGTCCTCAGGTTCCACAG  636

Qy  6061 TAAGCTCCTTAATTGAAATGCTGTGGTTGTGTTTTTCTTTAAAATAAAAAACGTAT  6120
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Db  1534 TTTTACAAGCATCCATTAGATCTGCCATTATACAGTTGAAGACCAATGTTCTCTTGGA  1593

Db  6288 TAAGCTCCTTAATTGAAATGCTGTGGTTGTGTTTTTCTTTAAAATAAAAAACGTAT  6347
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   637 TTTTACAAGCATCCATTAGATCTGCCATTATACAGTTGAAGACCAATGTTCTCTTGGA  696

Qy  6121 GTATAATTAAGTAAGGTGAA  6135
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Db  6348 GTATAATTAAAAAAAA  6362

Db  1594 AGGAGCTGGAGTCAACTAAAGCTGTATTTATGGGAGAAAACTGCTGTTGTGTGAAATAGATA  1653
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   697 AGGAGCTGGAGTCAACTAAAGCTGTATTTATGGGAGAAAACTGCTGTTGTGTGAAATAGATA  756

Qy  1654 CCTTTCCCGAGGAGTAATTTAATTAATACCTAGTTATAGCATTTCACCTTTTGGATACT  1713
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Db   757 CCTTTCCCGAGGAGTAATTTAATTAATACCTAGTTATAGCATTTCACCTTTTGGATACT  816

Db  1714 TTTTGGCAATTCATATCGTAGCAGAGAAAAAGAAAAAATTTTAAAGATAA  1773
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Qy   817 TTTTGGCAATTCATATCGTAGCAGAGAAAAAGAAAAAATTTTAAAGATAA  876

Qy  1774 TGGGACTTCATGATACTGCCTTTGGCTTTCCTGGGTTCTTCTATATACAAGTTTAATTT  1833
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   877 TGGGACTTCATGATACTGCCTTTGGCTTTCCTGGGTTCTTCTATATACAAGTTTAATTT  936

Db  1834 TTCTTATGTCCCTTCTTATGGCAGTCATTGCGACAGCTTCTTGTATTCCTCAAAGTA  1893
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Qy   937 TTCTTATGTCCCTTCTTATGGCAGTCATTGCGACAGCTTCTTGTATTCCTCAAAGTA  996

Qy  1894 GCAGCATTGTGATATTTCTGTCTTTTTCCTTATGGATATCATCGTATTTTTGCTT  1953
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Db   997 GCAGCATTGTGATATTTCTGTCTTTTTCCTTATGGATATCATCGTATTTTTGCTT  1056

Db  1954 TAATGCTGACACCTCTTTAAAAATCAAAACATGTGGGAATAGTTGAATTTTTGTTA  2013
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1057 TAATGCTGACACCTCTTTAAAAATCAAAACATGTGGGAATAGTTGAATTTTTGTTA  1116

Qy  2014 CTGTGGCTTTTGGATTTATTGGCCTTATGATAATCCTATCAGAAAGTTTCCCAAATCGT  2073
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Db  1117 CTGTGGCTTTTGGATTTATTGGCCTTATGATAATCCTATCAGAAAGTTTCCCAAATCGT  1176

Db  2074 TAGTGTGGCTTTCAGTCCTTGCTCACTGTACTTTGTGATTGGTATTGCACAGGTCA  2133
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Qy  1177 TAGTGTGGCTTTCAGTCCTTGCTCACTGTACTTTGTGATTGGTATTGCACAGGTCA  1236

Qy  2134 TGCATTTAGAAGATTTTAATGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCATATC  2193
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Db  1237 TGCATTTAGAAGATTTTAATGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCATATC  1296

Db  2194 CTCTAATTATTACAATTACATGCTCACACTTAATTAATAGTATATTCATGTCATGATGCAGTCCACCA  2253
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Qy  1297 CTCTAATTATTACAATTACATGCTCACACTTAATTAATAGTATATTCATGTCATGATGCAGTCCAG  1356

Qy  2254 TCTATCTTGATCAAGTCAATTGGCTTACGGAGATCATCTTATATTTTTC  2313
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Db  1233 ...
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RESULT 3
US-10-090-458-4
; Sequence 4, Application US/10090458
; Publication No. US20020123107A1
GENERAL INFORMATION:
;   APPLICANT: Chen, Hongyun
;   APPLICANT: Kilinski, Ligia
;   APPLICANT: Le Bihan, Stephane
;   TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
;   FILE REFERENCE: 100103.403
;   CURRENT APPLICATION NUMBER: US/10/090,458
;   CURRENT FILING DATE: 2002-03-01
;   NUMBER OF SEQ ID NOS: 5
;   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
;   LENGTH: 5475
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 25
;   OTHER INFORMATION: n = A, T, C or G
US-10-090-458-4

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Query Match             82.3%;   Score 5373.2;  DB 13;  Length 5475;
Best Local Similarity   99.9%;   Pred. No. 0;
Matches 5375;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   994 AGGTTTATTCAGAAAAACATGTCCACTGCAATTAGGGAGGTTGGAGACAGGTTGGAGACAGACCA  1053
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1054 GAACACTTCTACTGAAGAATATTCTTACTTAATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGG  1113
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Db   157 GAACACTTCTACTGAAGAATTACTTAATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGG  216

Qy  1114 AAATTCTTTTCCACTATTTTTTTTTTTTTTTTGTTAATATTAATTAATTAGCATGATGCATCCAA  1173
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Db   217 AAATTCTTTTCCACTATTTTTTTTTTTTTTTTGTTAATATTAATTAGCATGATGCATCCAA  276

Qy  1174 ATAAGAAATATGAAGAGAGTGCTAATATAGAACTCAATATAGAACTCATCCATGGACAAGTTACTCTTT  1233
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Db  1233
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Db        1357 TCTATCTTGATCAAGTCATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 1416

Qy        2314 TGAAGCCTTCATATTGGTCAAAGAGTAAAAGAAATTATGAGGAGTTATCAGAGGGCAATG 2373
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Db        1417 TGAAGCCTTCATATTGGTCAAAGAGCAAAAGAAATTATGAGGAGTTATCAGAGGGCAATG 1476

Qy        2374 TTAATGGAAATATTAGTTTTAGTGAAATTATTGAGCCAGTTTCTTCAGAATTTGTAGGAA 2433
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Db        1477 TTAATGGAAATATTAGTTTTAGTGAAATTATTGAGCCAGTTTCTTCAGAATTTGTAGGAA 1536

Qy        2434 AAGAAGCCATAAGAATTAGTGGTATTCAGAAGACATACAGAAAGAAGGGTGAAAATGTGG 2493
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Db        1537 AAGAAGCCATAAGAATTAGTGGTATTCAGAAGACATACAGAAAGAAGGGTGAAAATGTGG 1596

Qy        2494 AGGCTTTGAGAAATTTGTCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCC 2553
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Db        1597 AGGCTTTGAGAAATTTGTCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCC 1656

Qy        2554 ACAGTGGAACAGGAAAGAGTACATTGATGAATATTCTTTGTGGACTCTGCCCACCTTCTG 2613
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Db        1657 ACAGTGGAACAGGAAAGAGTACATTGATGAATATTCTTTGTGGACTCTGCCCACCTTCTG 1716

Qy        2614 ATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA 2673
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Db        1717 ATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA 1776

Qy        2674 GAAAAATGATTGGCATTTGTCCACAGTTAGATATACACTTTGATGTTTTGACAGTAGAAG 2733
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1777 GAAAAATGATTGGCATTTGTCCACAGTTAGATATACACTTTGATGTTTTGACAGTAGAAG 1836

Qy        2734 AAAATTTATCAATTTTGGCTTCAATCAAAGGGATACCAGCCAACAATATAATACAAGAAG 2793
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1837 AAAATTTATCAATTTTGGCTTCAATCAAAGGGATACCAGCCAACAATATAATACAAGAAG 1896

Qy        2794 TGCAGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAAT 2853
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1897 TGCAGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAAT 1956

Qy        2854 TAAGTGGTGGTCAAAAAAGAAAGCTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGA 2913
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1957 TAAGTGGTGGTCAAAAAAGAAAGCTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGA 2016

Qy        2914 TACTGCTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGA 2973
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2017 TACTGCTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGA 2076

Qy        2974 ATCTTTTAAAATACAGAAAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTCATGGATG 3033
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2077 ATCTTTTAAAATACAGAAAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTCATGGATG 2136

Qy        3034 AAGCTGACATTCTTGCAGATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTG 3093
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2137 AAGCTGACATTCTTGCAGATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTG 2196

Qy        3094 GTTCTTCAATGTTCCTCAAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAG 3153
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2197 GTTCTTCAATGTTCCTCAAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAG 2256

Qy        3154 ACAAATATTGTGCCACAGAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTA 3213
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2257 ACAAATATTGTGCCACAGAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTA 2316

Qy        3214 CTTTATTACAACAGAATGACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACA 3273
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2317 CTTTATTACAACAGAATGACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACA 2376

Qy        3274 AATTTTCAGGTTTGTTTTCTGCCCTAGACAGTCATTCAAATTTGGGTGTCATTTCTTATG 3333
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2377 AATTTTCAGGTTTGTTTTCTGCCCTAGACAGTCATTCAAATTTGGGTGTCATTTCTTATG 2436

Qy        3334 GTGTTTCCATGACGACTTTGGAAGACGTATTTTTAAAGCTAGAAGTTGAAGCAGAAATTG 3393
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2437 GTGTTTCCATGACGACTTTGGAAGACGTATTTTTAAAGCTAGAAGTTGAAGCAGAAATTG 2496

Qy        3394 ACCAAGCAGATTATAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAAT 3453
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2497 ACCAAGCAGATTATAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAAT 2556

Qy        3454 CTTTTGATGAAATGGAACAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCTCTAGTGA 3513
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2557 CTTTTGATGAAATGGAACAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCTCTAGTGA 2616

Qy        3514 GCACCATGAGCCTTTGGAAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCT 3573
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2617 GCACCATGAGCCTTTGGAAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCT 2676

Qy        3574 TGAAACGTGAAAGTAAATCAGTGAGATCAGTGTTGCTTCTGCTTTTAATTTTTTTCACAG 3633
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2677 TGAAACGTGAAAGTAAATCAGTGAGATCAGTGTTGCTTCTGCTTTTAATTTTTTTCACAG 2736

Qy        3634 TTCAGATTTTTATGTTTTTGGTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAAC 3693
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2737 TTCAGATTTTTATGTTTTTGGTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAAC 2796

Qy        3694 TTGTTCCAGACTTATATTTTCTAAAACCTGGAGACAAACCACATAAATACAAAACAAGTC 3753
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2797 TTGTTCCAGACTTATATTTTCTAAAACCTGGAGACAAACCACATAAATACAAAACAAGTC 2856

Qy        3754 TGCTTCTTCAAAATTCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGCC 3813
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2857 TGCTTCTTCAAAATTCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGCC 2916

Qy        3814 AGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTG 3873
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2917 AGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTG 2976

Qy        3874 CGGCTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTA 3933
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2977 CGGCTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTA 3036

Qy        3934 CTATGGTTTATTCTTTACCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCATT 3993
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3037 CTATGGTTTATTCTTTACCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCATT 3096

Qy        3994 TAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGATA 4053
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3097 TAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGATA 3156

Qy        4054 TAGTTTTTAAAATTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAA 4113
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3157 TAGTTTTTAAAATTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAA 3216

Qy        4114 TGCCACCTTACTTTGCCATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATACTCAAC 4173
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3217 TGCCACCTTACTTTGCCATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATACTCAAC 3276

Qy        4174 TTAAACTTTCAGGTCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCC 4233
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3277 TTAAACTTTCAGGTCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCC 3336

Qy        4234 CCTTATTTTTATCATTCTTATTTTGATGCTAGGAAGCTTACTGGCATTTCATTATGGAT 4293
               |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db        3337 CCTTATTTTTATCATTCTTATTTTGATGCTAGGAAGCTTATTGGCATTTCATTATGGAT 3396

Qy        4294 TATATTTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTTGCCTTATTGGTTATGTTCCAT 4353
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3397 TATATTTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTTGCCTTATTGGTTATGTTCCAT 3456

Qy        4354 CAGTTATTCTGTTCACTTATATTGCTTCTTTCACCTTTAAGAAAATTTTAAATACCAAAG 4413
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3457 CAGTTATTCTGTTCACTTATATTGCTTCTTTCACCTTTAAGAAAATTTTAAATACCAAAG 3516

Qy        4414 AATTTGGTCATTTATCTATTCTGTGGCAGCGTTGNCTTGTATTGCAATCACTGAAATAA 4473
               |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        3517 AATTTGGTCATTTATCTATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAA 3576
```

Qy 4474 CTTCCTTTATGGGATACACAATTGCAACTATTCTTCATTATGCCTTTTGTATCATCATTC 4533
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Db 3577 CTTTCTTTTATGGGATACACACAATTGCAACTATTCTTCATTATGCCTTTTGTATCATCATTC 3636

Qy 4534 CAATCTATCCACTTCTAGGTTGCCTGATTTCTTCATAAAGATTTCTTGGAGAATGTAC 4593
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3637 CAATCTATCCACTTCTAGGTTGCCTGATTTCTTCATAAAGATTTCTTGGAGAATGTAC 3696

Qy 4594 GAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTGACTTGTTATATCGGCCTT 4653
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3697 GAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTGACTTGTTATATCGGCCTT 3756

Qy 4654 ACCTGCAGTGTGTACTGTGGATTTCCTCTTACAATACTATGAGAAAAATATGGAGGCA 4713
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3757 ACCTGCAGTGTGTACTGTGGATTTCCTCTTACAATACTATGAGAAAAATATGGAGGCA 3816

Qy 4714 GATCAATAAGAAAAGATCCCTTTTCAGAAACCTTTCAACGAAGTCTAAAAATAGGAAGC 4773
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3817 GATCAATAAGAAAAGATCCCTTTTCAGAAACCTTTCAACGAAGTCTAAAAATAGGAAGC 3876

Qy 4774 TTCCAGAACCACCAGACAATGAGGATGAAGATGTCAAAGCTGAAAGACTAAAGG 4833
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3877 TTCCAGAACCACCAGACAATGAGGATGAAGATGTCAAAGCTGAAAGACTAAAGG 3936

Qy 4834 TCAAAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCATCCATTATGGTCAGCAATT 4893
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3937 TCAAAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCATCCATTATGGTCAGCAATT 3996

Qy 4894 TGCATAAAGAATGATGACAAGAAAGATTTCTCTTTCAAGAAAGTAAAGAAAGTGG 4953
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3997 TGCATAAAGAATGATGACAAGAAAGATTTCTCTTTCAAGAAAGTAAAGAAAGTGG 4056

Qy 4954 CAACTAAATACATCTCTTTCTGTGTGAAAAAAGGAGAATCTTAGGACTATTGGGTCCAA 5013
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4057 CAACTAAATACATCTCTTTCTGTGTGAAAAAAGGAGAATCTTAGGACTATTGGGTCCAA 4116

Qy 5014 ATGGTGCTGCAAAAGCACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAG 5073
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Db 4117 ATGGTGCTGCAAAAGCACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAG 4176

Qy 5074 GCCAGGTATTTTTTAGGAGATTATTCTTCAGAGACAAGTGAAGGTGAAGATGATGAAGT 5133
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Db 4177 GCCAGGTATTTTTTAGGAGATTATTCTTCAGAGACAAGTGAAGGTGAAGATGATGAAGT 4236

Qy 5134 GTATGGGTTACTGTCCCAGATAAACCCTTGTGGCCAGATACTACATTGCAGGAACATT 5193
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4237 GTATGGGTTACTGTCCCAGATAAACCCTTGTGGCCAGATACTACATTGCAGGAACATT 4296

Qy 5194 TTGAAAATTATGGAGCTGTCAAGGAATGCAAGTGCAATGACAATGAAGAAGTCATAAGTC 5253
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Db 4297 TTGAAAATTATGGAGCTGTCAAGGAATGCAAGTGCAATGACAATGAAGAAGTCATAAGTC 4356

Qy 5254 GAATAACACATGCAAACGAAGTTGTGTTTTTGCCTTAAAGAAGAACATCCTCAGATTACTT 5313
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Db 4357 GAATAACACATGCAAACGAAGTTGTGTTTTTGCCTTAAAGAAGAACATCCTCAGATTACTT 4416

Qy 5314 CAGGAATCAAACGAAAGTTGTGTTTGCTCTAAGTATGCTAGGGAATCCTAGATTACTT 5373
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4417 CAGGAATCAAACGAAAGTTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTAGATTACTT 4476

Qy 5374 TGCTAGATGAACCATCTACAGGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAA 5433
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4477 TGCTAGATGAACCATCTACAGGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAA 4536

Qy 5434 TTCGAACTGCATTTAAAAACAGAAAGCCGGCTCTATTCTGACCACTCCACTATATGGAGG 5493
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4537 TTCGAACTGCATTTAAAAACAGAAAGCCGGCTCTATTCTGACCACTCCACTATATGGAGG 4596

Qy 5494 AGGCAGAGAGCGCTGTCGTGATCGAGTAGCTATCATGGTTGTCTGGGCAGTTAAGATGTATCG 5553
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4597 AGGCAGAGAGCGCTGTCGTGATCGAGTAGCTATCATGGTTGTCTGGGCAGTTAAGATGTATCG 4656

Qy 5554 GAACAGTACAACATCTAAAGAGTAAATTTGGAAAGGCTACTTTTGGAAATTAAATTGA 5613

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
4657 GAACAGTACAACATCTAAAGAGTAAATTTGGAAAGGCTACTTTTGGAAATTAAATTGA 4716

Qy 5614 AGGACTGGATAGAAAAACCTAGAAGTAGAGCCCTTCAAAGAGAAATTCAGTATATTTTCC 5673
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4717 AGGACTGGATAGAAAAACCTAGAAGTAGACCGCCCTTCAAAGAGAAATTCAGTATATTTTCC 4776

Qy 5674 CAAATGCAAGCCGTCAGGAAAGTTTTCTTCTATTTGGCTTATAAAAATTCCTAGGGAAG 5733
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4777 CAAATGCAAGCCGTCAGGAAAGTTTTTCTTCATTTGGCTTATAAAAATTCCTAGGAAG 4836

Qy 5734 ATGTTCAGTCCCTTCACAATCTTTTTAGCTGAAGAAGCTAAACATGCTTTTGCCA 5793
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4837 ATGTTCAGTCCCTTCACAATCTTTTTAAGCTGAAGAAGCTAAACATGCTTTTGCCA 4896

Qy 5794 TTGAAGAATATAGCTTTTCTCAAGCAACATTGGAACAGGTTTTTGTAGAACTCACTAAAG 5853
         ||||||||||||||||||||||||||| ||||||||||||| |||||||||||||||||
Db 4897 TTGAAGAATATAGCTTTTCTCAAGCACATTGGAACAGGTTTTGTAGAACTCACTAAAG 4956

Qy 5854 AACAAGAGGAGGAAGAATAATAGTTGTGGAACTTAAACAGCACACTTGGTGGGAACGAA 5913
         ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db 4957 AACAAGAGGAGGAAGAATAATAGTTGTGGAACTTAAACAGCACACTTGGTGGGAACGAA 5016

Qy 5914 CACAAGAAGATAGAGTAGTATTTGTATTGTCGGTCTGCTTACTGGGGACTTCT 5973
         |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db 5017 CACAAGAAGATAGAGTAGTATTTGTATTGTCCGGTCTGCTTACTGGGGACTTCT 5076

Qy 5974 TTCTTTTTCACTTAATTTAACTTTGGTTTAAAAAGTTTTTATTGGAATGGTAACTGGA 6033
         ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db 5077 TTCTTTTTCACTTAATTTTAACTTTGGTTTAAAAAGTTTTTATTGGAATGGTAACTGGA 5136

Qy 6034 GAACCAAGAACGCACTGAAATTTTCTAAGCTCCTTAAATTAAGTGAAGTGCATGTTTGTATTGA 6093
         ||||||||||||||| |||||||||||||||||||||| |||||||||||||||||||
Db 5137 GAACCAAGAACGCACTTGATTTTTCTAAGCTCCTTAAATTAAGTGAAGTGCATGTTGGTGTG 5196

Qy 6094 TTTGCTTTTCTTAAATAAAACGTATGTATAAATAAAACGTATGTATAATAAAACGTGTATTGA 6153
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5197 TTTGCTTTTCTTAAATAAAACGTATGTATAAATAAAACGTATGTATAATAAAACGTGTATTGA 5256

Qy 6154 AGTATATTGAACTATATAGTTGTATGTCATCTTTTCACCATTCAGAAACAGTGCTTCT 6213
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Db 5257 AGTATATTGAACTATATAGTTGTATGTCATCTTTTCACCATTCAGAAACAGTGCTTCT 5316

Qy 6214 GAATTTGTGATTTAAAGGAATTGTATAGAATGTAATAAAACTAATACATAA 6273
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Db 5317 GAATTTGTGATTTAAAGGAATTGTATAGAATGTAATAAAACTAATACATAA 5376

Qy 6274 TATGCCATCTTCTTAAATAAGTACGTAATGTTCCAATCTAAATAAAAACTAATACATAA 6333
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5377 TATGCCATCTTCTTAAATAAGTACGTAATGTTCCAATCTAAATAAAAACTAATTCATAA 5436

Qy 6334 CTAATGCATAGAAAAAGATACATAAAGCAATGTGAAAGTT 6372
         |||||||||||||||||||||||||||||||||||||||
Db 5437 CTAATGCATAGAAAAAGATACATAAAGCAATGTGAAAGTT 5475

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 25, 2888, 2889
; OTHER INFORMATION: n = A,T,C or G
US-10-090-458-1

Query Match      80.5%;  Score 5255.8;  DB 13;  Length 5463;
Best Local Similarity  98.9%;  Pred. No. 0;  Indels  8;  Gaps  3;
Matches 5340;  Conservative  0;  Mismatches  0;
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Qy    994 AGGTTTATTCAGAAACATGTCCACTGCAATTAGGAGGAGTTGGAGACAGACCA 1053
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Db     97 AGGTTTATTCAGAAACATGTCCACTGCAATTAGGAGGAGTTGGAGACAGACCA  156

Db   1054 GAACACTTCTACTGAAGAATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGG 1113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    157 GAACACTTCTACTGAAGAATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGG  216

Qy   1114 AAATTCTTTTCCACATATTTTTTTATTTTGGTTAATATTAATTAGCATGATGCATCCAA 1173
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Db    217 AAATTCTTTTCAC TATTTTTTTATTTTGGTTAATATTAATTAGCATGATGCATCCAA   276

Qy   1174 ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTACTCTTT 1233
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Db    277 ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTACTCTTT  336

Qy   1234 CTAATCTAATTCTTGGATATACTCCAGTGACTAATAATTACAAGCAGCATCATCATCCAGTGACTAATAATTACAAGCAGCATCATCAGCAGAAAG 1293
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 CTAATCTAATTCTTGGATATACTCCAGTGACTAATAATTACAAGCAGCATCATCAGCAGAAAG  396

Qy   1294 TGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAGAAA 1353
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Db    397 TGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAGAAA  456

Qy   1354 TGTTAAATCCAGTCTCTCTAAGCGCAACTTTGTAGGTGTTGGTTTCAAAGACTCCA 1413
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457 TGTTAAATCCAGTCTCTCTAAGCGCAACTTTGTAGGTGTTGGTTTCAAAGACTCCA 516

Qy   1414 TGTCCTATGAACTTCGTTTTTTTCCTGATATGATTCCAGTACTTCATTTATATGGATT 1473
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    517 TGTCCTATGAACTTCGTTTTTTTCCTGATATGATTCCAGTACTTCATTTATATGGATT 576

Qy   1474 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTCACAG 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    577 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTCACAG  636

Qy   1534 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGA 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    637 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGA  696

Qy   1594 AGGAGCTGAGTCAACTAAAGCTGTTATTATGGGAGAAACTGCTGTTGTTGTAGAAATAGATA 1653
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Db    697 AGGAGCTGAGTCAACTAAAGCTGTTATTATGGGAGAAACTGCTGTTGTTGTAGAAATAGATA  756

Qy   1654 CCTTTCCCCGAGGAGTAATTTAATATAACCTAGTTATATAGCATTTGGATTACCTTTTGGATACT 1713
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1714 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAAATAAAAGAAATTTTAAAGATAA 1773
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    817 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAAATAAAAGAAATTTTAAAGATAA  876

Qy   1774 TGGGACTTCATGATACTGCTCCTTTGGCTTCTCTGGGTTCCTGGGTTCTCATATACAAGTTTAATTT 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    877 TGGGACTTCATGATACTGCTCCTTTGGCTTCTCTGGGTTCCTGGGTTCTCATATACAAGTTTAATTT  936

Qy   1834 TTCTTATGTCCCTTCTTATGGCAGTCATTGCGACAGCTTCTTTGTTATTTCCTCAAAGTA 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    937 TTCTTATGTCCCTTCTTATGGCAGTCATTGCGACAGCTTCTTTGTTATTTCCTCAAAGTA  996

Qy   1894 GCAGCATTGTGATATTTCTGCTTTATGGAATCATCTGTATTTTGCTT 1953
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   1894 GCAGCATTGTGATATTTCTGCTTTATGGAATCATCTGTATTTTGCTT 1953
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Db    997 GCAGCATTGTGATATTTCTGCTTTTTTTCCTTATGGAATTATCTGTATTTTGCTT 1056
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Qy   1954 TAATGCTGACACCTCTTTTTAAAAATCAAAACATGTGGAATAGTTGAATTTTTGTTA 2013

Db   1057 TAATGCTGACACCTCTTTTTAAAAATCAAAACATGTGGAATAGTTGAATTTTTTGTTA 1116
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Qy   2014 CTGTGGCTTTTGGATTAATTGGCCTATGAATAATCCTCATAGAAAGTTTCCCAAATCGT 2073

Db   1117 CTGTGGCTTTTGGATTAATTGGCCTATGAATAATCCTCATAGAAAGTTTCCCAAATCGT 1176
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Qy   2074 TAGTGTGGCTTTTCAGTCCTTTCGTCGTGTCGTCACTGTACTTTGTGATTGGTATTGCACAGGTCA 2133

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Db   1237 TGCATTTAGAAGATTTAATGAAGTGCTTCATTTCAATTTCAAATTGACTGCAGGCCCATATC 1296
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Db   1357 TCTATCTTGATCAAGTCATTCCAGGGGAATTTGGCTTACGGAGTAATTCTTATATTTTC 1416
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Qy   2314 TGAAGCCTCATATGGTCAAAGACTAAAAGAGTAAAAAGCAAAAGAAAATTATGAGGGCAATG 2373

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Qy   2374 TTAATGAAATATTAGTTTAGTGAAATTAGTGAGCCAGTTCTTCAGAAATTTGTAGGAA 2433

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Db   1537 AAGAAGCCATAAGAATTAGTGGTATTCAGAAGACATACAGAAAGAAGAAGGGGTGAAAATGTGG 1596
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Db   1597 AGGCTTGAGAAATTGTCATTTGACATATATGAGGTCAGATTACTGCCTTACTTGGCC 1656
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Qy   2554 ACAGTGAACAGGAAAAGTACATTGATGAATATTCTTGTGGGACTTGTGCCCACCTTCTG 2613

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Qy   2614 ATGGGTTTGCATCTATATATGACACAGAGTTCTCAGAAATGTTTGAAGCAA 2673

Db   1717 ATGGGTTTGCATCTATATATGACACAGAGTTCTCAGAAATGTTTGAAGCAA 1776
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Qy   2674 GAAAAATGATTGCCATTTTGGCTTCAAGATTTAGACATGCCACCTTTGATGTTTTGACATGTAGAGAAAG 2733

Db   1777 GAAAAATGATTGCCATTTTGGCTTCAAGATTTAGACATGCCACCTTTGATGTTTTGCACAGTTTGCACAGTAGAGAAAG 1836
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Qy   2734 AAAATTTATCAATTTTGGCTTCAATCAAAGGATAACAAGAAGTATCAAAGATCGCGACTATCAAAGAT 2793

Db   1837 AAAATTTATCAATTTTGGCTTCAATCAAAGGATAACAAGAAGTATCAAAGATCGCGACTATCAAAGAT 1896
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Qy   2794 TGCAGAAGGTTTTACTAGATTTAGACATGTTACTAGATTTAAAGATAA 2853

Db   1897 TGCAGAAGGTTTTACTAGATTTAGACATGTTACTAGATTTAAAGATAA 1956
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Qy   2854 TAAGTGGTGGTCAAAAAGAAAGCTGTCATTAGGAATTGCTGTCTTGGGAACCCAAAGA 2913

Db   1957 TAAGTGGTGGTCAAAAAGAAAGCTGTCATTAGGAATTGCTGTCTTGGGAACCCAAAGA 2016
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Qy   2914 TACTGCTGCTAGATGAACCAAGCTGGAATGGACCCCCGTTCTCGACATATTGTATGGA 2973

Db   2017 TACTGCTGCTAGATGAACCAAGCTGGAATGGACCCCCGTTCTCGACATATTGTATGGA 2076
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Qy   2974 ATCTTTAAAATACAGAAAAGCCAATCGGTGACAGTTCAGTACTCATTCATGGATG 3033

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Qy 4096 G-AATCATTGTTACTGCAATGCCACCTTACTTGCCATGGAAAATGCAGAGAATCATAAG 4154
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Db 3217 GAAATCATTGTAACTGCAATGCCACCCTACTTCTGCCATGGAAAATGCAGAGAATCATA-- 3274

Qy 4155 ATCAAAGCTTATACTACTCAACTTAAACTTCAGGTCTTTGCCATCTGCATATTGATTGGA 4214
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Db 3275 -----------------AGGTCTTTGCCATCTGCATATTGATTGGA 3305

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Qy 4275 CTGGCATTCATTATGATTATATATTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTTGC 4334
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Db 3846 AAGTCTAAAAATAGGAAGCTTCCAGAACAATGGCAACTAAATACATCTCTTTCTGTGAAGATGAGATGTC 3905

Qy 4815 AAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGTTGCCAGTGTGTGAGGAGAAACCA 4874
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Db 3906 AAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGTTGCCAGTGTGTGAGGAGAAACCA 3965

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Db 2137 AAGCTGACATTCTTGCAGATAGGAAAGCTGTGATATCACAAGGAATGTGTGTG 2196

Qy 3094 GTTCCTTCAATGTTCCTCAAAGTAAATGGGGATCGGCTACCGCCTGAGCCATGTGACATAG 3153
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Qy 3334 GTGTTTCCATGACAGCTTTGGAAGACGTATTTTTAAAGTAGAAGTTGAAGCAGAAATTG 3393
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Qy 3754 TGCTTCCTCAAAATTCTGCT------------GACTCAGATATCAGTGATCTTA 3795
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Db 2857 TGCTTCCTCAAAATTCTGCTGTTNNGTGAGAGTGTTNAGACTCAGATATCAGTGATCTTA 2916

Qy 3796 TTAGCTTTTCACAAGCCAGACATAATGTGACGATGATTAATGACAGTGACTATGTAT 3855
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Qy 3916 CAGCTGTTTTCAACAGTACTATGGTTTATTCTTTACCTATATATTAGTCATTAGTA 3975
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Qy 4036 TTCAAGAAATTACTGATTACTTTTAAAAATTGAGCTGTATTTTCAAGCCAGCTTTGCTTG 4095
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Db  5346  TTTAAGTTATCTTTAAGTTTATGCGCCATCTTCTTAAATAAGTACGTAAGTGTTCCAATCTAA 5405
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Db  5406  ATAAAAAACTAAATTCATAACTAATGCTACATAGAAAAGATACATAAAGCAATGTGAAAGTT 5463
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RESULT 5
US-09-971-121-5
; Sequence 5, Application US/09971121
; Patent No. US2002011477A1
; GENERAL INFORMATION:
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: US20020111477A1el Human Transporter Proteins and Polynucleot.
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 5262
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-971-121-5

Query Match   80.4%;   Score 5247.4;   DB 9;   Length 5262;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 5248;   Conservative 4;   Mismatches 4;   Indels 0;   Gaps 0;

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Db    61  TTTCAGAGCTGACAGATTGCTGCTCCAGTTCCTTAAGAGAGACAGCT  120

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Qy   937  ATTACATGCAGTTACTGCGTGGCTCCGGTTGTTGTTGTTTCCTCTTAATAGG  996
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Qy  1117  TTCTTTTTCCACTATTTTTTTTATTTTGGTTAATATTAGCATGATGCATCCAAATA  1176
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Qy  1177  AGAAATATGAAGAGTGCCTAATATAGAAACTCAAACCTATAGCAAGTTACTCTTTCTA  1236
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Db   481  ATCTAATTCTTGATATATCCAGTGACTAATTACTACAAGCAGCATCATGAGAAAGTGT  540

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Db  4266  ACTACATTGCAGGAACATTTGAAATTTATGGAGCTGTCAAGAATGAGTGCAAGTGAC  4325
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Qy  5835  TTTGTAGAACTCACTAAAGAACAAGAGGAAGAATAATAGTTGTGGAACTTAAACAGC  5894
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Qy  5895  ACACTTTGGTGGAACGAACACAAGAAGAAGAAGATAGAGTATTTTGAATTTGTATTGTTCGG  5954
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4986  ACACTTTGTGGTGGAACGAACACAAGAAGAAGAAGATAGAGTATTTTGAATTTGTATTGTTCGG  5045

Qy  5955  TCTGCTTACTGGGACTTCTTTCTTTTCACTTAACTTTGGTTAAAAAGTTTTT  6014
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5046  TCTGCTTACTGGGACTTCTTTCTTTTTCACTTAACTTTGGTTAAAAAGTTTTT  5105

Qy  6015  TATTGGAATGGTAACTGGAACCAAGACGCACTTGAAATTTTCTAAGCTTCCTTAATT  6074
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5106  TATTGGAATGGTAACTGGAACCAAGACGCACTTGAAATTTTCTAAGCTTCCTTAATT  5165

Qy  6075  GAAATGCTGCTGGTTGTGTTTTGCTTTTCTTAAATAAAAACGTATGCAATAATTAAGTGA  6134
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5166  GAAATGCTGCTGGTTGTGTTTTGCTTTTCTTAAATAAAAACGTATGCAATAATTAAGTGA  5225

Qy  6135  AGCTTGCATGTTGTATTGAAGTAATTGAACTATATAGTTGTAATGTCATCTTTTTCACC  6194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5226  AGCTTGCATGTTGTATTGAAGTAATTGAACTATATAGTTGTAATGTCATCTTTTTCACC  5285

Qy  6195  ATTCAGAAACAGTGCTTCTGAATTTGTGATTTAAGGAATTGTAATAGAATTAGTTTTATT  6254
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5286  ATTCAGAAACAGTGCTTCTGAATTTGTGATTTAAGGAATTGTAATAGAATTAGTTTTATT  5345

Qy  6255  TTTAAGTTATCTTTAAGTTTATGCGCCATCTTCTTAAATAAGTACGTAAGTGTTCCAATCTAA  6314
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1357  TAACATCCAGTCTCTCTAAGCCGAGCAACTTGTAGGTGTGGTTTCAAAGACTCCATGT  1416
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  TAACATCCAGTCTCTCTAAGCCGAGCAACTTGTAGGTGTGGTTTCAAAGACTCCATGT   660

Qy    1417  CCTATGAACTTCGTTTTTTCCTGATATGATTCCAGTATCTTCATTTATATGGATTCAA  1476
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  CCTATGAACTTCGTTTTTTCCTGATATGATTCCAGTATCTTCATTTATATGGATTCAA   720

Qy    1477  GAGCTGGCTGTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTCACAGTTT  1536
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  GAGCTGGCTGTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTCACAGTTT   780

Qy    1537  TACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTGGAAGG  1596
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781  TACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTGGAAGG   840

Qy    1597  AGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAAACTGCTCGTGTGAGAAATAGATACCT  1656
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  AGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAAACTGCTCGTGTGAGAAATAGATACCT   900

Qy    1657  TTCCCGAGGAGTAATTTTAATATACCTAGTTATAGACATTTTCACCTTTTGGATACTTTT  1716
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  TTCCCGAGGAGTAATTTTAATATACCTAGTTATAGACATTTTCACCTTTTGGATACTTTT   960

Qy    1717  TGGCAATTCATATCGTAGCAGAAAGAAAAAAAAAAGAATTTTTAAAGATTTTAAAGATAATGG  1776
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  TGGCAATTCATATCGTAGCAGAAAGAAAAAAAAAAGAATTTTTAAAGATTTTAAAGATAATGG  1020

Qy    1777  GACTTCATGATACTGCCTTTGGCTTCCTGGGTTCTTCTATATACAAGTTTAATTTTTC  1836
            ||||||||||||||||||||||||||||||||||||||||| :|||||||||||||||
Db    1021  GACTTCATGATACTGCCTTTGGCTTCCTGGGTTCTTCTATAWACAAGTTTAATTTTTC  1080

Qy    1837  TTATGTCCCTTCTTATGGCAGTCATTGCCACAGCTTCTTGTTATTTCCTCAAAGTAGCA  1896
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  TTATGTCCCTTCTTATGGCAGTCATTGCCACAGCTTCTTGTTATTTCCTCAAAGTAGCA  1140

Qy    1897  GCATTGTGATATTCTGCTTTTTTCCTTATGGATTATCATCTGTATTTTTTGCTTTAA  1956
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141  GCATTGTGATATTCTGCTTTTTTCCTTATGGATTATCATCTGTATTTTTTGCTTTAA  1200

Qy    1957  TGCTGACACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTTGTTACTG  2016
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201  TGTGGCTTTTTCAGTCCTTTCTGTCCACTGTACTTTTGTGATTGGTAATTTTGTTACTG  1260

Qy    2017  TGGCTTTTGGATTTATTGGCCTTATGATAATCCTCATAGAAAAGTTTTCCCAAATCGTTAG  2076
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261  TGGCTTTTGGATTTATTGGCCTTATGATAATCCTCATAGAAAAGTTTTCCCAAATCGTTAG  1320

Qy    2077  TGTGGCTTTTCAGTCCTTTCTGTCCACTGTACTTTGTGATTGGTATTGCCACAGGTCATGC  2136
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321  TGTGGCTTTTCAGTCCTTTCTGTCCACTGTACTTTGTGATTGGTATTGCCACAGGTCATGC  1380

Qy    2137  ATTTAGAAGATTTTAATGAAGTGCTTCATTTCAAATTGACTGCGAGGCCCCATATCCTC  2196
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381  ATTTAGAAGATTTTAATGAAGTGCTTCATTTCAAATTGACTGCGAGGCCCCATATCCTC  1440

Qy    2197  TAATTATTACAACATTATCATGCTCACACTTAATAGTATATTCTATGTCCTCTTGGCTGTCT  2256
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441  TAATTATTACAATTATCATGCTCACACTTAATAGTATATTCTATGTCCTCTTGGCTGTCT  1500

Qy    2257  ATCTTGATCAAGTCATTCCAGGGGAATTTGGCTTACGGAGGGAATCATCTTTATATTTTCTGA  2316
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501  ATCTTGATCAAGTCATTCCAGGGGAATTTGGCTTACGGAGGGAATCATCTTTATATTTTCTGA  1560

Qy    2317  AGCCTTCATTATTGGTCAAAGAGTAAAAGAAAATTATGAGGGAGTTATCAGAGGGCCAATGTTA  2376
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561  AGCCTTCATTATTGGTCAAAGAGTAAAAGAAAATTATGAGGGAGTTATCAGAGGGCCAATGTTA  1620

Qy    2377  ATGGAAATATTAGTTTTAGTGAAATTATTGAGCCAGTTTCTTCAGAATTTGTAGGAAAAG  2436
            ||||||||||||||||||||||||||||||||||||||||||: |||||||||||||||
Db    1621  ATGGAAATATTAGTTTTAGTGAAATTATTGAGCCAGTTTCTTCAGAATTTGTAGAGAAAAG  1680

Qy    2437  AAGCCATAAGAATTAGTGTATTCAGAAGACATACAGAAGAAGGGTGAAAATGTGGAGG  2496
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Db    1681  AAGCCATAAGAATTAGTGTATTCAGAAGACATACAGAAGAAGGGTGAAAATGTGGAGG  1740

Qy    2497  CTTTGAGAAATTGTCATTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACA  2556
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741  CTTTGAGAAATTGTCATTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACA  1800

Qy    2557  GTGGAACAGGAAAGAGTACATTGATGAATATTCTTGTGGACTCTCGCCCACCTTCTGATG  2616
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801  GTGGAACAGGAAAGAGTACATTGATGAATATTCTTGTGGACTCTCGCCCACCTTCTGATG  1860

Qy    2617  GGTTTGCATCTATATGACACAGAGTCTCAGAAATGAGAAATGTTTGAAGCAAGAA  2676
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861  GGTTTGCATCTATATGACACAGAGTCTCAGAAATGAGAAATGTTTGAAGCAAGAA  1920

Qy    2677  AAATGATTGGCATTTGTCCACAGTTAGATATACACTTTGATGTTTTGACAGTAGAAGAAA  2736
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921  AAATGATTGGCATTTGTCCACAGTTAGATATATACACTTTGATGTTTTGACACAGTAGAAGAAA  1980

Qy    2737  ATTTATCAATTTGGCTTCAATCAAAGGGATACCAGCCAACAATATAATACAAGAAGTGC  2796
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981  ATTTATCAATTTGGCTTCAATCAAAGGGATACCAGCCACCAATATAATACAAGAAGTGC  2040

Qy    2797  AGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAA  2856
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041  AGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAA  2100

Qy    2857  GTGGTGGTGCAAAAAGAAAGCTGTCATTAGGAAATTGCTGTGTTCTTGGGAACCCAAAGATAC  2916
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101  GTGGTGGTGCAAAAAGAAAGCTGTCATTAGGAAATTGCTGTGTTCTTGGGAACCCAAAGATAC  2160

Qy    2917  TGCTGCTAGATGAACCACAGCTGGAATGGACCCCCTGTTCCGACATATTGTATGGAATC  2976
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161  TGCTGCTAGATGAACCACAGCTGGAATGGACCCCCTGTTCCGACATATTGTATGGAATC  2220

Qy    2977  TTTTAAAAATACAGAAAAGCCAATCGGGTGACAGTGTTCAGTACTCATTCATGATGAAG  3036
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221  TTTTAAAAATACAGAAAAGCCAATCGGGTGACAGTGTTCAGTACTCATTCATGATGAAG  2280

Qy    3037  CTGACATTCTTGCAGATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTGGTT  3096
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281  CTGACATTCTTGCAGATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTGGTT  2340

Qy    3097  CTTCAATGTTCCTCAAAGTAAATGGGGATCGGCGTCACCGGCTACCGCTGAGCATGTACATAGACA  3156
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341  CTTCAATGTTCCTCAAAGTAAATGGGGATCGGCGTCACCGGCTACCGCTGAGCATGTACATAGACA  2400

Qy    3157  AATATTGTGCCACAGAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTT  3216
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401  AATATTGTGCCACAGAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTT  2460

Qy    3217  TATTACAACAGAATGACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAAAT  3276
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461  TATTACAACAGAATGACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAAAT  2520

Qy    3277  TTTCAGGTTGTTGTTTCTGCCCTAGACAGTCATTCAAATTTGGGTGTCATTCTTATGGTG  3336
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521  TTTCAGGTTGTTGTTTCTGCCCTAGACAGTCATTCAAATTTGGGTGTCATTCTTATGGGG  2580

Qy    3337  TTTCCATGACGACTTTGGAAGACGTATTTTTAAAGCTACCTGAGGAAGAAGAATTGACC  3396
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581  TTTCCATGACGACTTTGGAAGACGTATTTTTAAAGCTACCTGAGGAAGAAGAATTGACC  2640

Qy    3397  AAGCAGATTATATGTGTATTTACTCAGCCACTGAGAGAAGAAATGGATTCAAAATCTT  3456
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641  AAGCAGATTATATGTGTATTTACTCAGCCACTGAGAGAAGAAATGGATTCAAAATCTT  2700

Qy    3457  TTGATGAAATGGAACAGAGCTTACTTATTCCTTCTCTAGTGAGCA  3516
            |||||||||||||||||||||||| :||||||||||||||||||
Db    2701  TTGATGAAATGGAACAGAGCTTACTTATTCCTCTGAAACCAAGGCTKCTCTAGTGAGCA  2760

Qy    3517  CCATGAGCCCTTTGGAAACAACCAGATGTATACAATAGCACAAGTTCATTTCCTTTACCTTGA  3576
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Qy   2511 TCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAACAGGAAAG 2570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAACAGGAAAG 1560

Qy   2571 AGTACATTGATGAATATTCTTTGTGGACTCTGCCCACCTTCTGATGGGTTTGCATCTATA 2630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 AGTACATTGATGAATATTCTTTGTGGACTCTGCCCACCTTCTGATGGGTTTGCATCTATA 1620

Qy   2631 TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGATTGGCATT 2690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGATTGGCATT 1680

Qy   2691 TGTCCACAGTTAGATATACACTTTGATGTTTTGACAGTAGAAGAAAATTTATCAATTTTG 2750
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TGTCCACAGTTAGATATACACTTTGATGTTTTGACAGTAGAAGAAAATTTATCAATTTTG 1740

Qy   2751 GCTTCAATCAAAGGGATACCAGCCAACAATATAATACAAGAAGTGCAGAAGGTTTTACTA 2810
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1741 GCTTCAATCAAAGGGATACCAGCCACCAATATAATACAAGAAGTGCAGAAGGTTTTACTA 1800

Qy   2811 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 2870
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 1860

Qy   2871 AGAAAGCTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA 2930
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AGAAAGCTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA 1920

Qy   2931 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAATACAGA 2990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAATACAGA 1980

Qy   2991 AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTCATGGATGAAGCTGACATTCTTGCA 3050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTCATGGATGAAGCTGACATTCTTGCA 2040

Qy   3051 GATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTGGTTCTTCAATGTTCCTC 3110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTGGTTCTTCAATGTTCCTC 2100

Qy   3111 AAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACA 3170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 AAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACA 2160

Qy   3171 GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAT 3230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAT 2220

Qy   3231 GACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAATTTTCAGGTTTGTTT 3290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAATTTTCAGGTTTGTTT 2280

Qy   3291 TCTGCCCTAGACAGTCATTCAAATTTGGGTGTCATTTCTTATGGTGTTTCCATGACGACT 3350
          ||||||||||||||||||||||||||||||| |||||||||||| |||||||||||||||
Db   2281 TCTGCCCTAGACAGTCATTCAAATTTGGGTGGCATTTCTTATGGGGTTTCCATGACGACT 2340

Qy   3351 TTGGAAGACGTATTTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGT 3410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TTGGAAGACGTATTTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGT 2400

Qy   3411 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATGGAA 3470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATGGAA 2460

Qy   3471 CAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG 3530
          |||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db   2461 CAGAGCTTACTTATTCTTTCTGAAACCAAGGCTKCTCTAGTGAGCACCATGAGCCTTTGG 2520

Qy   3531 AAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCTTGAAACGTGAAAGTAAA 3590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 AAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCTTGAAACGTGAAAGTAAA 2580
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Qy   3591 TCAGTGAGATCAGTGTTGCTTCTGCTTTTAATTTTTTTCACAGTTCAGATTTTTATGTTT 3650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TCAGTGAGATCAGTGTTGCTTCTGCTTTTAATTTTTTTCACAGTTCAGATTTTTATGTTT 2640

Qy   3651 TTGGTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTATAT 3710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TTGGTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTATAT 2700

Qy   3711 TTTCTAAAACCTGGAGACAAACCACATAAATACAAAACAAGTCTGCTTCTTCAAAATTCT 3770
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TTTCTAAAACCTGGAGACAAACCACATAAATACAAAACAAGTCTGCTTCTTCAAAATTCT 2760

Qy   3771 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGCCAGAACATAATGGTGACG 3830
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGCCAGAACATAATGGTGACG 2820

Qy   3831 ATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGGCTTTAAATGTGATG 3890
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   2821 ATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGGCTTTAAATGTGRTG 2880

Qy   3891 CATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTATTCTTTA 3950
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTATTCTTTA 2940

Qy   3951 CCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCATTTAAATGTGACTGAAACC 4010
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCATTTAAATGTGACTGAAACC 3000

Qy   4011 ATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGATATAGTTTTTAAAATTGAG 4070
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 ATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGATATAGTTTTTAAAATTGAG 3060

Qy   4071 CTGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCC 4130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 CTGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCC 3120

Qy   4131 ATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATACTCAACTTAAACTTTCAGGTCTT 4190
          |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db   3121 ATGGAAAATGCAGAGAATCATAAGATCAAAGCTTAYACTCAACTTAAACTTTCAGGTCTT 3180

Qy   4191 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCCTTATTTTTTATCATT 4250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCCTTATTTTTTATCATT 3240

Qy   4251 CTTATTTTGATGCTAGGAAGCTTACTGGCATTTCATTATGGATTATATTTTTATACTGTA 4310
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   3241 CTTATTTTGATGCTAGGAAGCTTATTGGCATTTCATTATGGATTATATTTTTATACTGTA 3300

Qy   4311 AAGTTCCTTGCTGTGGTTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACT 4370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 AAGTTCCTTGCTGTGGTTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACT 3360

Qy   4371 TATATTGCTTCTTTCACCTTTAAGAAAATTTTAAATACCAAAGAATTTTGGTCATTTATC 4430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TATATTGCTTCTTTCACCTTTAAGAAAATTTTAAATACCAAAGAATTTTGGTCATTTATC 3420

Qy   4431 TATTCTGTGGCAGCGTTGNCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGATAC 4490
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   3421 TATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGATAC 3480

Qy   4491 ACAATTGCAACTATTCTTCATTATGCCTTTTGTATCATCATTCCAATCTATCCACTTCTA 4550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 ACAATTGCAACTATTCTTCATTATGCCTTTTGTATCATCATTCCAATCTATCCACTTCTA 3540

Qy   4551 GGTTGCCTGATTTCTTTCATAAAGATTTCTTGGAAGAATGTACGAAAAAAATGTGGACACC 4610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 GGTTGCCTGATTTCTTTCATAAAGATTTCTTGGAAGAATGTACGAAAAAAATGTGGACACC 3600

Qy   4611 TATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTACTG 4670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTACTG 3660

Qy   4671 TGGATTTTCCTCTTACAATACTATGAGAAAAAAATATGGAGGCAGATCAATAAGAAAAGAT 4730
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Db  4741  CAATCTTTTTTAAGCTGGAGAAGCTAAACATGCTTTGCCATTGAAGAATATAGCTTT      4800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5811  TCTCAAGCAACATTGGAACACAGGTTTTTGTAGAACTCACTAAAGAACAAGGAGGAAGAT  5870
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4801  TCTCAAGCAACATTGGAACACAGGTTTTTGTAGAACTCACTAAAGAACAAGGAGGAAGAT  4860
Qy  5871  AATAGTTGTGGAACTTAAACAGCACACTTTGGTGGGAACGAACCAAGAAGAGATAGAGTA  5930
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4861  AATAGTTGTGGAACTTAAACAGCACACTTTGGTGGGAACGAACCAAGAAGAGATAGAGTA  4920
Qy  5931  GTATTTTGA  5939
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Db  4921  GTATTTTGA  4929
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RESULT 7
US-10-090-458-3
; Sequence 3, Application US/10090458
; Publication No. US20020123107A1
; GENERAL INFORMATION:
;   APPLICANT: Chen, Hongyun
;   APPLICANT: Kilinski, Ligia
;   APPLICANT: Le Bihan, Stephane
;   TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
;   FILE REFERENCE: 100103.403
;   CURRENT APPLICATION NUMBER: US/10/090,458
;   CURRENT FILING DATE: 2002-03-01
;   NUMBER OF SEQ ID NOS: 5
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 4917
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2775, 2776
;   OTHER INFORMATION: n = A,T,C or G
US-10-090-458-3

Query Match   73.7%;   Score 4807.4;   DB 13;   Length 4917;
Best Local Similarity   98.8%;   Pred. No. 0;
Matches 4891; Conservative   0; Mismatches   7; Indels 50; Gaps 3;

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Qy  1011  ATGTCCACTGCAATTAGGGAGGTAGGAGTTGGAGACAGACCAGAACACTTCTACTGAAG   1070
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Db     1  ATGTCCACTGCAATTAGGGAGGTAGGAGTTGGAGACAGACCAGAACACTTCTACTGAAG     60
Qy  1071  AATTACTAATTAAATGCAGAACCAAAAAGAGTAGTTCAGGAATTCTTTTTCCACTA    1130
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  AATTACTAATTAAATGCAGAACCAAAAAGAGTAGTTCAGGAATTCTTTTTCCACTA     120
Qy  1131  TTTTTTTTATTTGTTAATTAATTAGCATGGACAAGTTACTCTTCTAATCTAATTCTTGGA  1190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  TTTTTTTTATTTGTTAATTAATTAGCATGGACAAGTTACTCTTCTAATCTAATTCTTGGA   180
Qy  1191  GTGCCTAATATAGAACTAGAACTCAATCCATGGACAAGCATCATCAAGAATATGAAGAA   1250
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  GTGCCTAATATAGAACTAGAACTCAATCCATGGACAAGCATCATCAAGAATATGAAGAA   240
Qy  1251  TATACTCCAGTGACTAATATTACAGGAATATACAAATGAAAAAGAATGTCTACTGATCATCTA  1310
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  TATACTCCAGTGACTAATATTACAGGAATATACAAATGAAAAAGAATGTCTACTGATCATCTA  300
Qy  1311  CCTGATGTCATAATTACTGAAGAATTTCCCAAATGCAAGCCGTCAG    1370
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CCTGATGTCATAATTACTGAAGAATTTCCCAAATGCAAGCCGTCAG     360
Qy  1371  TCTAAGCCGGCAACTTGTAGGTGTGGTTTCAAAGACTTCAGTTCCCTTCA    1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  TCTAAGCCGGCAACTTTGTAGGTGTGGTTTCAAAGACTTCAGTTCCCTTCA    420
Qy  1431  TTTTTCCTGATATGATTCCAGTATCTTCTATTTATATGGATTCAAGAGCTGGCTGTTCA  1490
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Db  3661  TGGATTTTCCTCTACAATACTATGAGGAAAAATATGAGGCAGATCAATAAGAAAGAT    3720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4731  CCCTTTTCAGAAACCTTTCAACGAAGCTTAAAAATAGGAGAAGCTTCCAGAACCACCAGAC  4790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  CCCTTTTCAGAAACCTTTCAACGAAGCTTAAAAATAGGAGAAGCTTCCAGAACCACCAGAC  3780
Qy  4791  AATGAGGATGAAGATGAAGAGTCAAAGTGAAAGACTAAAGTCAAGAGCTGATGGGT    4850
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  AATGAGGATGAAGATGAAGAGTCAAAGTGAAAGACTAAAGTCAAGAGCTGATGGGT     3840
Qy  4851  TGCCAGTGGTGTGAGGAGAAACCATCATTATGGTCAGCAATTGCATAAAGAATATGAT  4910
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  TGCCAGTGGTGTGAGGAGAAACCATCATTATGGTCAGCAATTGCATAAAGAATATGAT  3900
Qy  4911  GACAAGAAAGATTTCTTCTTCTTCAAGAAAGTAAGAAAGTGCAACTAAATACATCTCT  4970
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901  GACAAGAAAGATTTCTTCTTCTTCAAGAAAGTAAGAAAGTGCAACTAAATACATCTCT  3960
Qy  4971  TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGTCTGGCAAAAGC  5030
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961  TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGTCTGGCAAAAGC  4020
Qy  5031  ACAATTATTAATATTCTGGTTGGTGATATTGACCAACTTCAGGCCAGGTATTTTTAGGA  5090
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021  ACAATTATTAATATTCTGGTTGGTGATATTGACCAACTTCAGGCCAGGTATTTTTAGGA  4080
Qy  5091  GATTATTCTTCAGAGACAAGACAAGTGAAGATGATTCACTGAAGTGTATGGTTACTGTCCT  5150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081  GATTATTCTTCAGAGACAAGACAAGTGAAGATGATTCACTGAAGTGTATGGTTACTGTCCT  4140
Qy  5151  CAGATAAACCCTTTGTGGCCAGATACTACATTGCCAGGAACATTTGAAATTTATGGAGCT  5210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141  CAGATAAACCCTTTGTGGCCAGATACTACATTGCCAGGAACATTTGAAATTTATGGAGCT  4200
Qy  5211  GTCAAGGAATGAGTGCAAGTGCAAGTGCAAGATGACATGAAGAGTCATAAGTCGAATAACACATGCACTT  5270
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201  GTCAAGGAATGAGTGCAAGTGCAAGTGCAAGATGACATGAAGAGTCATAAGTCGAATAACACATGCACTT  4260
Qy  5271  GATTAAAAGAACACATCTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAG  5330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4261  GATTAAAAGAACACATCTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAG  4320
Qy  5331  TTGTGTTTTGCTCTAAGTATGTCTAAGAATCCTCAGATTACTTTGCTAGATGAACCATCT  5390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4321  TTGTGTTTTGCTCTAAGTATGTCTAAGAATCCTCAGATTACTTTGCTAGATGAACCATCT  4380
Qy  5391  ACAGGTATGGATCCCAAAGCCAAAACAGCACAAGCAACAATTCGAACTGCATTTAAA    5450
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4381  ACAGGTATGGATCCCAAAGCCAAAACAGCACAAGCAACAATTCGAACTGCATTTAAA     4440
Qy  5451  AACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGGCTGTCTGT  5510
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4441  AACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGGCTGTCTGT  4500
Qy  5511  GATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCCGGAACAGTACAACATCTA  5570
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4501  GATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCCGGAACAGTACAACATCTA  4560
Qy  5571  AAGAGTAAATTTGGAAAAGCTACTTTTTGGAAATTAAATTCAGTATATTTCCCAAATGCCCGTCAG  5630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4561  AAGAGTAAATTTGGAAAAGCTACTTTTTGGAAATTAAATTCAGTATATTTCCCAAATGCCCGTCAG  4620
Qy  5631  CTAGAAGTAGACCGCCTTCAAAGAGAATTCAGTATATTTCCCAAATGCAAGCCGTCAG  5690
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4621  CTAGAAGTAGACCGCCTTCAAAGAGAATTCAGTATATTTCCCAAATGCAAGCCGTCAG  4680
Qy  5691  GAAAGTTTTCTATTTGGCTTATAAAATCCTTAGGAAGAAGATGTTCAGTCCCTTTCA  5750
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4681  GAAAGTTTTCTATTTGGCTTATAAAATCCTTAGGAAGAAGATGTTCAGTCCCTTTCA  4740
Qy  5751  CAATCTTTTTTAAGCTGGAGAAGCTAAACATGCTTTGCCATTGAAGAATATAGCTTT  5810
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Db   421 TTTTTCCTGATAATGATTCCAGTATCCTTCATTATATGATTCAAGAGCTGGCTGTTCA   480

Qy  1491 AAATCATGTGAGGCTGCTCACTACTGGTCCTCAGTTTCACAGTTTACACAGCATCCATA 1550
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAATCATGTGAGGCTGCTCACTACTGGTCCTCAGTTTCACAGTTTACACAGCATCCATA  540

Qy  1551 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 1610
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT  600

Qy  1611 AAAGCTGTTATTATGGGAGAAACTGCTGTTGTGAGAAATAGATACCTTTCCCGAGGAGTA 1670
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AAAGCTGTTATTATGGGAGAAACTGCTGTTGTGAGAAATAGATACCTTTCCCGAGGAGTA  660

Qy  1671 ATTTTAATATACCTAGTTATAGCATTTGGATACTTTTGGCAATTCATATC 1730
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATTTTAATATACCTAGTTATAGCATTTGGATACTTTTGGCAATTCATATC  720

Qy  1731 GTAGCAGAAAAGAAATAAAATAAAAGAATTTTAAAGATAAATGGGACTTCATGATACT 1790
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GTAGCAGAAAAGAAATAAAATAAAAGAATTTTAAAGATAAATGGGACTTCATGATACT  780

Qy  1791 GCCTTTTGGCTTTCCTGGGTTCTTCTATATACAAGTTTAATTTTTCTTATGTCCCTTCTT 1850
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GCCTTTTGGCTTTCCTGGGTTCTTCTATATACAAGTTTAATTTTTCTTATGTCCCTTCTT  840

Qy  1851 ATGGCAGTCATTGCGACGCTTCTTGTATTCCTCAAAGTAGCAGCATTGTGATATTT 1910
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ATGGCAGTCATTGCGACGCTTCTTGTATTCCTCAAAGTAGCAGCATTGTGATATTT  900

Qy  1911 CTGCTTTTTTCCTTATGGATTATCATCTGTATTTTTGCTTTAATGCTGACACCTCTT 1970
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CTGCTTTTTTCCTTATGGATTATCATCTGTATTTTTGCTTTAATGCTGACACCTCTT  960

Qy  1971 TTTAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTTACTGTGCTTTTGGATTT 2030
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTTAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTTACTGTGCTTTTGGATTT 1020

Qy  2031 ATTGGCCTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCAGT 2090
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 ATTGGCCTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCAGT 1080

Qy  2091 CCTTTCTGTGTCACTGTACTTTGTGATTGGTATTGCACAGGTCATGCATTTAGAGATTTT 2150
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CCTTTCTGTGTCACTGTACTTTGTGATTGGTATTGCACAGGTCATGCATTTAGAGATTTT 1140

Qy  2151 AATGAAGGTGCTTCATTTCAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAATT 2210
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 AATGAAGGTGCTTCATTTCAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAATT 1200

Qy  2211 ATCATGCTCACACTTATTTGAGCCAGTTCTTCTTCTGGCTGTCTCTGCTGTCATCGATCAAGTC 2270
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 ATCATGCTCACACTTATTTGAGCCAGTTCTTCTTCTGGCTGTCTCTGCTGTCATCGATCAAGTC 1260

Qy  2271 ATTCCAGGGGAATTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 2330
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 ATTCCAGGGGAATTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 1320

Qy  2331 TCAAAGAGTAAAAGAAAATATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT 2390
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 TCAAAGAGTAAAAGAAAATATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT 1380

Qy  2391 TTTAGTGAAATTATTGAGCCAGTTCTTCAGAATTGTAGGAAAAGAAGCCATAAGAATT 2450
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 TTTAGTGAAATTATTGAGCCAGTTCTTCAGAATTGTAGGAAAAGAAGCCATAAGAATT 1440

Qy  2451 AGTGGTATTCAGAAGACATACAGAAGAGGGTGAAAATGTGGAGGCTTTGAAAATTTG 2510
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 AGTGGTATTCAGAAGACATACAGAAGAGGGTGAAAATGTGGAGGCTTTGAAAATTTG 1500

Qy  2511 TCATTGACATATAGAGGGTCAGATTACTTGCCCTTACTTGGCCCACAGTGAACAGGAAAG 2570
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 TCATTGACATATAGAGGGTCAGATTACTTGCCCTTACTTGGCCCACAGTGAACAGGAAAG 1560


Qy  2571 AGTACATTGATGAATATTCTTTGTGGACTCTGCGCCACCTTCTGATGGGTGTTGCATCTATA 2630
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 AGTACATTGATGAATATTCTTTGTGGACTCTGCGCCACCTTCTGATGGGTGTTGCATCTATA 1620

Qy  2631 TATGGACACAGAGTCTCAGAAATAGATGAAAATGTTGAAGCAAGAAAAATGATTGGCATT 2690
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TATGGACACAGAGTCTCAGAAATAGATGAAAATGTTGAAGCAAGAAAAATGATTGGCATT 1680

Qy  2691 TGTCCACAGTTAGTATATACACTTTGATGTTTTGACAGTAGCAGTAGAAGAAAATTATCAATTTTG 2750
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 TGTCCACAGTTAGTATACACTTTGATGTTTTGACAGTAGCAGTAGAAGAAATTATCAATTTTG 1740

Qy  2751 GCTTCAATCAAAGGGATACCAGCCAACATATAATACAGAGTGCAGAAGGTTTTACTA 2810
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 GCTTCAATCAAAGGGATACCAGCCAACATATAATACAGAGTGCAGAAGGTTTTACTA 1800

Qy  2811 GATTTAGACATGCAGCATCAAAGATAACCAAGCTAAAAAATTAAGCTGGTGGTCAAAAA 2870
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 GATTTAGACATGCAGCATCAAAGATAACCAAGCTAAAAAATTAAGCTGGTGGTCAAAAA 1860

Qy  2871 AGAAAGCTGTCATTAGGAATTGCTGTTCTGGAACCCAAAGATACTGCTGCTGACGATGAA 2930
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Db  1861 AGAAAGCTGTCATTAGGAATTGCTGTTCTGGAACCCAAAGATACTGCTGCTGACGATGAA 1920

Qy  2931 CCAACAGCTGGAATGGAATGACCCCTGTTCTCGACATATGTATGGAAATCTTTAAAATACAGA 2990
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CCAACAGCTGGAATGGAATGACCCCTGTTCTCGACATATTGTATGGAATCTTTAAAATACAGA 1980

Qy  2991 AAAGGCCAATCGGGTGACAGTGTTCAGTGTTCATTCAGTGACTACTTCTTGCA 3050
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 AAAGGCCAATCGGGTGACAGTGTTCAGTGTTCATTCAGTGACTACTTCTGCA 2040

Qy  3051 GATAGGAAAGCTGTGATATCACAAGGAAATGCTGAAAGTGTTGGTTCTTCAATGTTCCTC 3110
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 GATAGGAAAGCTGTGATATCACAAGGAAATGCTGAAAGTGTTGGTTCTTCAATGTTCCTC 2100

Qy  3111 AAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACA 3170
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 AAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACA 2160

Qy  3171 GAATCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTCAAACAGAAT 3230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GAATCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTCAAACAGAAT 2220

Qy  3231 GACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAAATTTCAGGTTTGTTT 3290
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAAATTTCAGGTTTGTTT 2280

Qy  3291 TCTGCCCTAGACAGTCATTCAAATTGGGTGTCATTCTTATGGTGTTCCATGACGACT 3350
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TCTGCCCTAGACAGTCATTCAAATTGGGTGTCATTCTTATGGTGTTCCATGACGACT 2340

Qy  3351 TTGGAAGACGTATTTTAAAGTAGAAGTTGAAGCAGCAAATTGACCAAGCAGATTATAGT 3410
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TTGGAAGACGTATTTTAAAGTAGAAGTTGAAGCAGCAAATTGACCAAGCAGATTATAGT 2400

Qy  3411 GTATTACTCAGCAGCCACTGGATTCAAAATCTTTTGATGAAATGAAG 3470
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GTATTACTCAGCAGCCACTGGATTCAAAATCTTTTGATGAAATGAAG 2460

Qy  3471 CAGAGCTTACTTCTTTCTGAAACCAAGGCTTCTCAGTGAGCTGAGCCTTTGG 3530
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGAGCTTACTTCTTTCTGAAACCAAGGCTGCTCAGTGAGCTGAGCCTTTGG 2520

Qy  3531 AAACAACAGATGTATACAAGTTCATTCTTTACCTTGAAACGTGAAAGTAA 3590
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 AAACAACAGATGTATACAAGTTCATTCTTTACCTTGAAACGTGAAAGTAA 2580

Qy  3591 TCAGTGAGATCAGTTGCTTCTGCTTTAATTTTTCACAGTTCAGATTTTTATGTTT 3650
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 TCAGTGAGATCAGTTGCTTCTGCTTTAATTTTTCACAGTTCAGATTTTTATGTTT 2640
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Db  4770 CATTGAAGAATATAGCTTTTCTCAAGCAACATTGGAAGCAGTGTTTTGTGAGAACTCACTAA 4829
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5852 AGAACAAGAGAGGAGGAAGATAATAGTTGTGGAACTTAAACAGCACACTTGGTGGGAACG 5911
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Db  4830 AGAACAAGAGAGGAGGAAGATAATAGTTGTGGAACTTAAACAGCACACTTGGTGGGGAACG 4889

Qy  5912 AACACAAGAAGAGATAGAGTAGTATTTTGA 5939
                    ||||||||||||||||||||||||||||||
Db  4890 AACACAAGAAGAGATAGAGTAGTATTTTGA 4917

RESULT 8
US-09-971-121-3
; Sequence 3, Application US/09971121
; Patent No. US2002011477A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris:
; TITLE OF INVENTION: No. US2002011477A1e1 Human Transporter Proteins and Polynucleoti
; TITLE OF INVENTION:  Same
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 4785
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-971-121-3

  Query Match             72.9%;   Score 4754.8;   DB 9;   Length 4785;
  Best Local Similarity   99.8%;   Pred. No. 0;
  Matches 4756;   Conservative 4;   Mismatches  7;   Indels  0;   Gaps  0;
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Qy  1011 ATGTCCACTGCAATTAGGGAGGAGGTAGGACTAGTTTGGAGACAGACCAGAACACTTCACTGAAG 1070
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Db     1 ATGTCCACTGCAATTAGGGAGGAGGTAGGACTAGTTTGGAGACAGACCAGAACACTTCACTGAAG   60
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Qy  1071 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCTTTTTCCACTA 1130
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCTTTTTCCACTA  120
```

```
Qy  1131 TTTTTTTTATTTTGGTTAATAATTAGCATGATGACATCCAAATAAGAAATATGAAGAA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTTTTTTTATTTTGGTTAATAATTAGCATGATGACATCCAAATAAGAAATATGAAGAA  180
```

```
Qy  1191 GTGCCTAATATAGAACTCAATCCTATGGACAACTTTACTCTTTCTAATCTAATTCTTGGA 1250
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTGCCTAATATAGAACTCAATCCTATGGACAACTTTACTCTTTCTAATCTAATTCTTGGA  240
```

```
Qy  1251 TATACTCCAGTGACTAATTACAAGCAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TATACTCCAGTGACTAATTACAAGCAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA  300
```

```
Qy  1311 CCTGATGTCATAATTACTGAAGAATTACAAATACAAAATGAAAAAGAAAATGTTAACATCCAGTCTC 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCTGATGTCATAATTACTGAAGAATTACAAATACAAAATGAAAAAGAAAATGTTAACATCCAGTCTC  360
```

```
Qy  1371 TCTAAGCCGAGCAACTTGTAGGTGGTTTGGTTTTCAAAGACTCCATGTCCTATGAACTTCGT 1430
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TCTAAGCCGAGCAACTTGTAGGTGGTTTGGTTTTCAAAGACTCCATGTCCTATGAACTTCGT  420
```

```
Qy  1431 TTTTTTCCTGATATGAGGCTGCCTCAGTACTGGGTCCTCAAGAGCTTCACAGTTTTATATGGATTCATATAATGGATT 1490
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TTTTTTCCTGATATGAGGCTGCCTCAGTACTGGGTCCTCAAGAGCTTCACAGTTTTATATGGATTCATATAATGGATT  480
```

```
Qy  1491 AAATCATGTAGAGGCTGCCTCAGTACTGGGTCCTCAGGTTTCACAGTTTTACAAGCATCCATA 1550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAATCATGTAGAGGCTGCCTCAGTACTGGGTCCTCAGGTTTCACAGTTTTACAAGCATCCATA  540
```

```
Qy  1551 GATGCTGCCATTATACAGTGAAGACCAATGTTTCTCTTGAAGGAGTGGAGTCAACT 1610
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GATGCTGCCATTATACAGTGAAGACCAATGTTTCTCTTGAAGGAGTGGAGTCAACT  600
```

```
Qy  1611 AAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGAGATACCTTTCCCGAGGAGTA 1670
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGAGATACCTTTCCCGAGGAGTA  660
```

```
Qy  1671 ATTTTAATATACCTAGTTATAGACATTTCACCTTTGGATACTTTTGGCAATTCATATC 1730
              |||-||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATTTTAATATACCTAGTTATAGACATTTCACCTTTGGATACTTTTGGCAATTCATATC  720
```

```
Qy  1731 GTAGCAGAAAAAAGAAAAAAAATAAAAGAATTTTAAAGATAATAATGGGACTTCATGATACT 1790
              |||||||||||||||||||||||||||-|||||||||||||||||||||||||||||||||
Db   721 GTAGCAGAAAAAAGAAAAAAAATAAAAGAATTTTAAAGATAATAATGGGACTTCATGATACT  780
```

```
Qy  1791 GCCTTTTGGCTTCCTGGGTTCTTCTATATACAGTTTAATTTTCTTATGTCCCTTCTT 1850
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db   781 GCCTTTTGGCTTCCTGGGTTCTTCTATAWACAAGTTTAATTTTCTTATGTCCCTTCTT  840
```

```
Qy  1851 ATGGCAGTCATTGCGACAGCTTCTTGTATTCCTCAAAGTAGCAGCATTGTGATATTT 1910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ATGGCAGTCATTGCGACAGCTTCTTGTATTCCTCAAAGTAGCAGCATTGTGATATTT  900
```

```
Qy  1911 CTGCTTTTTTTTCCTTATGGATTATCATCGTGTATTTTTTTGCTTAATGCTGACACCTCTT 1970
              |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db   901 CTGCTTTTTTTTCCTTATGGATTATCATCGTGTATTTTTTTGCTTAATGCTGACACCTCTT  960
```

```
Qy  1971 TTTAAAAATTCAAAACATGTGGGAATAGTTGAATTTTTGTTACTGTGGCTTTTGGATTT 2030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTTAAAAATTCAAAACATGTGGGAATAGTTGAATTTTTGTTACTGTGGCTTTTGGATTT 1020
```

```
Qy  2031 ATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTAGTGTGGCTTTTCAGT 2090
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 ATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTAGTGTGGCTTTTCAGT 1080
```

```
Qy  2091 CCTTTCGTCACTGTACTTTGTGATTGGTATTGCACAGGTCATGCATTAGAAGATTT 2150
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CCTTTCGTCACTGTACTTTGTGATTGGTATTGCACAGGTCATGCATTAGAAGATTT 1140
```

```
Qy  2151 AATGAAGGTGCTTCATTTCAAATTGACTGCAGGCCCATATCCTCTAATTATTACAATT 2210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 AATGAAGGTGCTTCATTTCAAATTGACTGCAGGCCCATATCCTCTAATTATTACAATT 1200
```

```
Qy  2211 ATCATGTCCACACTTAATAGTATATTCTATGTCCTCTGGCTGTCTATCTTGATCAAGTC 2270
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 ATCATGTCCACACTTAATAGTATATTCTATGTCCTCTGGCTGTCTATCTTGATCAAGTC 1260
```

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Qy  2271 ATTCCAGGGGAATTGGCTTACCGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 2330
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 ATTCCAGGGGAATTGGCTTACCGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 1320
```

```
Qy  2331 TCAAAGAGTAAAAGAAATTATGAGCCAGTTTCTTCAGAATTGTAAGGCAATGTTAATGGAAATATTAGT 2390
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 TCAAAGAGTAAAAGAAATTATGAGCCAGTTTCTTCAGAATTGTAAGGCAATGTTAATGGAAATATTAGT 1380
```

```
Qy  2391 TTTAGTGAAATTATTGAGCCAGTTTCTTCAGAATTGTAGGAGAGAGCCATAAGAATT 2450
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 TTTAGTGAAATTATTGAGCCAGTTTCTTCAGAATTGTAGGAGAGAGCCATAAGAATT 1440
```

```
Qy  2451 AGTGGTATTCAGAGACATACAGAAAGAGGGTGAAAATGTGAAGCCTTGAGAAATTTG 2510
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 AGTGGTATTCAGAGACATACAGAAAGAGGGTGAAAATGTGAAGCCTTGAGAAATTTG 1500
```

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Qy  2511 TCATTGACATATATGAGGGTCAGATTACTGCCCTTACTTGGCCACAGTGGAACAGGAAAG 2570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 TCATTGACATATATGAGGGTCAGATTACTGCCCTTACTTGGCCACAGTGGAACAGGAAAG 1560
```

```
Qy  2571 AGTACATTGATGAATATTCTTTGTGGACTTCTGCCCACCTTCGATGGGTTTGCATCCATA 2630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 AGTACATTGATGAATATTCTTTGTGGACTTCTGCCCACCTTCGATGGGTTTGCATCCATA 1620
```

```
Qy  2631 TATGGACACAGAGTCTCAGAAATAGATGAAATGTTGAAGCAAGAAAAATGATTGGCATT 2690
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```
Db  2701 TTTCTAAAACCTGGAGCAAACCACATAAATACAAACAAGCTGTCTTCTTCAAAATTCT 2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3771 GCTGACTCAGATATCAGTGATCTGATCTTATTAGCTTTTCACAAGCCAGAACATAATGGTGACG 3830
Db  2761 GCTGACTCAGATATCAGTGATCTGATCTTATTAGCTTTTCACAAGCCAGAACATAATGTGACG 2820

Qy  3831 ATGATTAATGACAGTGACTATCGTATCGTGCTCCCATAGTGCGGCTTTAAATGTGATG 3890
Db  2821 ATGATTAATGACAGTGACTATCGTATCGTGCTCCCATAGTGCGGCTTTAAATGTGRTG 2880

Qy  3891 CATTCAGAAAAGGACTATGTTTTGCAGCTGTTTCAACAGTACTATGGTTATTCTTA 3950
Db  2881 CATTCAGAAAAGGACTATGTTTTGCAGCTGTTTCAACAGTACTATGGTTATTCTTA 2940

Qy  3951 CCTATATTAGTGAATATCATYAGTAACTACTATCTTTATCATTAAATGTGACTGAAAAC 4010
Db  2941 CCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCATTAAATGTGACTGAAAAC 3000

Qy  4011 ATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGATATAGTTTTAAAATTGAG 4070
Db  3001 ATCCAGATCTGGAGTACCCCATTCTTTCAAGAAATTACTGATATAGTTTTAAAATTGAG 3060

Qy  4071 CTGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCC 4130
Db  3061 CTGTATTTTCAAGCAGCTTTGCTTGGAATCATTGTTACTGCAATGCCACCTTACTTTGCC 3120

Qy  4131 ATGGAAAATGCAGAGAATCATAAGATCAAAGCTTATACTCAACTTAAACTTTCAGTGTCTT 4190
Db  3121 ATGGAAAATGCAGAGAATCATAAGATCAAAGCTTAYACTCAACTTAAACTTTCAGTGTCTT 3180

Qy  4191 TTGCCATCTGCATATTGGATTGGACAAGCTGTGTTGATATCCCCTTATTTTTATCATT 4250
Db  3181 TTGCCATCTGCATATTGGATTGGACAAGCTGTGTTGATATCCCCTTATTTTTATCATT 3240

Qy  4251 CTTATTTTGATGCTAGGAAGCTTACTGGCATTCATTATGATTATATTTTATACTGTA 4310
Db  3241 CTTATTTTGATGCTAGGAAGCTTACTGGCATTCATTATGATTATATTTTATACTGTA 3300

Qy  4311 AAGTTCCTTGCGTGTGTTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACT 4370
Db  3301 AAGTTCCTTGCGTGTGTTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACT 3360

Qy  4371 TATATTGCTTCTTCACCTTTAAGAAAATTTAAATACCAAAGAATTTGGTCATTTATC 4430
Db  3361 TATATTGCTTCTTCACCTTTAAGAAAATTTAAATACCAAAGAATTTGGTCATTTATC 3420

Qy  4431 TATTCTGTGGCAGCGTTGNCTTGTATTGCAATCACTGAAATAACTTCTTTATGGGATAC 4490
Db  3421 TATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACTTCTTTATGGGATAC 3480

Qy  4491 ACAATTGCAACTATCTTCTTGTATCTATCCAATCTATCCACTTCTA 4550
Db  3481 ACAATTGCAACTATCTTCTTGTATCTATCCAATCTATCCACTTCTA 3540

Qy  4551 GGTTGCCTGATTTCTTTCTTCATAAGATTTCTTGGAGAATGTACGAAAAAATGTGGACACC 4610
Db  3541 GGTTGCCTGATTTCTTTCTTCATAAAGATTTCTTGGAAGAATGTACGAAAAAATGTGGACACC 3600

Qy  4611 TATAATCCATGGATAGGCTTCAGTAGCTTTCACACGGCTTACCTGCGAGTGTCTACTG 4670
Db  3601 TATAATCCATGGATAGGCTTCAGTAGCTTTCACACGGCTTACCTGCGAGTGTCTACTG 3660

Qy  4671 TGGATTTCCTCTTACAAATACTATGAGAAAAATATGGAGGCAGATCAATAAGAAAAGAT 4730
Db  3661 TGGATTTCCTCTTACAAATACTATGAGAAAAATATGGAGGCAGATCAATAAGAAAAGAT 3720

Qy  4731 CCCTTTTTCAGAAACCTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCACCAGAC 4790
Db  3721 CCCTTTTTCAGAAACCTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCACCAGAC 3780

Qy  4791 AATGAGGATGAAGATGAAGATGTCAAAGGTCAAAGAGCTGATGGGT 4850
Db  3781 AATGAGGATGAAGATGAAGATGTCAAAGGTCAAAGAGCTGATGGGT 3840
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Db  1621 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TATGGACACAGAGTCTCAGAAATAGATGAAATGTTGAGCAAGAAAAATGATTGGCATT 1680

Qy  2691 TGTCCACAGTTAGTATATACACTTTGATGTTGTTGACAGTAGAAGAAAAATTATCAATTTTG 2750
Db  1681 TGTCCACAGTTAGTATATACACTTTGATGTTGTTGACAGTAGAAGAAAAATTATCAATTTTG 1740

Qy  2751 GCTTCAATCAAAGGGATACCAGCCAACCAATATAATACAAGAGAGTTTTACTA 2810
Db  1741 GCTTCAATCAAAGGGATACCAGCCAATATAATACAAGAGAGTTTTACTA 1800

Qy  2811 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 2870
Db  1801 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 1860

Qy  2871 AGAAAGCTGTCATTAGGAATTGCTGTTCTGGGAACCCAAAGATACTGCTGCTAGATGAA 2930
Db  1861 AGAAAGCTGTCATTAGGAATTGCTGTTCTGGGAACCCAAAGATACTGCTGCTAGATGAA 1920

Qy  2931 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGATGGAATCTTTAAAATACAGA 2990
Db  1921 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGATGGAATCTTTAAAATACAGA 1980

Qy  2991 AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTCATTCAGTGTGTTCTTCAATGTTCCTC 3050
Db  1981 AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTCATTCAGTGTGTTCTTCAATGTTCCTC 2040

Qy  3051 GATAGGAAAGCTGTGTATATCACAAGGAATGCTGAAATGTCAAAGCTGAAAGTGTTCCTC 3110
Db  2041 GATAGGAAAGCTGTGTATATCACAAGGAATGCTGAAATGTCAAAGCTGAAAGTGTTCCTC 2100

Qy  3111 AAAAGTAAATGGGGATCGGCTACCGCCTGAGCCTACTTTATTACAACAGAAT 3170
Db  2101 AAAAGTAAATGGGGATCGGCTACCGCCTGAGCCTACTTTATTACAACAGAAT 2160

Qy  3171 GAATCTCTTCTTCACTGGTTAAAACAACATTATTACAACAGAAT 3230
Db  2161 GAATCTCTTCTTCACTGGTTAAAACAACATTATTACAACAGAAT 2220

Qy  3231 GACCAACAACTTGTGTATAGCTTGCCTTCAAGGACATGGACAAAATTTCAGGTTGTTT 3290
Db  2221 GACCAACAACTTGTGTATAGCTTGCCTTCAAGGACATGGACAAAATTTCAGGTTGTTT 2280

Qy  3291 TCTGCCCTAGACAGTCATTCAAATTGGGTGTCATTGTTCCATGACGACT 3350
Db  2281 TCTGCCCTAGACAGTCATTCAAATTGGGTGTCATTGTTCCATGACGACT 2340

Qy  3351 TTGGAAGAGCTATTTTAAAGCTAGAAGTTGAAGCAGAAAATTGACCAAGCAGATTATAGT 3410
Db  2341 TTGGAAGAGCTATTTTAAAGCTAGAAGTTGAAGCAGAAAATTGACCAAGCAGATTATAGT 2400

Qy  3411 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTGATGAAAATGGAA 3470
Db  2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTGATGAAAATGGAA 2460

Qy  3471 CAGAGCTTACTTATTCTTCTGAAACCAAGGCTTCTCAGTGAGCACCATGAGCCTTTGG 3530
Db  2461 CAGAGCTTACTTATTCTTCTGAAACCAAGGCTKCTCAGTGAGCACCATGAGCCTTTGG 2520

Qy  3531 AAACAACAGATGTATACAATAGCAAAGTTTCATTCTTTCATTCTTCTTTAATGTTTT 3590
Db  2521 AAACAACAGATGTATACAATAGCAAAGTTTCATTCTTTCATTCTTCTTTAATGTTTT 2580

Qy  3591 TCAGTGAGATCAGTGTTGCTTCTGCTTTAATTTTTTTCACAGTTCAGATTTTTATGTTT 3650
Db  2581 TCAGTGAGATCAGTGTTGCTTCTGCTTTAATTTTTTTCACAGTTCAGATTTTTATGTTT 2640

Qy  3651 TTGGTTCATCACTCTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCGACTTATAT 3710
Db  2641 TTGGTTCATCACTCTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCGACTTATAT 2700

Qy  3711 TTTCTAAAACCTGGAGCAACAAACCACATAAATACAAAACAAGCTGTCTTCTTCAAAATTCT 3770
Db  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 160
; LENGTH: 3347
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-160

Query Match        49.9%;    Score 3258.2;    DB 16;    Length 3347;
Best Local Similarity    98.5%;    Pred. No. 0;
Matches 3327;    Conservative 0;    Mismatches 0;    Indels 47;    Gaps 2;
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Qy  2999  TCGGGTGACAGTGTTCAGTACTCATTCATTCATGGATGAAGCTGACATTCTTGAGATAGGAA  3058
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  TCGGGTGACAGTGTTCAGTACTCATTCATTCATGGATGAAGCTGACATTCTTGAGATAGGAA    60

Qy  3059  AGCTGTGATATCACAAGGAATGCTGAAATGTGTTGGTTCTTCCTCCACAAAGTAA  3118
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  AGCTGTGATATCACAAGGAATGCTGAAATGTGTTGGTTCTTCCTCCACAAAGTAA   120

Qy  3119  ATGGGGGATCGGCTACCGCCTGAGCATGCATAGACAAATATTGTGCCACAGAATCTCT  3178
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  ATGGGGGATCGGCTACCGCCTGAGCATGCATAGACAAATATTGTGCCACAGAATCTCT   180

Qy  3179  TTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAATGACCAACA  3238
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAATGACCAACA   240

Qy  3239  ACTTGTGTATAGCTTGCCTTCAAGGACATGGACAAATTTCAGGTTGTTTTCTGCCCT  3298
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ACTTGTGTATAGCTTGCCTTCAAGGACATGGACAAATTTCAGGTTGTTTTCTGCCCT   300

Qy  3299  AGACAGTCATTCAAATTGGGTGTCATTTCTTATGGTGTTTCCATGACGACTTTGGAAGA  3358
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AGACAGTCATTCAAATTGGGTGTCATTTCTTATGGTGTTTCCATGACGACTTTGGAAGA   360

Qy  3359  CGTATTTTTAAAGCTAGAGTTGAAGCAGAAATGACCAAGCAGATTATAGTGTATTTAC  3418
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  CGTATTTTTAAAGCTAGAGTTGAAGCAGAAATGACCAAGCAGATTATAGTGTATTTAC   420

Qy  3419  TCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTGATGAAATGGACAGAGCTT  3478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  TCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTGATGAAATGGACAGAGCTT   480

Qy  3479  ACTTATTCTTTCTGAAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTGGAAACAACA  3538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  ACTTATTCTTTCTGAAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTGGAAACAACA   540

Qy  3539  GATGTATACAATAGCAAAGTTCATTCTTCATTTCTTCTTCACCTTGAAAGTAAATCAGTGAG  3598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GATGTATACAATAGCAAAGTTCATTCTTCATTTCTTCTTCACCTTGAAAGTAAATCAGTGAG   600

Qy  3599  ATCAGTGTTGCTTCGCTTTAATTTTTCACAGTTCAGATTTTTTGGTTCA  3658
          ||||||||||||||||||||||||||||||||||||||||||||
Db   601  ATCAGTGTTGCTTCGCTTTAATTTTTCACAGTTCAGATTTTTTGGTTCA   660

Qy  3659  TCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACAAAACAAGCTGCTTCTTCAAATTCTGCT--------  3718
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  TCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACAAAACAAGCTGCTTCTTCAAATTCTGCT   720

Qy  3719  ACCTGGAGACAAACCCATAAATACAAAACAAGCTGCTTCTTCAAAATTCTGCT----  3773
          |||||||||||||||||||||||||||||||||||||
Db   721  ACCTGGAGACAAACCCATAAATACAAAACAAGCTGATCTTATTAGCTTTTCACAAGCCAGAACATAA   780

Qy  3774  ----------GACTCAGATATCGAT  3822
          ||||||||||
Db   781  GAGTGTGAAGACTCAGATATCTGTGATCTTATTAGCTTTTTCACAAGCCAGAACATAA   840

Qy  3823  TGGTGACGATGAATAACAGTGACTATGTATCCGTGGCTCCCCATAGTGCGGCTTTAA  3882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  4851  TGCCAGTGTTGTGAGGAGAAACCATCCATTATGTGCAATTGCATAAAGAATATGAT  4910
          ||||||||||||||||||||||||||||||||||||||||||
Db  3841  TGCCAGTGTTGTGAGGAGAAACCATCCATTATGTGCAATTGCATAAAGAATATGAT  3900

Qy  4911  GACAAGAAAGATTTTCTTCTTCAGAAAAGTAAAGAAGTGGCAACTAAATACATCTCT  4970
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901  GACAAGAAAGATTTTCTTCTTCAGAAAAGTAAAGAAGTGGCAACTAAATACATCTCT  3960

Qy  4971  TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGCTGGCAAAAGC  5030
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961  TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGCTGGCAAAAGC  4020

Qy  5031  ACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTTAGGA  5090
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021  ACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTTAGGA  4080

Qy  5091  GATTATTCTTCAGAGACAAGTGAAGATGATGAGTGTACTGAAGTGTATGGGTTACTGTCCT  5150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081  GATTATTCTTCAGAGACAAGTGAAGATGATGAGTGTACTGAAGTGTATGGGTTACTGTCCT  4140

Qy  5151  CAGATAAACCCTTGTGGGCCAGATACTACACATTTGAAATTTATGGAGCT  5210
          ||||||||||||||||||||||||||||||||||||||||||
Db  4141  CAGATAAACCCTTGTGGGCCAGATACTACACATTTGAAATTTATGGAGCT  4200

Qy  5211  GTCAAAGGAATGAGTGCAAGTGACATGAAAGAGTCATAAGTCGAATAACACATGCACTT  5270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201  GTCAAAGGAATGAGTGCAAGTGACATGAAAGAGTCATAAGTCGAATAACACATGCACTT  4260

Qy  5271  GATTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAG  5330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4261  GATTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAG  4320

Qy  5331  TTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT  5390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4321  TTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT  4380

Qy  5391  ACAGGTATGGATCCCAAAGCCAAACAGCACACAGTGGCGCAATTCGAACTGCATTTAAA  5450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4381  ACAGGTATGGATCCCAAAGCCAAACAGCACACAGTGGCGCAATTCGAACTGCATTTAAA  4440

Qy  5451  AACAGAAAGCGGGGCTGCTATTCTGACCTCACTATATGGAGGAGGCGCTGTCTGT  5510
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  4441  AACAGAAAGCGGGGCTGCTATTCTGACCTCACTATATGGAGGAGGCGCTGTCTGT  4500

Qy  5511  GATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTA  5570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4501  GATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTA  4560

Qy  5571  AAGAGTAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTAAATTGAAGAGACTGGATAGAAAAC  5630
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4561  AAGAGTAAATTGGAAAAGGCTACTTTTTGGAAATTAAATTAAATTGAAGAGACTGGATAGAAAAC  4620

Qy  5631  CTAGAAGTAGACCCGCCTTCAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAG  5690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4621  CTAGAAGTAGACCCGCCTTCAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAG  4680

Qy  5691  GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTTCA  5750
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4681  GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTTCA  4740

Qy  5751  CAATCTTTTTTAAGCTGGAAGAAGCT  5777
          ||||||||||||||||||
Db  4741  CAATCTTTTTTAAGCTGGAAGAAGGT  4767
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RESULT 9
US-10-108-260A-160
; Sequence 160, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
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Db 841 TGGTGACGATGATTAATGACAGTGACTACTATGTATCCGTGCTCCCATAGTGCGGCTTTAA 900

Qy 3883 ATGTGATGACATTCAGAAAGGACTACATGGTTTTGCAGCTGTTTCAACAGTACTATGGTTT 3942
              |||| ||||||||||||||| ||||||| ||||||||||||||||||||||||||||||
Db 901 ATGTGATGCATTCAGAAAGGACTACATGGTTTTGCAGCTGTTTCAACAGTACTATGGTTT 960

Qy 3943 ATTCTTACCTATATTAGTGAATATCATTAGTAGTAACTACTACATCTTTATCATTTAAATGA 4002
              ||||||||||||||||||| ||||||||||||| ||||||||||| |||||||||||||
Db 961 ATTCTTTATCTATATTAGTGAATATCATTAGTAACTACTACATCTTTATCATTTAAATGTGA 1020

Qy 4003 CTGAAAACCATCCAGAGTCTGGAGTACCCCATTCTTCAAGAAAATTACTGCATAAGTTTTA 4062
              ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db 1021 CTGAAAACCATCCAGATCTGGAGTACCCCATTCTTCAAGAAAATTACTGCATATAGTTTTA 1080

Qy 4063 AAATTGAGCTGTATTTCAAGCAGCTTGCTTGGAATCATTGTTACTGCAATGCCACCTT 4122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 AAATTGAGCTGTATTTCAAGCAGCTTGCTTGGAATCATTGTTACTGCAATGCCACCTT 1140

Qy 4123 ACTTTGCCATGGAAAATGCAGAGAATCATAAAGATCAAAGCTTATACTCAACTTAAACTTT 4182
              ||||||||||||||||||||
Db 1141 ACTTTGCCATGGAAAATGCAGAGAATCATA------------------------------ 1170

Qy 4183 CAGTGTCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCCTTATTTT 4242
              ||| |||||| |||||||||||||||||||| |||||||||||||||||||||||||||
Db 1171 -AGGTCTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCCTTATTTT 1229

Qy 4243 TTATCATTCTTATTTGATGCTAGGAAGCTTACTGGAAGCTTATTGGCATTCATTATGGATGATAATTTT 4302
              ||| |||||||||||||||| ||||||||| ||||||| |||| |||||||||||||
Db 1230 TTATCATTCTTATTTGATGCTAGGAAGCTTACTGGAAGCTTATTGGCATTCATTGGATATATTTT 1289

Qy 4303 ATACTGTAAAGTTCCTTGCCTGTGGTTTTTGCCCTTATTGGTTATGTTCCATCAGTTATTC 4362
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1290 ATACTGTAAAGTTCCTTGCCTGTGGTTTTTGCCCTTATTGGTTATGTTCCATCAGTTATTC 1349

Qy 4363 TGTTCACTTATATTGCTTCTTCTTTAAGGAAAATTTAAATACCAAAGAATTTTGGT 4422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1350 TGTTCACTTATATTGCTTCTTCTTTAAGGAAAATTTAAATACCAAAGAATTTTGGT 1409

Qy 4423 CATTTATCATTCTGTGGCAGCGTTGNCTTGGCTTGTATTGCAATCACTGAAATAACTTCTTA 4482
              ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db 1410 CATTTATCTATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACTTTCTTA 1469

Qy 4483 TGGGATACACAATTGCGAACTATTCTTCATTATGCCTTTTGTATCATCATTCCAATCTATC 4542
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1470 TGGGATACACAATTGCGAACTATTCTTCATTATGCCTTTTGTATCATCATTCCAATCTATC 1529

Qy 4543 CACTTCTAGGTTGCCTGATTTCTTCAGTTGTTATATCGGCTTACCTGCAGT 4602
              |||||| |||||| |||||||||| |||||||||||||||||||||||||||
Db 1530 CACTTCCAGGTTGCCTGATTTCTTCAGTAGTGTTATATCGGCTTACCTGCAGT 1589

Qy 4603 TGGACACCTATAATCCATGGGATATCCTTACAATAATATGAGAAAAATATGAGGCAGATCAATAA 4662
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1590 TGGACACCTATAATCCATGGGATATCCTTACAATAATATGAGAAAAATATGAGGCAGATCAATAA 1649

Qy 4663 GTGTACTGTGGATTTTCTCTTACAATACTATGAGAAAAATATGAGGAGGCAGATCAATAA 4722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1650 GTGTACTGTGGATTTTCTCTTACAATACTATGAGAAAAATATGAGGAGGCAGATCAATAA 1709

Qy 4723 GAAAAGATCCCTTTTTCAGAAACCTTTCAAGAAAACCTTTCAAGAAGTCTAAAGAACTTCCAGAAC 4782
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1710 GAAAAGATCCCTTTTTCAGAAACCTTTCAAGAAAACCTTTCAAGAAGTCTAAAATAGAAGCTTCCAGAAC 1769

Qy 4783 CACCAGACAATGAGGATGAAGATGTCAAAGCTCAAAGTCAAAGAGC 4842
              |||||||||||||||||||||||||||||||||||||||||||||||
Db 1770 CACCAGACACAATGAGGATGAAGATGTCAAAGCTCAAAGTCAAAGAGC 1829

Qy 4843 TGATGGGTTGCCAGTGTTTGTGAGGAGAAACCATCATTATGTCAGCAATTTGCATAAAG 4902
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1830 TGATGGGTTGCCAGTGTTTGTGAGGAGAAACCATCATTATGTCAGCAATTTGCATAAAG 1889

Qy 4903 AATATGATGACAAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAAAGTGGCAACTAAAT 4962
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1890 AATATGATGACAAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAAAGTGGCAACTAAAT 1949

Qy 4963 ACATCTCTTTCTGTGTGAAAAAAGGAGGATCTTAGGACTATTGGGTCCAAATGGTGCTG 5022
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1950 ACATCTCTTTCTGTGTGAAAAAAGGAGGATCTTAGGACTATTGGGTCCAAATGGTGCTG 2009

Qy 5023 GCAAAAGCACAATTATTAATATTCTCGTTGGTGATATTGAACCAACTTCAGGCCAGGTAT 5082
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2010 GCAAAAGCACAATTATTAATATTCTCGTTGGTGATATTGAACCAACTTCAGCGCCAGGTAT 2069

Qy 5083 TTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGAAGATGATTCACTGAAGGTATGGGTT 5142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2070 TTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGAAGATGATTCACTGAAGTGTATGGGTT 2129

Qy 5143 ACTGTCCTCAGATAAACCCTTGTGCCAGATACTACATTGCAGGAGAACATTTTGAAATTT 5202
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2130 ACTGTCCTCAGATAAACCCTTGTGCCAGATACTACATTGCAGGAGAACATTTTGAAATTT 2189

Qy 5203 ATGGAGCTGTCAAAGAAGTGAGTGCAAGTGCAAGTGCAATGCTCAAGTGCAATAACAC 5262
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2190 ATGGAGCTGTCAAAGAAGTGAGTGCAAGTGCAAGTGCAATGCTCAAGTGCAATAACAC 2249

Qy 5263 ATGCACTTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCA 5322
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Db 2250 ATGCACTTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCA 2309

Qy 5323 AACGAAAGTTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTGCTCTAGATG 5382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2310 AACGAAAGTTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTGCTCTAGATG 2369

Qy 5383 AACCATCTACAGGGTATGGATCCCAAAGCCAAACAGCACATGCTGGCGAGCAATTCGAACTG 5442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2370 AACCATCTACAGGGTATGGATCCCAAAGCCAAACAGCACATGCTGGCGAGCAATTCGAACTG 2429

Qy 5443 CATTTAAAAACAGAACAGCGGGCGTGCTATTCTGACCACTCACTATGGAGGCAGAGG 5502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2430 CATTTAAAAACAGAACAGCGGGCGTGCTATTCTGACCACTCACTATGGAGGCAGAGG 2489

Qy 5503 CTGTCTGATCGAGTAGCTATCATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTAC 5562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2490 CTGTCTGATCGAGTAGCTATCATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTAC 2549

Qy 5563 AACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTAAATTGAAGGACTGGA 5622
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2550 AACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTAAATTGAAGGACTGGA 2609

Qy 5623 TAGAAAACCTAGAAGTAGAGACCGCCTTCAAAGAGAAATTCAGTATATATTTCCAAGAGAAGTTCAA 5682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2610 TAGAAAACCTAGAAGTAGAGACCGCCTTCAAAGAGAAATTCAGTATATATTTCCAAGAGAAGTTCAA 2669

Qy 5683 GCCGTCAGGAAGTTTCTCTATTTGGCTGGAAGAGCTAAACATGCTTTGCCATTGAAGAATGTTCAGT 5742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2670 CCCGTCAGGAAGTTTCTCTATTTGGCTGGAAGAGCTAAACATGCTTTGCCATTGAAGAATGTTCAGT 2729

Qy 5743 CCCTTTCACAATCTTTTTTTAAGCTGGAAGAGCTAAACATGCTTTTGCCATTGAAGAAT 5802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2730 CCCTTTCACAATCTTTTTTTTAAGCTGGAAGAGCTAAACATGCTTTTGCCATTGAAGAAT 2789

Qy 5803 ATAGCTTTTCTCAAGCAACATTGGAACCAGGTTTTGTAGAAACTCACTAAAGAACAAGAGAG 5862
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2790 ATAGCTTTTCTCAAGCAACATTGGAACCAGGTTTTGTAGAAACTCACTAAAGAACAAGAGAG 2849

Qy 5863 AGGAAGATATAAGTAGTGTGGAACTTAAACAGCACACTTGGTGGAACGAACAACAAGAAG 5922
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2850 AGGAAGATAATAGTAGT-GTGGAACTTAAACAGCACACTTGGTGGAACGAACAACAAGAAG 2909

Qy 5923 ATATGAGTAGTATTTGAATTGTAATTGTGTTCGGCTGCTTACTGGGACTTCTTCTTTTTC 5982
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2910 ATATGAGTAGTATTTGAATTTGTAATTGTGTTCGGTCGTGCTTACTGGGACTTCTTCTTTTTTTC 2969

Qy 5983 ACTTAATTTAACTTTGGTTTAAAAAGTTTTTATTGGAATGGTAACTGGACCAAGA 6042
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2970 ACTTAATTTAACTTTGGTTTAAAAAGTTTTTTTATTGGAATGGTAACTGGACCAAGA 3029

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Qy   6043  ACGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGTGTGTTTGCTTT  6102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3030  ACGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGTGTGTTTGCTTT  3089

Qy   6103  TCTTTAAATAAACGTATGTATAATTAAGTGAAGCTGCATGTTTGTATTGAAGTATATTG  6162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3090  TCTTTAAATAAACGTATGTATAATTAAGTGAAGCTGCATGTTTGTATTGAAGTATATTG  3149

Qy   6163  AACTATATAGTTGTATGTCATCTTTTCACCATTCAGAAACAGTGCTTCTGAATTTGTG  6222
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3150  AACTATATAGTTGTATGTCATCTTTTCACCATTCAGAAACAGTGCTTCTGAATTTGTG  3209

Qy   6223  ATTTAAAGGAATTGTAATAGAATAGTTTATTTTTAAGTTATCTTTAAGTTATGCCATC  6282
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3210  ATTTAAAGGAATTGTAATAGAATAGTTTATTTTTAAGTTATCTTTAAGTTATGCCATC  3269

Qy   6283  TTCTTAAATAAGTAGTACGTAATGTTCCAATCTAAATAAAAACTAATACATAACTAATGCAT  6342
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3270  TTCTTAAATAAGTAGTACGTAATGTTCCAATCTAAATAAAAACTAATACATAACTAATGCAT  3329

Qy   6343  AGAAAAGATACATAAAGC  6360
           ||||||||||||||||||
Db   3330  AGAAAAGATACATAAAGC  3347
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           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66  TGTGCCACAGAATCTCTTTCTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTA  125

Qy   3222  CAACAGAATGACCACAACAACTGTGTATAGCTTGCCTTCAAGGACATGGACAAATTTCA  3281
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126  CAACAGAATGACCACAACAACTGTGTATAGCTTGCCTTCAAGGACATGGACAAATTTCA  185

Qy   3282  G-----------------------------GTTTGTTTTCTGCCCTAGACAGTCAT  3308
           |                             ||||||||||||||||||||||||||
Db    186  GGAATTGCTTGATAGACAAAGGATGTGTATTGATGTTTGTTTTCTGCCCTAGACAGTCAT  245

Qy   3309  TCAAATTTGGGTGTCATTTCTTATGGTGTTCCATGAGACTTTGGAAGACGTGTATTTTA  3368
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246  TCAAATTTGGGTGTCATTTCTTATGGTGTTCCATGAGACTTTGGAAGACGTGTATTTTA  305

Qy   3369  AAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGTGTATTTACTCAGCAGCCA  3428
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306  AAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGTGTATTTACTCAGCAGCCA  365

Qy   3429  CTGGAGGAAGAAAATGGATTCAAAATCTTTTGATGAAATGAAAATCTTTGATGAAATGAAAATG  3488
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366  CTGGAGGAAGAAAATGGATTCAAAATCTTTTGATGAAATGAAACAACAGAGCTTACTTATTCTT  425

Qy   3489  TCTGAAACCAAGGCTTCTCGTGAGCACCATGGCCTTTGGAAACAACAGATGTATACA  3548
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426  TCTGAAACCAAGGCTTCTCGTGAGCACCATGGCCTTTGGAAACAACAGATGTATACA  485

Qy   3549  ATAGCAAAGTTCATTTCTTTACCTGAAACGTGAAAGTAAATCAGTGAGATCAGTGTTG  3608
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486  ATAGCAAAGTTCATTTCTTTACCTGAAACGTGAAAGTAAATCAGTGAGATCAGTGTTG  545

Qy   3609  CTTCTCGTTTAATTTTTTCACAGTTCAGATTTCAGATTTTTGGTTCATCACTCTTT  3668
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546  CTTCTCGTTTAATTTTTTCACAGTTCAGATTTCAGATTTTTGGTTCATCACTCTTT  605

Qy   3669  AAAAATGTCGTGGTCCCATCAAAACTGTTCCAGACTTATATTTCTAAAACCTGGAGAC  3728
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606  AAAAATGTCGTGGTCCCATCAAAACTGTTCCAGACTTATATTTCTAAAACCTGGAGAC  665

Qy   3729  AAACCACATAAATACAAAACAAGTCTGCTTCTCTCAAAATTCTGCTGACTCAGATATCAGT  3788
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666  AAACCACATAAATACAAAACAAGTCTGCTTCTCTCAAAATTCTGCTGACTCAGATATCAGT  725

Qy   3789  GATCTTATTAGCTTTTTCACAAGCCAGAACATAATGGTGACGATGATTAATGACAGTGAC  3848
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726  GATCTTATTAGCTTTTTCACAAGCCAGAACATAATGGTGACGATGATTAATGACAGTGAC  785

Qy   3849  TATGTATCCGTGGCTCCCCATAGTGCGGCTTTAAATGTGATGCATTCAGGAAAAGGACTAT  3908
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786  TATGTATCCGTGGCTCCCCATAGTGCGGCTTTAAATGTGATGCATTCAGGAAAAGGACTAT  845

Qy   3909  GTTTTTGCAGTGTGTTTCAACAGTACTATGGTTTATTCTTACCTATATTAGTAGTGAATATC  3968
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846  GTTTTTGCAGTGTGTTTCAACAGTACTATGGTTTATTCTTACCTATATTAGTAGTGAATATC  905

Qy   3969  ATTAGTAACTACATCTTTATCATTTATAAATGTGACTGAAAACCATCCAGATCTGGAGTACC  4028
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906  ATTAGTAACTACATCTTTATCATTTATAAATGTGACTGAAAACCATCCAGATCTGGAGTACC  965

Qy   4029  CCATTCTTCAAGAAATTACTGATATAGTTTTAAAATTGAGCGTGTATTTCAAGCAGCAGCT  4088
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966  CCATTCTTCAAGAAATTACTGATATAGTTTTAAAATTGAGCGTGTATTTCAAGCAGCAGCT  1025

Qy   4089  TTGCTTGGAATCATTGTTACTGCAATGCCAACCTTACTTGCCATGGAAAATGCAGAGAAT  4148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026  TTGCTTGGAATCATTGTTACTGCAATGCCAACCTTACTTGCCATGGAAAATGCAGAGAAT  1085

Qy   4149  CATAAGATCAAAGCTTATACTCAACTTAAACTTCAGTCTTTTGCCATCGCATATTGG  4208
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1086  CATAAGATCAAAGCTTATACTCAACTTAAACTTCAGTCTTTTGCCATCGCATATTGG  1145

Qy   4209  AATTGGACAAGCTGTGTGGTTGATATCCCCTTATTTTATCATTTTGATGCTAGGA  4268
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Query Match           48.7%;  Score 3178;  DB 15;  Length 3268;
Best Local Similarity 98.8%;  Pred. No. 0;
Matches 3224;  Conservative 0;  Mismatches 0;  Indels 33;  Gaps 1;

Qy   3102  ATGTTCCTCAAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATAT  3161
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6  ATGTTCCTCAAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATAT  65

Qy   3162  TGTGCCACAGAATCTCTTTCTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTA  3221
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Qy 5349 ATGCTAGGGAATCCTCAGATACTTTGCTCAGATGACCATCTCACAGGTATGGGATCCCAAA 5408
         ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db 2286 ATTCTAGGGAATCCTCAGATTACTTTGCTCAGATGACCATCTCACAGGTATGGGATCCCAAA 2345

Qy 5409 GCCAAACAGCACACATGTGGCGAGCAATTCGAACTGCATTTAAAACACAGAAAGCGGGCTGCT 5468
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2346 GCCAAACAGCACACATGTGGCGAGCAATTCGAACTGCATTTAAAACACAGAAAGCGGGCTGCT 2405

Qy 5469 ATTCTGACCACTCACTATATGGAGAGGCAGAGGCGTGTCTGATCGAGTAGCTATCATG 5528
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2406 ATTCTGACCACTCACTATATGGAGAGGCAGAGGCGTGTCTGATCGAGTAGCTATCATG 2465

Qy 5529 GTGTCTGGCAGTTAAGATGTATCGGAACAGTACACATCTCAAAGATAAATTGGAAAA 5588
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2466 GTGTCTGGGCAGTTAAGATGTATCGGAACAGTACACATCTCAAAGATAGATTGGAAAA 2525

Qy 5589 GGCTACTTTTTGGAAATTAAATTGAAGGACTGGATAGAAAACCTAGAAGTAGAACCGCCCTT 5648
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2526 GGCTACTTTTTGGAAATTAAATTGAAGGACTGGATAGAAAACCTAGAAGTAGAACCGCCCTT 2585

Qy 5649 CAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATT 5708
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2586 CAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATT 2645

Qy 5709 TTGGCTTATAAAATTCCTAAGGAGAGATGTTCAGTCCCTTCACAATCTTTTTTAAGCTG 5768
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2646 TTGGCTTATAAAATTCCTAAGGAGAAGATGTTCAGTCCCTTCACAATCTTTTTTAAGCTG 2705

Qy 5769 GAAGAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTTTCTCAAGCAACATTGGAA 5828
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2706 GAAGAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTTTCTCAGGCAACATTGGAA 2765

Qy 5829 CAGGTTTTTGTAGAACTCACTGGGAACGACATCTTCTTTTCTTTTTTAAGTTGTGGAACTTTA 5888
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2766 CAGGTTTTTGTAGAACTCACTGGGAACGACATCTTCTTTTCTTTTTTAAGTTGTGGAACTTTA 2825

Qy 5889 AACAGCACACTTTGGTGGGAACGACACTCTTCTTTTCTTTTTAACTTAATTTAACTTTGTATT 5948
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2826 AACAGCACACTTTGGTGGGAACGACACTCTTCTTTTCTTTTTAACTTAATTTAACTTTGTATT 2885

Qy 5949 GTTCGGTCTGCTTACTGGGACTTCTTCTTTTTCACTTAATTTTCACTTAATTTTCTAAGCTCC 6008
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2886 GTTCGGTCTGCTTACTGGGACTTCTTCTTTTTCACTTAATTTTCACTTAATTTTCTAAGCTCC 2945

Qy 6009 GTTTTTTATTGGAATGGTAACTGGAATGGTAACTGGAATGGTGTGTTTTGCTTTTTGCTTTTTTAAAAA 6068
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2946 GTTTTTTATTGGAATGGTAACTGGAATGGTAACTGGAATGGTGTGTTTTGCTTTTTGCTTTTTCTAAGCTCC 3005

Qy 6069 TTAATTGAAATGCTGTGGTTGTGTTTTGCTTTTCTTTAAATAAAACGTATGTATAATT 6128
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3006 TTAATTGAAATGCTGTGGTTGTGTTTTGCTTTTCTTTAAATAAAACGTATGTATAATT 3065

Qy 6129 AAGTGAAGCTGCATGTTGTATTGTAGGATTATTCTTCAGACATATATAGTTGTATGTCATCTTT 6188
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3066 AAGTGAAGCTGCATGTTGTATTGTAGGATTATTCTTCAGACATATATAGTTGTATGTCATCTTT 3125

Qy 6189 TTCACCATTCAGAAACAGTGCTTCTGAATTTGTGATTTAAAGGAATTGTAATAGAATAGT 6248
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3126 TTCACCATTCAGAAACAGTGCTTCTGAATTTGTGATTTAAAGGAATTGTAATAGAATAGT 3185

Qy 6249 TTTATTTTAAGTTATCTTATGCCATCTTCTTAAATAAGTACGTAATGTTCCA 6308
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3186 TTTATTTTAAGTTATCTTATGCCATCTCTTAAATAAGTACGTAATGTTCCA 3245

Qy 6309 ATCTAAATAAAAAAACTAATACAT 6331
         ||||||||||||||||||||||
Db 3246 ATCTAAATAAAAAAACTAATACAT 3268

RESULT 11
US-09-822-846-98
; Sequence 98, Application US/09822846

Db 1146 ATTGGACAAGCTGCTGTGATATCCCCTTATTTTTTATCATTCTTATTTTGATGCTAGGA 1205
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Qy 4269 AGCTTACTGGCATTCATTATGGATTATATTTTTATACTGTAAAGTTCCTTGCTGTGGTT 4328

Db 1206 AGCTTACTGGCATTCATTATGGATTATATTTTTATACTGTAAAGTTCCTTGCTGTGGTT 1265
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Qy 4329 TTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACTATATGCTTCTTTCCACC 4388

Db 1266 TTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACTATATGCTTCTTTCCACC 1325
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Qy 4389 TTTAAGAAAATTTAAATACCAAAGAATTTGGTCATTTATCATTCTCGTGGCAGCCGTTG 4448

Db 1326 TTTAAGAAAATTTAAAATACCAAAGAATTTGGTCATTTATCATTCTCGTGGCAGCCGTTG 1385
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Qy 4449 NCTTGTAATTGCAATCACTGAAAATAACTTTCTTATGGGATACACAATTGCAACTATTCTT 4508

Db 1386 GCTTGTAATTGCAATCACTGAAAATAACTTTCTTATGGGATACACAATTGCAACTATTCTT 1445
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4509 CATTATGCCTTTGTATCATCATTCCAATCATCCACTTCACTTGCTGTTGCCTGATTTCTTTC 4568

Db 1446 CATTATGCCTTTGTATCATCATTCCAATCATCCACTTCACTTGCTGTTGCCTGATTTCTTTC 1505
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Qy 4569 ATAAAGATTTCTTGGAAGAATGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGG 4628

Db 1506 ATAAAGATTTCTTGGAAGAATGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGG 1565
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4629 CTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTACTGTACTTTCCTCTTACAA 4688

Db 1566 CTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTACTGTACTTTCCTCTTACAA 1625
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Qy 4689 TACTATGAGAAAAAATATGGAGGCAGATCAATAGAAAGATCCCTTTTCAGAAACCTT 4748

Db 1626 TACTATGAGAAAAAATATGGAGGCAGATCAATAGAAAGATCCCTTTTCAGAAACCTT 1685
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4749 TCAACGAAGCTAAAAATAGGAGAGCTTCAAAGGTCAAAGAGAGGATGAAGATGAA 4808

Db 1686 TCAACGAAGCTAAAAATAGGAGAGCTTCAAAGGTCAAAGAGAGGATGAAGATGAA 1745
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4809 GATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCTTGCCAGTGTTGCCAGTGTGAGGAG 4868

Db 1746 GATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCTTGCCAGTGTTGCCAGTGTGAGGAG 1805
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4869 AAACCATCCATTATGGTCAGCAATTTGCATAAAGGTCAAAGAAAATATGATGCAAGAGAATTTCTT 4928

Db 1806 AAACCATCCATTATGGTCAGCAATTTGCATAAAGGTCAAAGAATATGATGCAAGAGAATTTCTT 1865
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4929 CTTTCAAGAAAAGTAAAGAAAGGTGGCAACTAAATACATCTCTTTCGTGTGTGAAAAAAGGA 4988

Db 1866 CTTTCAAGAAAAGTAAAGAAAGTAAAGAAAGGTGGCAACTAAATACATCTCTTTCGTGTGTGAAAAAAGGA 1925
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4989 GAGATCTTAGGACTATTGGGTCCAAAATGGTCGCAAAAGCACAACAATTATTAATAATTCTG 5048

Db 1926 GAGATCTTAGGACTATTGGGTCCAAAATGGTCGCAAAAGCACAACAATTATTAATAATTCTG 1985
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5049 GTTGGTGATATTGAACCAACTTCAGGCCCAGGTATTTTTAGGAGATTATTCTTCAGAGACA 5108

Db 1986 GTTGGTGATATTGAACCAACTTCAGGCCCAGGTATTTTTAGGAGATTATTCTTCAGAGACA 2045
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5109 AGTGAAGATGATTCACTGAAGTGTATGGGTTACTGTCCTCAGATAAACCCTTTGTGG 5168

Db 2046 AGTGAAGATGATTCACTGAAGTGTATGGGTTACTGTCCTCAGATAAACCCTTTGTGG 2105
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5169 CCAGATACTACATTGCAGGAACATTTATGGAGCTGTCAAAGGATGAGTAGTGCA 5228

Db 2106 CCAGATACTACATTGCAGGAACATTTATGGAGCTGTCAAAGGAATGAGTAGTGCA 2165
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5229 AGTGACATGAAAGAAGTCATAAGTCGAATAACATGCACTTGATTTAAAGAACATCTT 5288

Db 2166 AGTGACATGAAAGAAGTCATAAGTCGAATAACATGCACTTGATTTAAAGAACATCTT 2225
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Qy 5289 CAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAGGAAGTTGTGTTTTGCTTGTAAGT 5348

Db 2226 CAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAGGAAGTTGTGTTTTGCTTGTAAGT 2285

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Query Match     27.4%;  Score 1789.4;  DB 10;  Length 3928;
Best Local Similarity  98.2%;  Pred. No. 0;
Matches 1833;  Conservative  0;  Mismatches  0;  Indels 33;  Gaps 1;

Qy  1941  GTATTTTTGCTTAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTT  2000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  GTATTTTTGCTTAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTT    60

Qy  2001  GAATTTTTGTTACTGTGGCTTTTGGATTTATTGGCCTATGATAATCCTCATAGAAAGT  2060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GAATTTTTGTTACTGTGGCTTTTGGATTTATTGGCCTATGATAATCCTCATAGAAAGT   120

Qy  2061  TTTCCCAAATCGTTAGTGTGGCTTTTCAGTCCTTTCTGTCCACTGTACTTTGTGATTGGT  2120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  TTTCCCAAATCGTTAGTGTGGCTTTTCAGTCCTTTCTGTCCACTGTACTTTGTGATTGGT   180

Qy  2121  ATTGCACAGGTCATGCATTAGAAGATTTAATGAAGGTGCTTCATTTCAAATTTGACT  2180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ATTGCACAGGTCATGCATTAGAAGATTTAATGAAGGTGCTTCATTTCAAATTTGACT   240

Qy  2181  GCAGGCCCATATCCTAATTATTACAATTATCATGCTCACACTTAATAGTATATTCTAT  2240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GCAGGCCCATATCCTAATTATTACAATTATCATGCTCACACTTAATAGTATATTCTAT   300

Qy  2241  GTCCTCTTGGCTGTCTATCTTGATCAAGTCATTCCAGGGGAATTGGCTTACGGAGATCA  2300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  GTCCTCTTGGCTGTCTATCTTGATCAAGTCATTCCAGGGGAATTGGCTTACGGAGATCA   360

Qy  2301  TCTTTATATTTTCTGAAGCCTTCATATGGTCAAAGAGTTAAAAGAAATTATGAGGAGTTA  2360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  TCTTTATATTTTCTGAAGCCTTCATATGGTCAAAGAGTTAAAAGAAATTATGAGGAGTTA   420

Qy  2361  TCAGAGGGCAATGTAATGAAATATTAGTTTTAGTGAAATTATTGAGCCAGTTCTTCA  2420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  TCAGAGGGCAATGTAATGAAATATTAGTTTTAGTGAAATTATTGAGCCAGTTCTTCA   480

Qy  2421  GAATTTGTAGGAAAAGAAGCCATAAGAATTAGTGGTATTCAGAAGACATACAGAAAGAAG  2480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  GAATTTGTAGGAAAAGAAGCCATAAGAATTAGTGGTATTCAGAAGACATACAGAAAGAAG   540

Qy  2481  GGTGAAAATGTGGGAGGCTTTGAGAAATTTGTCATTGACATATGAGGGTCAGATTACT  2540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GGTGAAAATGTGGGAGGCTTTGAGAAATTTGTCATTGACATATGAGGGTCAGATTACT   600

Qy  2541  GCCTTACTTGGCCACAGTGGAAGAGGAAGAGTACAATGATGAATATCCTTGTGGACTC  2600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  GCCTTACTTGGCCACAGTGGAAGAGGAAGAGTACAATGATGAATATCTTGTGGACTC   660

Qy  2601  TGCCCACCTTCTGATGGTTTGCATCTATATATGGGACCACAGAGTCTCAGAAATAGATGAA  2660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  TGCCCACCTTCTGATGGTTTGCATCTATATATGGGACCACAGAGTCTCAGAAATAGATGAA   720

Qy  2661  ATGTTTGAAGCAAGAAAAATTATCAATTTGGCATTGTCCACAGTTAGATATACACTTTGATGTT  2720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ATGTTTGAAGCAAGAAAAATGATTGGCATTGTCCACAGTTAGATATACACTTTGATGTT   780

Qy  2721  TTGACAGTAGAAGAAATTATCAATTTGGCTTCAATCAAAGGGATACCAGCCAACAAT  2780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  TTGACAGTAGAAGAAATTATCAATTTGGCTTCAATCAAAGGGATACCAGCCAACAAT   840

Qy  2781  ATAATACAAGAAGTGCAGAAGTTTACTAGATTAGACATGGAGACATCAAAGATAAC  2840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  ATAATACAAGAAGTGCAGAAGTTTACTAGATTAGACATGCGAGACTATCAAAGATAAC   900

Qy  2841  CAAGGTAAAAATTAAGTCGTGGTCAAAAAAGAAAGTCTGTCATTAGGAATTGCTGTTCTT  2900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CAAGGTAAAAAATTAAGTCGTGGTCAAAAAAGAAAGCTGTCATTAGGAATTGCTGTTCTT   960

Qy  2901  GGGACCCAAAGATACTCGCTCTAGATGAACCACAGCTGGAATGGACCCCTGTTCTCGA  2960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  GGGACCCAAAGATACTGCTCTAGATGAACCACAGCTGGAATGGACCCCTGTTCTCCGA   1020

Qy  2961  CATATTGTATGGAATCTTTAAAATACAGAAAAGCCAATCGGTGACAGTGTTCAGTGTACT  3020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  CATATTGTATGGAATCTTTAAAATACAGAAAAGCCAATCGGTGACAGTGTTCAGTGTACT   1080

Qy  3021  CATTTCATGGATGAAGCTGACATTCTTGCAGATAGGAGAAGCTGTGATATCACAAGGAATG  3080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  CATTTCATGGATGAAGCTGACATTCTTGCAGATAGGAGAAGCTGTGATATCACAAGGAATG   1140

Qy  3081  CTGAAATGTGTGGTTCTTCAAGTCCTCAAAGTAAATGGGGATCGGCTACCGCCTG  3140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  CTGAAATGTGTTGGTTCTTCCAATGTCCTCAAAGTAAATGGGGATCGGCTACCGCCTG   1200

Qy  3141  AGCATGTACATAGACAAATATTGTCCACAGAATCTCTTCTTCACTGGTAAACACAT  3200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  AGCATGTACATAGACAAATATTGTCCACAGAATCTCTTCTTCACTGGTAAACACAT   1260

Qy  3201  ATACCTGGAGCTACTTATTACACAGATAATGACCAACAACTTGTGTAGAGCTGCCTTTC  3260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  ATACCTGGAGCTACTTATTACAACAGATAATGACCAACAACTTGTGTAGAGCTGCCTTTC   1320

Qy  3261  AAGGACATGGACAAATTTCAG-------------GTTTG  3287
          ||||||||||||||||||||||
Db  1321  AAGGACATGGACAAATTTCAGGGAATTGCTTGGATAGACAAAAGGATGTTATTGATGTTTG   1380

Qy  3288  TTTTCGCCCTAGACAGTCATTCAAATTTGGGGTGTCATTCCATGACGTGTTCCATGACG  3347
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  TTTTCGCCCTAGACAGTCATTCAAATTTGGGGTGTCATTCCATGACGTTCCATGACG   1440

Qy  3348  ACTTTGGAAGACGTATTTTAAAGCTAGAAGTGAAGCAGAAATTGACCAAGCAGATTAT  3407
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  ACTTTGGAAGACGTATTTTAAAGCTAGAAGTGAAGCAGAAATTGACCAAGCAGATTAT   1500

Qy  3408  AGTGTATTTACTCAGCAGCCACTGGAGGAAGAGAAATGAATCTTTGATGAAATG  3467
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  AGTGTATTTACTCAGCAGCCACTGGAGGAAGAGAAATGAATCTTTGATGAAATG   1560

Qy  3468  GAACAGAGCTTACTTATTCTTTCTGAACCAAGGCTTCTCAGTGAGCCATGAGCCTT  3527
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  GAACAGAGCTTACTTATTCTTTCTGAACCAAGGCTTCTCCTAGTGAGCCACCACGAGCCTT   1620
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Right column continuation markers:

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Db   481  ...GAAGAAGAAG   540
Db  2540  ...CGATTACT   2540
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Qy  3528 TGGAAACAACAGATGTATACAATAGCAAAGTTCATTTCTTTACCTTGAAACGTGAAAGT 3587
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TGGAAACAACAGATGTATACAATAGCAAAGTTCATTTCTTTACCTTGAAACGTGAAAGT 1680

Qy  3588 AAATCAGTAGAGATCAGTGTTGCTTCTGCTTTTAATTTTTTTCACAGTTCAGATTTTTATG 3647
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 AAATCAGTGAGATCAGTGTTGCTTCTGCTTTTAATTTTTTTCACAGTTCAGATTTTTATG 1740

Qy  3648 TTTTTGGTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTA 3707
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 TTTTTGGTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTA 1800

Qy  3708 TATTTTCTAAAACCTGGAGACAAACCACTACAAATACAAAACAAGTCTGCTTCTTCAAAT 3767
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 TATTTTCTAAAACCTGGAGACAAACCACTACAAATACAAAACAAGTCTGCTTCTTCAAAT 1860

Qy  3768 TCTGCTG 3774
         |||||||
Db  1861 TCTGCTG 1867
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RESULT 12
US-10-108-260A-1424
; Sequence 1424, Application US/10108260A
; Publication No. US2004005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1424
; LENGTH: 1943
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-1424

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Query Match      26.5%;  Score 1731.8;  DB 16;  Length 1943;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 1733;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy     1 AAAATGTTGATATTTCTCTTAGCAGGCTGTCAACCAGGTTAGGTCAGGTCATAAGTTT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   209 AAAATGTGATATTTCTCTTAGCAGGCTGTCAACCAGGTTAGGTCAGGTCATAAGTTT 268

Qy    61 CTACCCACATTCTTGAACTGTAGTGTCATTTAGTTTATTTTCAAAAACTTTTGCAG 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   269 CTACCCACATTCTTGAACTGTAGTTGTCATTTAGTTTATTTTTAGTTTATTTTCAAAAACTTTTGCAG 328

Qy   121 TACCTTTTTGGTCTGCTCTGTGTGTGCCTTGCCGTCAGTGAACAGTTGGACAGTGGT 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   329 TACCTTTTTGGTCTGCTCTGTGTGTGCCTTGCCGTCAGTGAACAGTTGGACAGTGGT 388

Qy   181 CTGTCTGTTAGTTCAGGAATTATTACAGGAATTAAAAAACAACTTTTTAGAGTGCTTTTCCTGAGCTC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   389 CTGTCTGTTAGTTCAGGAATTATTACAGGAATTAAAAAACAACTTTTTAGAGTGCTTTTCCTGAGCTC 448

Qy   241 TCCAGCTTGGGAATTATTACAGGAATTAAAAACAACTTTTTAGAGTCCTTTCCTGAGCTC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   449 TCCAGCTTGGGAATTATTACAGGAATTAAAAACAACTTTTTAGAGTCCTTTCCTGAGCTC 508

Qy   301 TCTTTCATTTGTCCCCCTTCTACTTTTTGCTTCCCGTGGTGCCTGTTCCTGTTCTATCCTCC 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   509 TCTTTCATTTGTCCCCCTTCTACTTTTTGCTTCCCGTGGTGCCTGTTCCTGTTCTATCCTCC 568

Qy   361 AGCCAGAGAGCTAGTGTTATTTCTCCATTGTTACACACTTGTCAGCTGCAACCAC 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   569 AGCCAGAGAGCTAGTGTTATTTCTCCATTGTTACACACTTGTCAGCTGCAACCAC 628

Qy   421 CATATCCAGGGCCCAATGGTAGGAGGTAGGAGAAGAAAGCAAAAGGGATTGGCCTCATCC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   629 CATATCCAGGGCCCAATGGTAGGAGGTAGGAGAAGAAAGCAAAAGGGATTGGCCTCATCC 688

Qy   481 TCTTACACGATAGTTCCATTGAATAGAGAGAGAGAGAGAAGGTTTCTGCCTCAGAGTGTTGGCT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   689 TCTTACACGATAGTTCCATTGAATAGAGAGAGAGAGAGAAGGTTTCTGCCTCAGAGTGTTGGCT 748

Qy   541 GCACTAGGCTTTTGTTACTGTAGTCTGCCCCTGTTACCATGGGATTGCTTGCATGTGGGG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   749 GCACTAGGCTTTTGTTACTGTAGTCTGCCCCTGTTACCATGGGATTGCTTGCATGTGGGG 808

Qy   601 ATACAGGAGAATTCAGAAAGAAAAAAAGATTTGCTATTTCTACATTCTCCCTGAGCATT 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   809 ATACAGGAGAATTCAGAAAGAAAAAAAGATTTGCTATTTCTACATTCTCCCTGAGCATT 868

Qy   661 AAGACCCTCCCTGCCCATTCCTCAATTCAAAGCTAGGCCTTCTTCTGGAGCTGCCTCTGT 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   869 AAGACCCTCCCTGCCCATTCCTCAATTCAAAGCTAGGCCTTCTTCTGGAGCTGCCTCTGT 928

Qy   721 GGGCGGTTCGGGAGATACCAAAGAGAAAAGTACCACTGTTGATATGGTGTATTCAA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   929 GGGCGGTTCGGGAGATACCAAAGAGAAAAGTACCACTGTTGATATGGTGTATTCAA 988

Qy   781 ATTCTGGTCTACCCTATTTCACATGCCTTGTTTACTTTTCAGAGGTTGACAGATTGCTGCT 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   989 ATTCTGGTCTACCCTATTTCACATGCCTTGTTTACTTTTCAGAGGTTGACAGATTGCTGCT 1048

Qy   841 CCATGCATTCTGTCCAGTTCCTAAGAGAGCAGCTTGGAGTATGCTTAATCCATCTTAC 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1049 CCATGCATTCTGTCCAGTTCCTAAGAGAGCAGCTTGGAGTATGCTTAATCCATCTTAC 1108

Qy   901 CTGGGACTGAAACAGCTGCTTATTTTGCCGTTAAAAATTACATGCAGTTTACTGCGTGGCC 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1109 CTGGGACTGAAACAGCTGCTTATTTTGCCGTTAAAAATTACATGCAGTTTACTGCGTGGCC 1168

Qy   961 TCCGGGTTGTTTGTTTGTTTGTTTCCTCTTTAATAGGTTTATTCAGAAAAACATGTCCACTG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1169 TCCGGGTTTGTTTGTTTGTTTCCTCTTTAATAGGTTTATTCAGAAAAACATGTCCACTG 1228

Qy  1021 CAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAATTACTTAA 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1229 CAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAATTACTTAA 1288

Qy  1081 TTAAATGTCAGAACCAAAAGAGTAGTGTTCAGGAGAATTCTTTTCCACTATTTTTTTTTAT 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1289 TTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAGAATTCTTTTCCACTATTTTTTTTTAT 1348

Qy  1141 TTTGGTTAATATTAATTAGACATGAATGCATGATGTAATCTTTCTCAAAACTTTTGCAG 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1349 TTTGGTTAATATTAATTAGACATGAATGCATGATGTAATCTTTCTCAAAACTTTTGCAG 1408

Qy  1201 TAGAACTCAATCCATGACAAGTTACTCTTCTCAATCTGATCATCTACCTGATGTCA 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1409 TAGAACTCAATCCATGACAAGTTACTCTTCTCAATCTGATCATCTACCTGATGTCA 1468

Qy  1261 TGACTAATATTACAAGAGCATCATGTTAACATCCAGTCTCTCTAAGCCGA 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1469 TGACTAATATTACAAGAGCATCATGTTAACATCCAGTCTCTCTAAGCCGA 1528

Qy  1321 TAATTACTGAAGAATATACAAATGAAAAGAAAATGTTAACATCCAGTCTCTCTAAGCCGA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1529 TAATTACTGAAGAATATACAAATGAAAAGAAAATGTTAACATCCAGTCTCTCTAAGCCGA 1588

Qy  1381 GCAACTTTGTAGGTGTGGTTTCCATGCCATGAACTTCGTTTTTTTCCTG 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1589 GCAACTTTGTAGGTGTGGTTTCCATGCCATGAACTTCGTTTTTTTCCTG 1648

Qy  1441 ATATGATTCCAGTATCTTCTATTTATATGGATTCAAATCATGTG 1500
         ||||||||||||||||||||||||||||||||||||||||||||
Db  1649 ATATGATTCCAGTATCTTCTATTTATATGGATTCAAATCATGTG 1708

Qy  1501 AGGCTGCTCAGTACTGGTCCTCAGGTTCACAGTTTTACAAGCAATCCATAGATGCTGCCA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  ...
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Query Match       26.4%;   Score 1722.8;   DB 15;   Length 1818;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1735;   Conservative   0;   Mismatches   0;   Indels   2;   Gaps   1;

Qy        1 AAAATGTTGATATTTCTCTTAGCAGGCTGCAACCAGGTTAGGTTCAGTCATAAGTTT     60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       81 AAAATGTTGATATTTCTCTTAGCAGGCTGCAACCAGGTTCAGGTTCAGTCATAAGTTT    140

Qy       61 CTACCCACATTCTTGAACTGTAGTGTCATTTAGTTATTTTCAAAAACTTTTGCAG    120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      141 CTACCCACATTCTTGAACTGTAGTGTCATTTAGTTATTTTCAAAAACTTTTGCAG    200

Qy      121 TACCTTTTTGGTCTGCTCTGTGTGTGTCCTTGCCAGTGAACAGTCTGGATTGGACAGTGGT    180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      201 TACCTTTTTGGTCTGCTCTGTGTGTGTCCTTGCCAGTGAACAGTCTGGATTGGACAGTGGT    260

Qy      181 CTGTCGTTAGTTCAGTTCTCAAGCCTTGTCACACTAATAGGATTGGATTTATGTATG    240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      261 CTGTCGTTAGTTCAGTTCTCAAGCCTTGTCACACTAATAGGATTGGATTTATGTATG    320

Qy      241 TCCAGCTTGGGAATTATTACAGGAGTAAAACAACTTTTAGAGTGCTTTCCTGAGCTC    300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      321 TCCAGCTTGGGAATTATTACAGGAGTAAAACAACTTTTAGAGTGCTTTCCTGAGCTC    380

Qy      301 TCTTTCTATTGTCCCCTCTACTTTTGCTTCCCGTGGCTGCTGTTCTATCCTCC    360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      381 TCTTTCTATTGTCCCCTCTACTTTTGCTTCCCGTGGCTGCTGTTCTATCCTCC    440

Qy      361 AGCCAGAGAGCTAGTGTTATTTTCTCCATTGTTACACACTTGTGCAGCTGCAACCAC    420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      441 AGCCAGAGAGCTAGTGTTATTTTCTCCATTGTTACACACTTGTGCAGCTGCAACCAC    500

Qy      421 CATATCCAGGGCCCAATGGTAGGAGTGAGAAGCAAAGGGATTGGCCTCATCC    480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      501 CATATCCAGGGCCCAATGGTAGGAGTGAGAAGCAAAGGGATTGGCCTCATCC    560

Qy      481 TCTTACAACGATAGTTCCATTGAATAGAGAGAGAGAAGGTTTCCTGCCTCAGAGTGTTGGCT    540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      561 TCTTACAACGATAGTTCCATTGAATAGAGAGAGAGAAGGTTTCCTGCCTCAGAGTGTTGGCT    620

Qy      541 GCACTAGGCTTTGTACTGTAGTCTCGGCCCTGTAGTCCATGGATTGCTTGCATGTGGGG    600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      621 GCACTAGGCTTTGTACTGTAGTCTCGGCCCTGTAGTCCATGGATTGCTTGCATGTGGGG    680

Qy      601 ATACAGGAGAATTCAGAAAGAAAAAGATTTGCTATTCTCCCGAGCATT    660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      681 ATACAGGAGAATTCAGAAAGAAAAAGATTTGCTATTTCTACATTCCCGAGCATT    740

Qy      661 AAGACCTCCCTGCCATTCCTCAATTCAAAGTGGCTTCCTCTGGAGCTGCCTCTGT    720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      741 AAGACTTCCCTGCCCATTCCTCAATTCAAAGCTCAAAGCTTCTTCTGGAGCTGCCTCTGT    800

Qy      721 GGGCGGTTCGGGAGTACCAAAGGAAAAAGTACCACTGTTGATATGGTGGTATTTCAA    780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      801 GGGCGGTTCGGGAGATACCAAAGGAAAAAGTACCACTGTTGATATGGTGGTATTTCAA    860

Qy      781 ATTCTGGTCTACCCTATTTCACATGGCCTTGTTTACTTTTCAGAGCTGACAGATTGCTGCT    840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      861 ATTCTGGTCTACCCTATTTCACATGCCTTGTTTACTTTTCAGAGCTGACAGATTGCTGCT    920

Qy      841 CCATGCATTCGTCCAGTTCCTAAGAGACAGCTTGGAGTATGCTTAATCCATCTTAC    900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      921 CCATGCATTCGTCCAGTTCCTAAGAGAGACAGCTTGGAGTATGCTTAATCCATCTTAC    980

Qy      901 CTGGGACTGAAACAGCTGCTTATTTTGCCGTTAAAAATTACATGCGTGGC    960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      981 CTGGGACTGAAACAGCTGCTTATTTTGCCGTTAAAAATTACATGCGTGGC   1040

Qy      961 TCCGGGTTTGTTTGTTGTTTTTCCT-CTTTAATAGGTTTATTCAGAGAAAAACATGTCCACT   1019
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     1041 TCCGGGTTTGTTTGTCGTTTTTCCTCCTTTAATAGGTTTATTCAGAGAAAACATGTCCACT   1100

Qy     1020 GCAATTAGGAGGTAGGAGTTGGAGACAGACCAAGAACACTTCTACTGAAGAATTACTTA   1079
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Db     1709 AGGCTGCTCAGTACTGGTCCTCAGGTTTCACAGTTTACAAGCATCCATAGATGCTGCCA   1768
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1561 TTATACAGTTGAAGACACCAATGTTCCTTTGGAAGGAGCTGGAGTCAACTAAAGCTGTTA   1620
            |||||||||||||||||||||| |||||||||||||||||||||||||||
Db     1769 TTATACAGTTGAAGACACCAATGTTCCTTTTGGAAGGAGCTGGAGTCAACTAAAGCTGTTA   1828

Qy     1521 TTATGGGAGAAACTGCTGTGTTGTAGAAAATAGATACCTTCCCCGAGGAGTAATTTAATAT   1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1829 TTATGGGAGAAACTGCTGTGTTGTAGAAAATAGATACCTTCCCCGAGGAGTAATTTAATAT   1888

Qy     1681 ACCTAGTTATAGCATTTCACCTTTTGGATACTTTTTGGCAATTCATATCGTAGC   1735
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1889 ACCTAGTTATAGCATTTTCACCTTTTTGGATACTTTTTGGCAATTCATATCGTAGC   1943
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RESULT 13
US-10-204-887-32
; Sequence 32, Application US/10204887
; Publication No. US20030124569A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PANZER, Scott R.
; APPLICANT: SPIRO, Peter A.
; APPLICANT: BANVILLE, Steven C.
; APPLICANT: SHAH, Purvi
; APPLICANT: CHALUP, Michael S.
; APPLICANT: CHANG, Simon C.
; APPLICANT: CHEN, Alice
; APPLICANT: D'SA, Steven A.
; APPLICANT: AMSHEY, Stefan
; APPLICANT: DAHL, Christopher R.
; APPLICANT: DAM, Tam C.
; APPLICANT: DANIELS, Susan E.
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: FLORES, Vincent
; APPLICANT: FONG, Willy T.
; APPLICANT: GREENAWALT, Lila B.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: JONES, Anissa L.
; APPLICANT: LIU, Tommy F.
; APPLICANT: ROSEBERRY, Ann M.
; APPLICANT: ROSEN, Bruce H.
; APPLICANT: RUSSO, Frank D.
; APPLICANT: STOCKDREHER, Theresa K.
; APPLICANT: DAFFO, Abel
; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: YAP, Pierre E.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: BRADLEY, Diana L.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: COHEN, Howard J.
; APPLICANT: HODGSON, David M.
; APPLICANT: LINCOLN, Stephen E.
; TITLE OF INVENTION: SECRETORY MOLECULES
; FILE REFERENCE: PT-1134 PCT
; CURRENT APPLICATION NUMBER: US/10/204,887
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/185,215; 60/185,216; 60/204,887
;   60/205,324; 60/205,286
; PRIOR FILING DATE: 2000-02-24; 2000-02-24; 2000-05-16; 2000-05-17;
;   2000-05-17; 2000-05-17
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PERL Program
;
; SEQ ID NO 32
; LENGTH: 1818
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030124569A1 LI:445188.1:2000MAY01
US-10-204-887-32

(columns on right, sequence positions:)
60/205, 232; 60/205,323; 60/205,287;

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Db   1101  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
           GCAATTAGGAGGTAGGAGTTTGGAGACTAGCCAGACACTTCTACTGAAGAATTACTTA  1160

Qy   1080  ATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATCTTTTTCCACTATTTTTTTA  1139
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161  ATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATCTTTTTCCACTATTTTTTTA  1220

Qy   1140  TTTTGGTTAATATTAATTAGCATGATGATGCATCCAAATAAGAAAATGAGAAGTGCCTAAT  1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221  TTTTGGTTAATATTAATTAGCATGATGATGCATCCAAATAAGAAAATGAGAAGTGCCTAAT  1280

Qy   1200  ATAGAACTCAATCCTATGGACAAGTTACTCTTTCTAATCTAATTCTTGGATATACTCCA  1259
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281  ATAGAACTCAATCCTATGGACAAGTTACTCTTTCTAATCTAATTCTTGGATATACTCCA  1340

Qy   1260  GTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTACCTGATGTC  1319
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341  GTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTACCTGATGTC  1400

Qy   1320  ATAATTACTGAAGAATATACAAATGAAAAAGAAGAAATGTTAACATCCAGTCTCTCTAAGCCG  1379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401  ATAATTACTGAAGAATATACAAATGAAAAAGAAGAAATGTTAACATCCAGTCTCTCTAAGCCG  1460

Qy   1380  AGCAACTTTGTAGGTGTGGTTTCAAAGACTCCTATGAACTTCGTTTTTTCCT  1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461  AGCAACTTTGTAGGTGTGGTTTCAAAGACTCCTATGAACTTCGTTTTTTCCT  1520

Qy   1440  GATATGATTCCAGTATCTTCTATTTATATGGATTCAAGAGCTCGCTGTGTTCAAAATCATGT  1499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521  GATATGATTCCAGTATCTTCTATTTATATGGATTCAAGAGCTCGCTGTGTTCAAAATCATGT  1580

Qy   1500  GAGGCTGCTCAGTACTGGTCCTCAGTTTCACAGTTTCACAAGCATCCATAGAGATGCTGCC  1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581  GAGGCTGCTCAGTACTGGTCCTCAGTTTCACAGTTTCACAAGCATCCATAGAGATGCTGCC  1640

Qy   1560  ATTATACAGTTGAAGACCAAATGTTCTCTTGGAAGGAGCTGGAGTCAACTAAAGCTGTT  1619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641  ATTATACAGTTGAAGACCAAATGTTCTCTTGGAAGGAGCTGGAGTCAACTAAAGCTGTT  1700

Qy   1620  ATTATGGGAGAAACTGCTGTTGTGTAGAAATAGATACCTTTCCCCGAGGAGTAATTTTAATA  1679
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701  ATTATGGGAGAAACTGCTGTTGTGTAGAAATAGATACCTTTCCCCGAGGAGTAATTTTAATA  1760

Qy   1680  TACCTAGTTATAGCATTTCACCTTTGGATACTTTTGGCAATTCATATCGTAGCAG  1737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761  TACCTAGTTATAGCATTTCACCTTTGGATACTTTTGGCAATTCATATCGTAGCAG  1818
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RESULT 14
US-09-822-846-97
; Sequence 97, Application US/09822846
; Publication No. US2003027139A1
; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS

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Query Match             23.7%;  Score 1543.8;  DB 10;  Length 1548;
Best Local Similarity   99.8%;  Pred. No. 5.3e-309;
Matches 1545;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy   3386  AGAAATTGACCAAGCAGCAGATTATAGTGTATTTACTCAGCAGCCACTCGAGGAAGAAATGGA  3445
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  AGAAATTGACCAAGCAGCAGATTATAGTGTATTTACTCAGCAGCCACTCGAGGAAGAAATGGA  60

Qy   3446  TTCAAAATCTTTGATGAAATGGAACAGAGCTTACTTATTCTTCTGAAACCAAGGCTTC  3505
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  TTCAAAATCTTTGATGAAATGGAACAGAGCTTACTTATTCTTCTGAAACCAAGGCTTC  120

Qy   3506  TCTAGTGAGCACCATGAGCCTTTGGAAACACAGCAGATGTATACAATAGCAAAGTTTCATTT  3565
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  TCTAGTGAGCACCATGAGCCTTTGGAAACACAGCAGATGTATACAATAGCAAAGTTTCATTT  180

Qy   3566  CTTTACCTTGAAACGTGAAAGTAAATCAGTGAGATAAATCAGTGGTTGCTTCTCGTCTTTTAATTTT  3625
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CTTTACCTTGAAACGTGAAAGTAAATCAGTGAGATAAATCAGTGGTTGCTTCTCGTCTTTTAATTTT  240

Qy   3626  TTTCACAGTTCAGATTTTATGTTTTGGTTCATCACTCTTTAAAAATGCTGTGGTTCC  3685
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  TTTCACAGTTCAGATTTTATGTTTTGGTTCATCACTCTTTAAAAATGCTGTGGTTCC  300

Qy   3686  CATCAAACTTGTTCCAGACTTATATTTTCTAAAACCTGGAGACAAACCACATAAAATACAA  3745
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CATCAAACTTGTTCCAGACTTATATTTTCTAAAACCTGGAGACAAACCACATAAAATACAA  360

Qy   3746  AACAAGTCTGCTTCTTCAAAATTCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTT  3805
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  AACAAGTCTGCTTCTTCAAAATTCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTT  420

Qy   3806  CACAAGCCAGAACATAATGGTGACGATGATTAATGACAGTGACTATGTTCCGTGGCTCC  3865
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CACAAGCCAGAACATAATGGTGACGATGATTAATGACAGTGACTATGTTCCGTGGCTCC  480

Qy   3866  CCATAGTGCGGCTTAAAATGTGATGCATTCAGAAAGGACTACATGTTTTGCAGCTGTTTT  3925
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  CCATAGTGCGGCTTAAAATGTGATGCATTCAGAAAGGACTACATGTTTTGCAGCTGTTTT  540

Qy   3926  CAACAGTACTATGGTTTATTCTTTACCTATATTAGTGAAATCATTAGTAACTACTATCT  3985
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CAACAGTACTATGGTTTATTCTTTACCTATATTAGTGAAATCATTAGTAACTACTATCT  600

Qy   3986  TTATCATTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTTCAAGAAAT  4045
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TTATCATTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCTTTCAAGAAAT  660

Qy   4046  TACTGATATAGTTTTAAAATTGAGCTGTATTTCAAGCAGCTTTGCTTGGAATCATTGT  4105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  TACTGATATAGTTTTAAAATTGAGCTGTATTTCAAGCAGCTTTGCTTGGAATCATTGT  720

Qy   4106  TACTGCAATGCCACCTTACTTTGCCATGGAAATCAGAGAATCATAAGATCAAAGCTTA  4165
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  TACTGCAATGCCACCTTACTTTGCCATGGAAATCAGAGAATCATAAGATCAAAGCTTA  780

Qy   4166  TACTCAACTTAAACTTTCAGGTCTTTTGCCATCTGCATCTGCATATTGGATTGGACAAGCTGTTGT  4225
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TACTCAACTTAAACTTTCAGGTCTTTTGCCATCTGCATCTGCATATTGGATTGGACAAGCTGTTGT  840
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Qy   4226 TGATATCCCCTTATTTTTATCATTCTTATTTTGATGCTAGGAAGCTTACTGGCATTCA 4285
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TGATATCCCCTTATTTTTATCATTCTTATTTTGATGCTAGGAAGCTTACTGGCATTCA 900

Qy   4286 TTATGGATTATATTTTTATACTGTAAAGTTCCTTGCGTGGTTTTTTGCCTTATTGGTTA 4345
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TTATGGATTATATTTTTATACTGTAAAGTTCCTTGCGTGGTTTTTTGCCTTATTGGTTA 960

Qy   4346 TGTTCCATCAGTTATTCTGTTCACTTATATGCTTCTTCTTAAGAAAAATTTTAAA 4405
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TGTTCCATCAGTTATTCTGTTCACTTATATGCTTCTTCTTAAGAAAAATTTTAAA 1020

Qy   4406 TACCAAAGAATTTGGTCATTTATCATTCTGTGGCAGCGTTGNCTTGTTATTGCAATCAC 4465
               ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1021 TACCAAAGAATTTGGTCATTTATCATTCTGTGGCAGCGTTGGCTTGTTATTGCAATCAC 1080

Qy   4466 TGAAATAACTTTCTTTATGGATACACAATTGCAACTATTCCTTCATTATGCCTTTTGTAT 4525
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGAAATAACTTTCTTTATGGATACACAATTGCAACTATTCCTTCATTATGCCTTTTGTAT 1140

Qy   4526 CATCATTCCAATCTATCCACTTCTAGGTTGCCTGATTTCTTTCATAAAGATTTCTTGGAA 4585
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CATCATTCCAATCTATCCACTTCTAGGTTGCCTGATTTCTTTCATAAAGATTTCTTGGAA 1200

Qy   4586 GAATGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTCAGTAGCTGTTAT 4645
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GAATGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTCAGTAGCTGTTAT 1260

Qy   4646 ATCGCCTTACCTGCAGTGTGTACTGTGGATTTCCTCTTACAATACTATGAGAAAAAATA 4705
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 ATCGCCTTACCTGCAGTGTGTACTGTGGATTTCCTCTTACAATACTATGAGAAAAAATA 1320

Qy   4706 TGGAGGCAGATCAATAAGACAAAAAGATCCCTTTTCAGAAACCTTCAACGAAGTCTAAAAA 4765
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TGGAGGCAGATCAATAAGACAAAAAGATCCCTTTTCAGAAACCTTCAACGAAGTCTAAAAA 1380

Qy   4766 TAGGAAGTTCCAGAACCACCAGGAGGATGAGGATGAGGATGAAGCTCAAAGCTCGAAAG 4825
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TAGGAAGTTCCAGAACCACCAGGAGGATGAGGATGAGGATGAAGCTCAAAGCTCGAAAG 1440

Qy   4826 ACTAAAGGTCAAAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCATCCATTATGGT 4885
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACTAAAGGTCAAAGAGCTGATGGGTTGCCAGTGTTGTGAGGAGAAACCATCCATTATGGT 1500

Qy   4886 CAGCAATTGCATAAAGAATATGCATAAAGAATATGACAAGAAGAAAGATTTCTTCTTTC 4933
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CAGCAATTGCATAAAGAATATGCATAAAGAATATGACAAGAAGAAAGATTTCTTCTTTC 1548
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US-09-962-436-337

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Query Match             18.1%;  Score 1182;  DB 9;  Length 1346;
Best Local Similarity   96.5%;  Pred. No. 3.9e-234;
Matches 1306; Conservative 0; Mismatches 29; Indels 19; Gaps 9;
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Qy   4786 CAGACAATGAGGATGAAGATGAAGATGAAGAGTCAAAGACTAAAGGTCAAAGAGCTGA 4845
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAGACAATGAGGATGAAGATGAAGATGAAGAGTCAAAGACTAAAGGTCAAAGAGCTGA 60

Qy   4846 TGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGAAT 4905
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGAAT 120

Qy   4906 ATGATGACAAGAAAGAATTTCTCTTCTTCAAGAAAAGTAAAGAAAGTGGCAACTAAAATACA 4965
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ATGATGACAAGAAAGAATTTCTCTTCTTCAAGAAAAGTAAAGAAAGTGGCAACTAAAATACA 180

Qy   4966 TCTCTTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGCTGGCA 5025
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCTCTTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGCTGGCA 240

Qy   5026 AAAGCACAATTATTAATATTCTGGTTGGTGTATATTGAACCAACTTCAGGCCAGTGTATTT 5085
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAAGCACAATTATTAATATTCTGGTTGGTGTATATTGAACCAACTTCAGGCCAGTGTATTT 300

Qy   5086 TAGGAGTATATTCTTCAGAGACAAGTGAAGAGATGATGATTCACTGAAGTGTATGGGTTACT 5145
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TAGGAGTATATTCTTCAGAGACAAGTGAAGAGATGATGATTCACTGAAGTGTATGGGTTACT 360

Qy   5146 GTCCTCAGATAAACCCTTGTGGCCAGATACTACATTGCAGGAACATTTGAAATTTATG 5205
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCCTCAGATAAACCCTTGTGGCCAGATACTACATTGCAGGAACATTTGAAATTTATG 420

Qy   5206 GAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAGAGTCATAAGTGAAAATGAAGCATG 5265
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAGAGTCATAAGTGAAAATGAAGCATG 480

Qy   5266 CACTTGATTTAAAAGAACATCTTCAGAAGAGACTGTAAAGAAAACTACCTGCAGGAATCAAAC 5325
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CACTTGATTTAAAAGAACATCTTCAGAAGAGACTGTAAAGAAAACTACCTGCNAGGAATCAAA 540

Qy   5326 GAAAGTTGTGTTTGCTCTAGTAATGCTAGGGAATCCTCAGATTACTTTGCTAGTDATGAAC 5385
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGAAAGTGTGTTTGCTCTAGTAATGCTAGGGAATCCTCAGATTACTTTGCTAGTGATGAAC 600

Qy   5386 CATCTACAGTGATGATGGATCCCAAA--GCCAAACAGCACAGTGGCAGCAATTCGAACTGC 5443
               |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db    601 CATCTACAGGTCTGATCCCAAATGCCAAACATGGCATGGCATGGCAATTCGAACTGC 660

Qy   5444 ATTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGAGGCAGAGGC 5503
               ||||||||      ||||||||||||||||||||||||||||||||||||||||||||
Db    661 AT-------AT-------NNAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGAGGC 711

Qy   5504 TGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTGAAGGTATCGGAACAGTACA 5563
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    712 TGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTGAAGGTATCGGAACAGTACA 771

Qy   5564 ACATCTAAAGAGTAAATTGGAAAAGCTACTTTTTGGAAATTAAATTGA-GGACTGGA 5622
               ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    772 ACATCTAAAGAGTAAATTGGAAAAG--NACTTTTTGGAAATTAAATTGAACGGACTGGA 829

Qy   5623 TAGAAAACCTAGAAG-TAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCA 5681
               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
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Qy   5682 AGCCGTCAGGAGAAAGTTTTTCTTTCTATTTTTGGCTTATAAAATTCCTAAGGAGAGATGTTCAG 5741
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    890 AGCCGTCA-GAAAGTTTTTCTTTCTATTTTTGGCTTCTTCTAAAATTAATAAGGAAGAATGTTCAG 948

Qy   5742 TCCCTTTCACAATCTTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTGAAGAA 5801
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    949 TCCCTTTCCCAATCTTTTTTTAAGCTGGAAGAAGCTAAACATGC-TTTGCCATTGAAGAA 1007
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RESULT 15

US-09-962-436-337

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; Sequence 337, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel
;   TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
;   TITLE OF INVENTION: Sets
;   FILE REFERENCE: 689290-75
;   CURRENT APPLICATION NUMBER: US/09/962,436
;   CURRENT FILING DATE: 2001-09-25
;   PRIOR APPLICATION NUMBER: US/60/235,082
;   PRIOR FILING DATE: 2000-09-25
;   PRIOR APPLICATION NUMBER: US/60/234,924
;   PRIOR FILING DATE: 2000-09-25
;   NUMBER OF SEQ ID NOS: 568
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 337
;   LENGTH: 1346
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: n=a,t,g or c
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Qy   5802 TATAGCTTTTCTCAAGCAACATTGGAACAGGTTTTGTAGAACTCACTAAAGAACAAGAG 5861
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Db   1008 TATAGC-TTTCTCAAGCAACATTGGAACAGGTTTTGTAGAACTCACTAAAGAACAAGAG 1066

Qy   5862 GAGGAAGATAATAGTTGTGGAACTTAAACAGCACACTTGGTGGGAACGAACAAGAA 5921
          ||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   1067 GAGGAAGATAATAGTTGTGGAACTTAAACAGCACACTTGGT-GGAACGAACACAGAA 1125

Qy   5922 GATAGAGTAGTATTTGAATTGTATTGTTCGGTCTGCTTACTGGGACTTCTTTCTTTTT 5981
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 GATAGAGTAGTATTTGAATTGTATTGTTCGGTCTGCTTACTGGGACTTCTTTCTTTTT 1185

Qy   5982 CACTTAATTTAACTTTGGTTTAAAAAGTTTTTTATTGGAATGGTAACTGGAGAACCAAG 6041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 CACTTAATTTAACTTTGGTTTAAAAAGTTTTTTATTGGAATGGTAACTGGAGAACCAAG 1245

Qy   6042 AACGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGTGTTTTGCTT 6101
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 AACGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGTGTTTTGCTT 1305

Qy   6102 TTCTTTAAATAAAACGTATGTATAATTAAGTGAA 6135
          ||||||||||||||||||||||||||||||||||
Db   1306 TTCTTTAAATAAAACGTATGTATAATTAAGTGAA 1339
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Search completed: December 4, 2004, 20:32:22
Job time : 2970 secs